

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRG
51 DTEWCLAPIP LGGYVKMVD REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNOGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQHTADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMMVAFFND VTRLLG*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFTRKRG	DTEWCLAPIP
g591	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFTRKRG	DTEWCLAPIP
	10	20	30	40	50	60
m591.pep	LGGYVKMVD	TREGEVSEAD	LPYAFDKQHP	AKRIAIVAAG	PLTNLALAVL	LYGLSFSFGVT
g591	LGGYVKMVD	TREGEVSEAD	LPYAFDKQHP	AKRIAIVAAG	PLTNLALAVL	LYGLSFSFGVT
	70	80	90	100	110	120
m591.pep	ELRPYVGTV	EPDTIAARAG	FQSGDKIQSV	NGTPVADWGS	AQTEIVLNLE	AGKVAVGVQTA
g591	ELRPYVGTV	EPDTVAARTG	FQSGDKIQSV	NGVSVQDWSS	AQTEIVLNLE	AGKVAVGVQTA
	130	140	150	160	170	180
m591.pep	SGAQTVRTI	DAAGTPEAGK	IAKNQGYIGL	MPFKITTVAG	GVEKGSPEAK	AGLKPGRDLTA
g591	SGAQTVRTI	DAAGTPEAGK	IAKNQGYIGL	MPFKITTVAG	GVEKGSPEAK	AGLKPGRDLTA
	190	200	210	220	230	240
m591.pep	ADGKPIASW	QEWANLTRQS	PGKKITLNYE	RAGQHTADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	ADGKPIASW	QEWANLTRQS	PGKKITLTYE	RAGQHTADIR	PDTVEQPDHT	LIGRVGLRPQ
	250	260	270	280	290	300
m591.pep	PDRAWDAQI	RRSYRPSVVR	AFGMGWEKTV	SHSWTTLKFF	GKLISGNASV	HISGPLTIAD
g591	PDRAWDAQI	RRSYRPSVVR	AFGMGWEKTV	SHSWTTLKFF	GKLISGNASV	HISGPLTIAD
	310	320	330	340	350	360
m591.pep	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLL	PVPVLDGGHL	VFYTAEWIRG	KPLGERVQNI
g591	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLL	PVPVLDGGHL	VFYTVIEWIRG	KPLGERVQNI
	370	380	390	400	410	420
m591.pep	GLRFGALMM	LMMVAFFND	VTRLLGX			
g591	GLRFGALMM	LMMVAFFND	VTRLLGX			
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:

a591.seq

```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCCG CGAAAAAGCA GGCCTGAAAC
701 CGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGCG AACTAATCA GCGGCAACGC CTCCTGACG
1051 CATATTTCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT GGCACCTGGT AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTTGC CCTCATGATG CTGATGATG
1301 CGGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIARAGF QSGDKIQSVN
151 GTPVADWGSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFLALMM LMMAVAFEND VTRLIG*

```

m591/a591 99.6% identity in 446 aa overlap

```

          10      20      30      40      50      60
m591.pep  LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGVFGKPFFFTRKRGDTEWCLAPIP
          |||
a591       LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSGVFGKPFFFTRKRGDTEWCLAPIP
          10      20      30      40      50      60

          70      80      90      100     110     120
m591.pep  LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT
          |||
a591       LGGYVKMVDTREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT
          70      80      90      100     110     120

          130     140     150     160     170     180
m591.pep  ELRPYVGTV E PDTIARAGFQSGDKIQSVNGTPVADWGSAQTEIVLNLEAGKVAVGVQTA
          |||
a591       ELRPYVGTV E PDTIARAGFQSGDKIQSVNGTPVADWGSAQTEIVLNLEAGKVAVGVQTA
          130     140     150     160     170     180

          190     200     210     220     230     240
m591.pep  SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
          |||
a591       SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
          190     200     210     220     230     240

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	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVVISLGVNLNLLPVPVLDGGHLV FYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVVISLGVNLNLLPVPVLDGGHLV FYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51  cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgccg ccgccgccgc cgaagtgaac caccctgttt cgcaaggtat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 ccgccttcac catcttgatt taccaacagc cttatggcga tttgagcggg
301 cgcgcgtcga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcctc gccgtcatcc tgtttatgtt tgccttttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctgggt ttggcgtggg tctatttcgg
501 cgcgggttgc aatgtgcctt tggctcggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctgcgcgcca tcctgctgct ctgccattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcataaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GGLGGLISQ TMMGIKRL YSNEAGMGS
51  PNAAAAAEVK HPVSQGMQIM LGVFVDIIIV CSCTAFIILI YQPPYGDLSG
101 AALTQAAIVS QVQWAGAGFL AVILFMFAPS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCTGA
51  CGCGGCAGCA GCGGCGTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCCTG TATTCCAACG AGGCGGGTAT GGGTCCGCG
151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 CCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG

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935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGATT CAACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQM LGVFVDTIIV CSCTAFIILI YQPYGDL SG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSA PNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQPYGDL SGAALTQAAIVSQVGQWGAGFL					
g592	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQPYGDL SGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFS TVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFS TVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVW X					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTA KLKMGKDPEF KLSEHPGLKRRIKSDVW X					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGCGCTG TATTCCAACG AGGCGGGTAT GGGTTCCGCG
 151 CCGAACGCGG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTCCG TATGCTGGT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGATT CAACTTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGSA
 51 PNAAAAAEVK HPVSQGMQM LGVFVDTIIV CSCTAFIILI YQPYGDL SG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMGMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMIQMLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1  atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcggcg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcatc
151 gtccggccgg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctgccttgt cggcacttgc
351 cgaagtccgg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgccct
451 tccctgctgt tgcctgatga atcgttttcc agtttggaac cgcatttgcg
501 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcgggcatc
551 ctgccgtttt ggtaacgcat tcgcccgaag aggcctgcac ggcgggcgac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga
651 aaccttgatt caaacgcctg ccggcggtgca ggtcgcccggt ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgtcc gcctgcccga
801 ctgcgtccgg ctttccgccc tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtagcgtc
901 cgcattccgc tcgatgaagg gcgtatcgtc cgtttccgat ga

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This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1  MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEI RL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAE R LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNQTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTTGG
101 GGCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

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201 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA TATGAGTGC GCGGAAAATG CGGCATTTCGG TTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTCC AGTTTGGACA CGCATTTGCG
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GCGGCATCC
551 CTGCCGTTTT GGTAACGCAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CTGCGTGCA GGTGCCCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
  1 MLELNLCKR FGKNTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
 51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTLRLGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGTPELTV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWNLDMRHA GAVSGKDTVR
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGKNTVADNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMQKMPKAEAEERLAMAALAEVG					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMQKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS					
	130	140	150	160	170	180
m593.pep	SLDTLRLGTLRRMTAERIRN					
g593	SLDTLRLDRMTAERIRK					
	130	140	150	160	170	180
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRIQLQYGTPELTVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPETLIQTAPAGVQVARLMGLPNTDD					
	190	200	210	220	230	240

938

	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDL-RHAGAVSGKDTV					
	: : : : : : : : : : : : : : : : : :					
g593	RHIPQNAVCLDNHGTCECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	::: :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
  1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
 51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTTGG
101  GCGCGTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TGCGGGCATC
151  GTCCGCGCGG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201  TATGCCGCCG GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251  TGTTTCCCCA TATGAGTGCA CTGGAAAATG CGGCATTTCG TTTGAAAATG
301  CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351  CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAN AAACCTTCCG
401  GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451  TCCCTGCTGC TGTGGACGA ATCGTTTTCC AGTTTGGACA CGCATTTCGC
501  CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GGCGGCATCC
551  CTGCCGTTTT GGTAACGCAT TCGCCGAAG AGGCCTGCAC GGCGGCAGAC
601  GAAATCGCCG TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCCGA
651  AACCTTGTTT CAAACGCCTG CCGGCGTGCA GGTCGCCCCAT CTGATGGGGC
701  TGCCCAATAC CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751  GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801  ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851  ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAAACGA TACGGTACGC
901  ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
  1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
 51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101  QKMPKAEAES LAMAALAEVG LENEHRKPX KLSGGEKQRL ALARALVVRP
151  SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201  EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLPNTDDD RHIPQHAVRF
251  DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301  IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFRGNKTVDNICTLVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
	: : : : : : : : : : : : : : : : : :					
a593	MLELNLCKRFRGGKTVADDICTLVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMQKMPKAEAEERLAMAALAEVG					
	: : : : : : : : : : : : : : : : : :					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMQKMPKAEAESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
	: : : : : : : : : : : : : : : : : :					
a593	LENEHRKPKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRILQYGT PETLVKTPSCVQVARLMGLPNTDDN					

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```

|||||:|||||:|:| | |||||:|:| | |||:|||||:|
a593      GGIPAVLVTHSPEEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDDD
          190      200      210      220      230      240

          250      260      270      280      290      300
m593.pep  RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDMRHAGAVSGKDTV
          |||||:|||||:|:| | |||||:|:| | |||:|||||:|
a593      RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDMPHAGEISGNDTV
          250      260      270      280      290      300

          310
m593.pep  IHIEEREIVRFRX
          ||||:|||||
a593      IHIEDREIVRFRX
          310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

```

g594.seq..
1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgttttt agcatactcc ggctgctggt ccgcacgga attgggatcg
101 gtaagttcgc cgttcaggcc ttccaggctc ttaagctgct gatctgtacg
151 gttgagcacc caaatcggtt tgccttgcca ctccggcggtc agcagctgac
201 ccgcttcgat ttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctttttccg aagggaaaaa actggccaca aacggcggtg ccacacccaa
301 tgctgccact ccgcccgcgc cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttggt gatttcttga ttatccatta ttcagtcgtc ctaatatattt
401 gggaatgccg agccattaaa cattgcaatt ttaccagtt tgcagtgata
451 ctcaaagcat tattaataat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```

g594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

```

m594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTTCG CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGCGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTGAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```

m594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRCQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1   ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GCGGCGCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTCAAG AAACGGCGGC
351 GGCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGGAAATACG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1   MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq..
1   atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggtttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagacca atccgccaac gaaggcggtt cggtcggtat cgccgtcaac

```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgatgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgccccca accgctcgcc
451 gactataaag cctacgttca aggcgagggt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacgca accgattgcc
601 gagctttttca gcgaactcga ccccgtcacg gatgcgtgtg aagacgactt
651 caaagacggg gcgaaagatg ccgggtttac cggcttccac cgtatcgaa
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcgaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaacg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcaccaa
```

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1051 gacggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga
 1151 tactcggtt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN
 51 DNACEPMNLT VPSGQVFN I KNNSGRKLEW EILKGMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVAD SGFKDTANEA DLEKLPQPLA
 151 DYKAYVQGEV KELA AKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGA SEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTD TNFKQV NEILAKYRTK
 351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRGILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTAGTAT CGCCGTCAAC
 151 GACAATGCCT GCGAACC GAT GGA ACTGACC GTGCCGAGCG GACAGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCAACCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
 551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCGCGTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGA AAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAAC TGATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAC TGATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CTTGCCCAA CTTGCGGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSI AVN
 51 DNACEPMELT VPSGQVFN I KNNSGRKLEW EILKGMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGA SEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTD TNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSI	AVNDNACEPMELT
g595	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGI	AVNDNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

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m595.pep	VPSGQVVFN	KNNSGRKLEWEIL	KGVMVVD	ERENIAPGL	SDKMTVTLL	PGEYEMTCGLLT
g595	VPSGQVVFN	KNNSGRKLEWEIL	KGVMVVD	ERENIAPGL	SDKMNRNLL	PGEYEMTCGLLT
	70	80	90	100	110	120
m595.pep	NPRGKLVV	TDSGFKDTANEAD	LEKLSQPLADY	KAYVQGEVKEL	VAKTKTFT	EAVKAGDIE
g595	NPRGKLVV	ADSGFKDTANEAD	LEKLPQPLADY	KAYVQGEVKEL	AAKTKTFT	EAVKAGDIE
	130	140	150	160	170	180
m595.pep	KAKSLFAD	TRVHYERIEPIA	ELFSELDPVID	AREDDFKDGA	KDAGFTGF	HRIEYALWVEK
g595	KAKSLFAA	TRVHYERIEPIA	ELFSELDPVID	ACEDDFKDGA	KDAGFTGF	HRIEHALWVEK
	190	200	210	220	230	240
m595.pep	DVSGVKEI	AAKLMTDVEAL	QKEIDALAF	PPGKVVGGA	SELIEEVAG	SKISGEEDRYSHTD
g595	DVSGVKET	AAKLMTDVEAL	QKEIDALAF	PPGKVVGGA	SELIEEAAG	SKISGEEDRYSHTD
	250	260	270	280	290	300
m595.pep	LSDFQANV	DGSKKIVDLFR	PLIEAKNKAL	LEKTDTNFKQ	VNEILAKYR	TKDGFETYDKLG
g595	LSDFQANAD	GSKKIVDLFR	PLIEAKNKAL	LEKTDTNFKQ	VNEILAKYR	TKDGFETYDKLS
	310	320	330	340	350	360
m595.pep	EADRKALQ	ASINALAEDLA	QLRGILGLKX			
g595	EADRKALQ	APINALAEDLA	QLRGILGLKX			
	370	380	389			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

a595.seq

1	ATGAGAAAAT	TCAATTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGGCGGTT	CGGTACGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCAGT	GGAACGTACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCACCCT	GTTGCCGGGC	GAATACGAAA	TGACTTGC
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTGCA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCTCTCC	GGCAAGGTGG	TCGGCGGCGC	GTCCGAACTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTGCGATT
951	GTTCCTGTCG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTG	GAAAAAACCG
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAA			

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

a595.pep

1	MRKFNL	TALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQ	TAN	EGGSVSI	IAVN
51	DNACEP	MELT	VPSGQVVFN	KNNSGRKLEW	EILKGVMVVD	ERENIAPGLS		

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTAHSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIAVNDNACEPMELT					
a595	MRKFNLTAHSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIAVNDNACEPMELT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a595	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a595	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLFADTRVHYERIEPIAELEFSELDVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	KAKSLFADTRVHYERIEPIAELEFSELDVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG					
a595	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTK DGFETYDKLG					
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX					
a595	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1  ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcggtgga
51  atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggtaa
101 cgcacgaccg ctacttcctc gacaacgccg ccgaatggat tttggaactc
151 gaccgcggac acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

```

945

```

451   ttcggcgata aagtgtgat tgacggtttg agcttcaaag tgccggcggg
501   cgcatattgtc ggcatcatcg gccggaacgg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcggggcaaa gagcagcccg attcggggcga agtgaaaatc
601   gggcaaaccg tgaaaatgag cttgattgac caaagccgcg aaggttttgc
651   aaacgacaaa accgtgttcg acaacattgc cgaagggtcg gatattttgc
701   aggtcgggaca gtttgaaatc cccgcccggc aatatattggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgga
801   acgcgggcgt ctgcacttg caaaaacctt gttggggcggc ggcaatgtgt
851   tgctgtctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgcg
901   ttggaagacg cattgttgga atttgccggc agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001  gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051  gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101  atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

m596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRQNAKG
101 RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNVSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLLDPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTG AAGATATTTT CCTTTCTTTC TTCCCCGGCG
101 CGAAATATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGTTTGAA GCGATTATTG
401 CCGCAGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCC
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CCGCGGTGAA AAACGCGCGC TTGCCTTGTC CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGC GC TCCCCGCA CAGTCGTTGC
651 GGTAACGCAC GACCCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAAAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001 AATCGTTTCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101 GCTGTTCAAA ATGATTTCGG GCAAAGAGCA GCCTGATTCC GGCGAGGTGA
1151 AAATCGGACA AACCCTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GCCCGACAT
1251 TTTGCAGGTT GGTCAAGTTT AAATTCCCGC CCGCCAATAT TTGGGGCGTT
1301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351 GGCGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTGTA GCGGCGGCAA
1401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451 TGGCGTTGGA AGACGCATTG TTGGAATTG CCGGCAGCGT GATGTTGATT
1501 TCGCACGACC GTTGGTTTCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1551 TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651 ATCAAATACA AACCCTGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1 MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51 RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGRHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

```

                160      170      180      190      200      210
m596.pep      LPEWDAKIDNLSGGEKRRVALCKLLSKPDMLLDEPTNHLDAESVEWLEQFLVRFPGTV
                ||||||||||||||||||
g596                MLLDEPTNHLDAESVEWLEQFLVRFPGTV
                        10      20      30

                220      230      240      250      260      270
m596.pep      VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
                ||||||||||||||||||
g596      VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
                40      50      60      70      80      90

                280      290      300      310      320      330
m596.pep      LEWVRQNAKGRQAKSKARLARFEEMSNEYEQKRNETQEIFIPVAERLGNEVIEFVNVSKS
                ||||||||||||||||||
g596      LEWVRQNAKGRQAKPKARLARFEEMSNEYEQKRNETQEIFIPVAERLGNEVIEFVNVSKS
                100      110      120      130      140      150

                340      350      360      370      380      390
m596.pep      FGDKVLIDDLSEFKVPAGAIVGIIGPNGAGKSTLFKMISGKEQPDGGEVKIGQTVKMSLID
                ||||||| :|||||
g596      FGDKVLIDGLSEFKVPAGAIVGIIGPNGAGKSTLFKMIAGKEQPDGGEVKIGQTVKMSLID
                160      170      180      190      200      210

                400      410      420      430      440      450
m596.pep      QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR
                |||||||
g596      QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR
                220      230      240      250      260      270

```

947

	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLDPEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
g596	LHLAKTLLGGGNVLLLDPEPSNDLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330

	520	530	540	550	559
m596.pep	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYKPVTRX				
g596	ACEGDSKWVFFDGNVQEYADKKRRLGKEGAKPKRIKYKPVTRX				
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CTTTCTTTT TTCCCCGCGC
101 CGAAAAATCGG TTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAAGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGAA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAATCGCT
451 GCCGACGCGC TCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCCGCG TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGC GC TCCCCGTA CAGTCGTTGC
651 CGTAACACAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGAGCAGA AAGAAAAACG TTTGGAAAAC GAGGCGAAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTCA AGCCAAGTCC AAAGCGGTT TGGCGCGTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTCGGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCGGC
1351 GGCGAACGCG GACGTTTGCA CTTGGCAAAA ACCTTGTG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCCTGC
1451 GCGCGTTGGA AGACGCATTG CTGGAATTTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGCGGAC TCCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.pep
1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHEHEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAEE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMKQELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSTFKVP
351 AGAIVGIIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451 GERGRHLAK TLLGGGNVLL LDPEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGTPKPR
551 IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADFD					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEEQGRLEAIIAAGSSTGGGAHEHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAAARVKAMKQELEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNIEVFVNVSFSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNIEVFVNVSFSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFKMISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSDQSKITGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEQYEADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYEQYEADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGAKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACGCAAAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```

```

151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTTCGTAT CGGGGAACTA TAAAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCTTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCTCCAAAG ATGCCCCGAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAAagcc
601 gaacaccgCA TtcaggAtgc ggAagcaaAA agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcgGc GATGTTTGGa AAGGCGTgTT CTATTCCACT
901 CGCGCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGCTACGGCA AAGTGGTcGT GATCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCCGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 ACPFSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.pep

```

1 MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTLNLRLKT EVAATKAQIS RFVSGNYKNS RPNVALFLK NAEPEGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPFSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAACAGCG CGAGGCTTGG GACAAGTTCC AAAAACTCAA TACCGAGCTG
151 AACCGTTTGA AAACGGAAAGT CGCCGCTACG AAAGCGCAGA TTTCCTGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTC
251 TGAAAAACGC CGAACCAGGT CAGAAAAACC GCTTTTTCGCG TTATACGCGT
301 TATGTAAACG CTCCAATCG GGAAGTTGTC AAGGATTTGG AAAAACAGCA
351 GAAGGCTTTG CGCGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAA TCAGGCAAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCGC AGACAGAATG CCAAATCGC
501 CAAAGATGCC CGAAAACCTGC TGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAA AGGCCGAACA CCGCATTGAG
601 GATGCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CTTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCAG AACCGGAGCG
851 GCGGCGATAT TTGGAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTCG ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGAG CGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAATA CGTTATCAAG GTCAGGTATT GAACCCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEERIRQE RIRQARGNLA SVNRKQREAW DKFQKLNTL
51 NLRKTEVAAT KAQISRFVSG NYKNSQPNVA ALFLKNAEPG QKNRFLRYTR
101 YVNASNREV V KLEKQKAL AVQEQKINNE LARLKKIQAN VQSLLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKGNE QQLNKLLSNL EKKKAEHRIQ
201 DAEAKRKLAE ARLAAAEKAR KEAAQQAEEA RRAEMSNLTA EDRNIQAPSV
251 MGIGSADGFS RMQRLKKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPTVTSY ADEL DGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGQVLNPS SWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRKLT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRKLT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFSVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFSVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVDHGENYISYAGLSEISAGKGYTVAAGSKI GT					
m597	APATVESIAPGTVSYADELDGYGKVVDHGENYISYAGLSEISVKGGMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLPNSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLPNSSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAG CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAAA CAGCGCGAGG CTTGGGACAA GTTCCAAAAA
151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCG CGTTTCGTAT CGGGGAACTA TAAAAACAGC CAGCCGAATG
251 CGGTTGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCCTC AATCGGGAAG TTGTCAAGGA
351 TTTGGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGGGCGGAA CAGACGGAAA GCCGCAGACA
501 GAATGCCAAA ATCGCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGGAGAA GAAAAAGGCC
601 GAACACCGCA TTCAGGATGC GGAAGCAAAA AGAAAATTGG CTGAAGCCAG
651 ACTGGCGGCA GCCGAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 AAGCACGACG TGCGGAAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGGTT TCAGCCGCAT
801 GCAAGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGACTTTTCG
851 GGCAGAACCG GAGCGCGGCG GATGTTTGGA AAGGCGTGT CTATTCCACT
901 GCACCGGCAA CGGTTGAAAG CATTGCGCCG GGAACGGTAA GCTATGCGGA

```

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTCGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTGA TCAAGGTCAG GTATTGAACC
1151 CTTGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

a597.pep

```

1 MLLHVSNSLK QLQEEIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51 LNTELNRKLT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGQ VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

a597.pep	10	20	30	40	50	60
m597	10	20	30	40	50	60
a597.pep	MLLHVSNSLKQLQEEIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRKLT					
m597	MLLHVSNSLKQLQEEIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRKLT					
a597.pep	70	80	90	100	110	120
m597	60	70	80	90	100	110
a597.pep	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
a597.pep	130	140	150	160	170	180
m597	120	130	140	150	160	170
a597.pep	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
a597.pep	190	200	210	220	230	240
m597	180	190	200	210	220	230
a597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
a597.pep	250	260	270	280	290	300
m597	240	250	260	270	280	290
a597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
a597.pep	310	320	330	340	350	360
m597	300	310	320	330	340	350
a597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
a597.pep	370	380	390			
m597	360	370	380			
a597.pep	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

g601.seq

```

1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTGATGATCA GCGACGTATC CGAAGCCGCC GCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTGCGCCG TACGCGCCCT
351 GAGCATGGGC AACTGCACC ACCTATGATG GGCATCGCC TCGGTCGCCA
401 TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTGCGCCG AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGTGTGCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCC aaagcggtca
551 tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

g601.pep

```

1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDGQWTAA KAVMSRSARV IMESWVRVPD
201 DCF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

m601.seq

```

1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTCTTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTGCTGG TACGCGCCCT
351 GAGCATGGGC AACTGCACC ACGCGATGAT GGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTCATGAG CCGTAGCGCA CGCGTGATGA TGAAGGTTG GGTCAGGGTG
601 CCTGAGGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

m601.pep

```

1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

g601      |||||:|||||
          TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLPVRALSMG
          70      80      90      100     110     120

          130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAECQDGQWT
          |||||:|||||
g601      KLHHAMMGIA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHPSGTLRVGAAECQDGQWT
          130     140     150     160     170

          190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |:|||||:|:|:|:|:|:|
g601      AAKAVMSRSARVIMESWVRVPDDCFX
          180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCCGTACGC TGGTCAACCT TGCCGAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGGAAGGTTG GGTCAGGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVREG HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

          10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          |||||
a601      MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          10      20      30      40      50      60

          70      80      90      100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
          |||||
a601      KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
          70      80      90      100     110     120

          130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAECQDGQWT
          |||||
a601      KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAECQDGQWT
          130     140     150     160     170     180

          190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |||||
a601      ATKAVMSRSARVMMEGWVRVPEDCFX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTCTGCT
 51 CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA Tgcgagatta TATCACTTGC TTTtggcgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
  1 MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
 51 LIDRQIAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKLSAA
101 CLQMRDYITC FWRLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAACGCGA CATATGCGTC CCCTTCTGCT
 51 CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
  1 MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
 51 LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	: : : :: : :: : : :					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60

	70	80	90	100	110
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAGEYTVN---LQMRDYITRF*QLHX				
	: : : : : : : :				
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKLSAACLQMRDYITCFWRLHX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
  1 ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
 51 CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
  1 MLLHQCDKAR HMRTLLGRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
 51 LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
a602	MLLHQCDKARHMRLLLLGRQVNRHGQTGNCGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAEYTVNLQMRDYITRFXLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFXLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

```

g603.seq
1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
101 CAGACGGCCC CGCACC AAAA AAACAACCAC AAAC TACAAG GAGAAACATC
151 ATGTCCGACC AACTCATCTT TGTCTGAAC TGCCTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
251 GGGAACGCCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCTCT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCACGGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTGCGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGGTAATGGG TACACGTTGC GGCACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCCgA actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTTAC CGGCGGTATC GCGGAAAAC
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATT CTGCGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGA AAAA CGTACGGCA ATTCGGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

```

g603.pep
1  MDSRLRGNDA RKYGIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPNANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISELPN DCRTLEIAAD EGREGARLAL
351 EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDLFLGL
401 HIDTKANMEK RYGNNGIISP TDSSPAVLV PTNEELMIAC DTAELAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

```

m603.seq
1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TGCGCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCCACTA AAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAMAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCAG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

m603 . pep

m603/g603

		10	20	30	40	50	60
m603 . pep		LSSRRRGRNND	KCGIRFAQ	RGLKHLAP	DCVCFSD	DP	TLKKQPQT
		:	:	:	:	:	:
g603		MDSRLRG-ND	ARKYGI	RFAQ	RGLKHT	PPNAHP	FS
		:	:	:	:	:	:
		10	20	30	40	50	
		70	80	90	100	110	120
m603 . pep		NCGSSSLKGA	VIDRXSG	SVVLSCL	GERLTT	PEAVIT	FNKDG
		:	:	:	:	:	:
g603		NCVSSSLKGA	VIDRXSG	SVVLSCL	GERLTT	PEAVIT	FNKDG
		:	:	:	:	:	:
	60	70	80	90	100	110	
		130	140	150	160	170	180
m603 . pep		LLNELEKHGL	HDRIKA	IGHRIA	HGGEKY	SESVLI	DQAVMD
		:	:	:	:	:	:
g603		LLNELEKHGL	HDRIKA	IGRRIA	HGGEKY	HESVLI	DQDVL
		:	:	:	:	:	:
	120	130	140	150	160	170	
		190	200	210	220	230	240
m603 . pep		LAAQEHFPGL	PNVGVM	DTSFHQ	TMPEAY	TYAVPR	ELRKKY
		:	:	:	:	:	:

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```

g603      LAAQEHFPGLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISELSND CRTLEIAADEGHEGARLAL EVM TYRLAK
          | | |||||:|||: ||||| |||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISELPND CRTLEIAADEGREGARLAL EVM TCRLAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVGC GVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:|:| ||||| ||||| ||||| ||||| ||||| |||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          ||||| ||||| ||||| ||||| ||||| |||||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTAGACGCA CCCACACC. AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTGTCTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAAGCGG CAGCGTCGTC CTAAGTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTGCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAAAA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG GCGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCAGTCTG CCAATGTCTG GCGTGATGGA TACTTCGTTT
601 CACCAAACCA TGCCGAGCG TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCCGTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAAAC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAAACGGC AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGTACGCGC TGCGGCGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCCG GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGTGC GCGG GCGGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TGCGACACTG CCGAACTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRLKHTPPN AHPFSDDPTX KKQPQTTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD ELNACIPLAP LHPANISGI LAAQEHFPGP PNVGVMDTSF

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201 HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ACILGKPLED
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
 301 YLTSHAGLDV AQVDEMLNKK SLLGISELS NDCRTLEIAA DEGHEGARLA
 351 LEVM TYRLAK YIASMAVGCG GVDALVFTGG IGENS RNIRA KTVSYLDFLG
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL
 451 *

m603/a603 96.7% identity in 450 aa overlap

m603.pep	10	20	30	40	50	60
	LSSRRRGRNDRKCGIRFAQGRGLKHLAPDVCXFSDDP	TLKKQPQTTRRNIMSDQLILVL				
a603	10	20	30	40	50	60
	LSSRRRGRNDRKCGIRFAQGRGLKHTPPNAHPFSDDPTXKKQPQTTRRNIMSDQLILVL					
m603.pep	70	80	90	100	110	120
	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDG	NKRQVPLSGRNCHAGAVGM				
a603	70	80	90	100	110	120
	NCGSSSLKGAVIDRKSGSVVLSCLGERLTTPEAVITFSKDG	NKRQVPLSGRNCHAGAVGM				
m603.pep	130	140	150	160	170	180
	LLNELEKHGLHDRIKAIGHRIAHGGEKYSV	LIDQAVMDELNACIPLAPLHN PANISGI				
a603	130	140	150	160	170	180
	LLNELEKHELHDRIQAVGHRIAHGGEKYSV	LIDQAVMDELNACIPLAPLHN PANISGI				
m603.pep	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDTSF	HQTMPERAYTYAVPRELRKKYAFRRYGFHG	TSMRYVAPEA			
a603	190	200	210	220	230	240
	LAAQEHFPGLPNVGVMDTSF	HQTMPERAYTYAVPRELRKKYAFRRYGFHG	TSMRYVAPEA			
m603.pep	250	260	270	280	290	300
	ARILGKPLEDIRMIIAHLNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
a603	250	260	270	280	290	300
	ACILGKPLEDIRMIIAHLNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS					
m603.pep	310	320	330	340	350	360
	YLTSHAGMDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLA	LEVMTYRLAK				
a603	310	320	330	340	350	360
	YLTSHAGLDVAQVDEMLNKKSGLLGISELSNDCRTLEIAADEGHEGARLA	LEVMTYRLAK				
m603.pep	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
a603	370	380	390	400	410	420
	YIASMAVGCGGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS					
m603.pep	430	440	450			
	PTDSSPAVLVVPTNEELMIACDTAELAGILX					
a603	430	440	450			
	PTDSSPAVLVVPTNEELMIACDTAELVGILX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT
 151 GTCGCGGCGG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG
 201 GCGCGACGAA GCGGGTTTC GCGGTGCGG CGCGGCGGC GGCTTCGGAT

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251 ACGTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC
301 AAATTTTTC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT
351 TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAAAACGGT CGGAATGCCC
401 GCGTTGATGA GCGTGGCTTT CAGACGACCT ATATTCGGCA CATCAATTTT
451 GTCGACCAA TTGCCGGTTG GGAACATACT GCCTTCgCG TCGGCTGGAT
501 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604 . pep

```

1 MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID
51 VGGVYGFAAG GGVIGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
101 KFFQRGGIVV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF
151 VDQIAGWEHT AFAVGWI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604 . seq

```

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
51 CCAGCGTACC GGGTACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCGTTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG
201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG AGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CCGCGGCATC GTTGTGATG TCGTCTGCA
351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCCGCT TGATGAGCGT GGCTTTCAA CGGCCTATAT TCGGCACATC
451 AATTTTCATG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATC

```

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604 . pep

```

1 MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51 IDVGGVHGFA TGGGVIGGGR DEGDFRRVRA SGSGFYVADQ THFQRTVSAD
101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

```

              10      20      30      40      50      60
m604 . pep    MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
              ||||| :|| :|| :|| ||||| :||| :|||
g604          MPEAHFFTRSAACGKVDQRTGEGG--DGDRGDAHHSVVQFAHAQGAYRQIDVGGVYGFA
              10      20      30      40      50

              70      80      90      100     110     120
m604 . pep    TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA
              :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
g604          AGGGVIGGGRDEGGFRRARAGGGFGYVADQTHFQRAICADGFKFFQRGGIVVDVVLQLFA
              60      70      80      90      100     110

              130     140     150     160     169
m604 . pep    CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
              ||||| :||| :||| :||| :||| :||| :||| :||| :|||
g604          RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX
              120     130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604 . seq

```

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCCTGCG GCAAGGTTGA
51 CCAGCGTACC GGGCACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA
101 CCCATCATCG CGTGGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA
151 ATCGATGTCG GCGGCATTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG

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960

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201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GGCGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA
401 ATGCCCAGCT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTTCATC ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAACT GCGCCGTTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101 FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI KFDLYFGCRE RYAVELKIAC FQNCVHLRY
201 MGNNGFADV FLPDFCDAVX *

```

m604/a604 97.0% identity in 169 aa overlap

```

              10      20      30      40      50      60
m604.pep      MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
a604           MPEAHFFTRS AACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA
              10      20      30      40      50      60
              70      80      90     100     110     120
m604.pep      TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFFLEFFQSRGIVVDVVLQLFA
a604           TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFFLEFFQSCGIVVDVVLQLFA
              70      80      90     100     110     120
              130     140     150     160     169
m604.pep      CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWI
a604           RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFVAGWIKKFDLYFGCRE
              130     140     150     160     170     180
a604           RYAVELKIACFQNCVHLHRYMGNNGFADVFLPDFCDAVX
              190     200     210     220

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCCGAC
151 TATATGACAG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATCtacCc cgGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA atCTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTTGCGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCcgCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCC GGCGATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQQRQA LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQENHHTYN LARMNMFHNL VNYNKFHIEL GDTLTNPKLK DSKPFDVVS
301 NPPYSIDFW SDDPTLINDD RFAPAGVLAP KSKADFALIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTICIAVNI
401 LVLKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LFADKADVPK
451 IAQNAAQQTV KDNNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTC TACCGCTTTC TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCCTG CCGCCGTCTT CAAAGGCGTG GCGGAACCTG ATTTGCGCAA
501 TTTTGAAAAC CACCACATCG ACCTTTTTCG CGATGCCTAC GAATACCTGA
551 TTTCCAACTA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCAAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCCGA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCC GGCGATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQQRQA LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

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101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
 151 KRLAAVLKGV AELDFGNFEN HHIDLFGBAY EYLISNYAAN AGKSGGEFFT
 201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF
 251 GQEIHTTYN LARMNMLHN VNYNQFHIEL GDTLTNPKLK DSKPFDIVS
 301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
 351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
 401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
 451 IAQNAAQQTVDKNGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
 501 LRREIDEVIA EIEA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADEVRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGV AELDFGNFENHHIDLFGBAY					
g605	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGV AELDFGNFEDHRIDLFGDAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEIHTTYNLARMNMLHN VNYNQFHIELGDTLTNPKLKDSKPFDIVS					
g605	DEHIEEGFFGQEIHTTYNLARMNMLHN VNYNKFHIELGDTLTNPKLKDSKPFDAVVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAFILHALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNVLIEEHIAEIVKLFADKADVP HIAQNAAQQTVDKNGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLTEEHIAEIVKLFADKADVP HIAQNAAQQTVDKNGYNLAVSSYVEAEDTRE					

963

	430	440	450	460	470	480
	490	500	510			
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
	: : : : : : :					
g605	VIDIRQLNAEISETVAKIERLRREIDEVIAEIEIX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1911>:

```

a605.seq
1   ATGATGACCG AAATACAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTCAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCACG CCGGAAATCA AAGACGATGC CGTCAAAGTC AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAAGA CATTAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAGAAC
451 AAGCGCTTGG CCGCGTCCTT AAAAGGCGTG GCGGAACTCG ATTTCCGGCAG
501 TTTTGAAGAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAATA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTAAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACAC
851 TGACCAATCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTTTCC
901 AATCCGCCCT ATTCCATCAA CTGGATAGGC AGCGGCGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CTGCAGGCGT ACTCGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTATTCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGCATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTCA
1151 TCGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATA
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AGGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTTG AACCAGAAGA CACCCGCGAA ATTATCGACA
1451 TCAAAACAGCT TAACGCCGAA ATCAGCGAAA CCGTTGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

```

a605.pep
1   MMTEIQRAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51  YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDFFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGSFED HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQEINHHTYN LARMNMFLHN VYNKFHIEL GDTLTNPKLK DSKPFDVAVS
301 NPPYSINWIG SGDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDAGGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQTV KDNNGYNLAVS SYVEPEDTRE IIDIKQLNAE ISETVAKIER
501 LRREIDEVIA EIEA*

```

m605/a605 98.1% identity in 514 aa overlap

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVGAVDGWDGFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	: : : : : :					
a605	MMTEIQRAQLHRQIWKIADEVGAVDGWDGFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					

g606.seq

1	ATGTCCAAAT	TTATCGCCAA	ACAATCGGTC	GGTGCGAAG	TCATCGACAC
51	GCCGcgCACC	GAAGAAGAAG	CCTGGGTTCT	GAACACTGTC	GAAGCCCAAg
101	cgcGGCAATG	GAATCTGAA	ACGCGAGAAG	TCGCCATCTA	CCACTCCCC
151	GAACCCAATG	CCTTTGCCAC	GGGCGCATCG	AGAAACAGT	CCCTGATCGC
201	CGTCAGCacc	ggtttgcctcg	accatATatg	GCGGACgaa	gtggaagccg
251	tgTTGGCGCA	CGAAATGGCG	CACGTCGGCA	ACGGCGACAT	GGTTACGCTG
301	ACGCTGatTC	AAGGCGTGGT	CAATACCTTT	GTCGTGTTCC	TGTCGCGCAT
351	TATTGCCAAC	CTGATTGCC	GAACAACGCA	CGGCAGCCAG	TCCCAGGGAA
401	CTTATTTCCT	AGTCAGCATG	GTATTCCAAA	TCCTGTTCGG	CTTCTTTGCC
451	AGCCTGATTG	TCATGTGGTT	CAGCCGCCAA	CGCGAATACC	GCGCCGAcgc
501	gggCGcggCA	AAACTGGTCG	GCGCACCgAA	AATGATTTC	GCCCTGCAAA
551	GGCTTAAAGG	CAACCCGGTC	GATTTGCCCG	AAGAAATGAA	CGCAATGGGC
601	ATCAGCCGAG	ATACGCGCGA	CTCCCTGCTC	AGCACCACC	CTTCGCTGGA
651	CAACCCGAATC	GCCCCCTCA	AATCGCTTTA	A	

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep
 1 MSKFIQKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
 51 EPNFATGAS RNSSLIIVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
 101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
 151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
 201 IAGDTRDSSL STHPSLDNRI ARLKSL*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq
 1 ATGTCCAAAT TTATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
 51 GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
 101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
 151 GAACCCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
 201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
 251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTACGCTG
 301 ACGCTGATC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
 351 TATTGCCAAC CTGATTGCCG GAAACAACGA CGGCAGCCAG TCCCAGGGAA
 401 CTTATTTTCCT GGTCAGCATG GTATTCCAAA TCCTGTTTCG CTTCCTTGCC
 451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
 501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTCG GCCCTGCAAA
 551 GGCTCAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
 601 ATCGCCGGAG ATACGCGCGA CTCCTGCTC AGCACCCACC CTTGCTGGA
 651 CAACCGTATC GCCCGCCTCA AATCGCTTTA A

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep
 1 MSKFIQKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
 51 EPNFATGAS RNSSLIIVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
 101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
 151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
 201 IAGDTRDSSL STHPSLDNRI ARLKSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

m606.pep	10	20	30	40	50	60
	MSKFIQKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
g606	MSKFIQKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIIVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIIVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GCGCGGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AACTGGTCG GCGCGCCGAA AATGATTTC GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTTGCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCGCGCTCA AATCGCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIQKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

```

m606.pep      10      20      30      40      50      60
MSKFIQKQSVGAEVIDTPRT EEEAWLLNTVEAQARQWNLKTPEVAIYHSP EPNAFATGAS
|||||
a606          10      20      30      40      50      60
MSKFIQKQSVGAEVIDTPRT EEEAWLLNTVEAQARQWNLKTPEVAIYHSP EPNAFATGAS

m606.pep      70      80      90      100     110     120
RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN
|||||
a606          70      80      90      100     110     120
RNSSLIAVSTGLLDHMTRDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN

m606.pep     130     140     150     160     170     180
LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
|||||
a606         130     140     150     160     170     180
LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS

m606.pep     190     200     210     220
ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX
|||||
a606         190     200     210     220
ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTcgaCCG CTTTTCTTt tccGTCTTCC TGAAAGAAAT
51  CCGCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTGGG CGGCGGTGGC TTTGGGCAGC AGCGGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATT TGTGTGGGC
351 GGCGATTACG CCGTCCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAtggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGTACACC GCGCACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGTGGCGCA

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601 GGTTCGGGCG TGGCGACAAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGACTGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGgcgcGCCA TCGGGCTGTC TTATTTTTTG GAAGccaGcg cGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTtccggCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTCG GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTTA AGCATCGCCT CCACCGTCCT
1101 GCTGTTCGCC GGCCTGTtcc aACCGGCAGA CTTCACCCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTCACCA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TCTGGGGCTG CCGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFLGILGIF GMILMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRLAHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFRSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AAFAWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCTTTT CCCGTCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAACC GACGAAGTGG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTC GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC CCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGAAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCGGTTC GCCGCTGGTA
1051 AGTATGTACA ACAAATGATC GCGGTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTCC AACCAGCAGA CTTACCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCCT TTTGGGGCTG CCGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSF PVFLKEVRLL TTLALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

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968

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101 IWFGFLGVEF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYT SSLNRPR LIM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFPSPLV
351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
401 AAAGWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
451 EMVRSHKAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLTTTALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVLFGMVLMWAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGFLGILGIFGMILMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYTSSLNRPR LIM LVSFAAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYASSLNRPR LIM LVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
	250	260	270	280	290	300
m607.pep	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIQSV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m607.pep	GSAGTVRIGFSLGRREFSRRARYISGVSLVLGWMLAVITVLSLVLFPSPLVSMYNNDDPAVL					
g607	GSAGTVRIGFSLGRREFSRRARYISGVSLVSGWVLAVITVLSLVLFPSPLASMYNNDDPAVL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m607.pep	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN					
g607	SIASVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
	430	440	450	460		
m607.pep	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLTTTALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFSVFLKEVRLLTALALPMLLAQVAQVGIGFVDVTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPIMIAQLYGAGKTDEVGETGRQGIWFGFLGLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPIMIAQLYGAGKTDEVGETGRQGIWFGFLGLGVFGMVLMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAMVHRLHAYTSSLNRPRLIMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAMVHRLHAYASSLNRPRLIMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240

              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGGISLSGILYMI PQSV
a607          WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGGISLSGILYMI PQSV
              250      260      270      280      290      300

              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFRSPLVSMYNN DPAVL
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMLAVITVLSLVLFRSPLVSMYNN DPAVL
              310      320      330      340      350      360

              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN
a607          SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420

              430      440      450      460
m607.pep      MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
a607          MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1  ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATcGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCTCGC CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCatCaaa cAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAIRKI LQGEPGAGD IRLEGLDILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1  ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCAG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCTCGC CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGACGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

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501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep
1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRS ELAAFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	:					
g608	MSALLPIINRLILQSPDSRS ELTSFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPEGAGDIGLEGLILG IAVLSLLGSLRSRASDELARIFGTQADIGS					
	:					
g608	TFRNSAIRKILQGGEPEGAGDIRLEGLDLILG IAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq
1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCCTGA
51 CAGCCGCTCG GAACTGCGC CCTTCGCAGG CAAAACACTG ACCCTGAACA
101 TTGCGGGTT GAACTGCGC GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGAAACG GCTTTCGAGA CACCGAAATC ACCTTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACCGG GCGGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCG ACATCGGACA CGGCATCAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep
1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLILG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

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```

m608.pep      MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a608           MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
                10      20      30      40      50      60
                70      80      90     100     110     120
m608.pep      TFRNSAVQKILQGGEPGAGDIGLEGLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608           TFRNSAVQKILQGGEPGAGDIGLEGLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
                70      80      90     100     110     120
                130     140     150     160     170     180
m608.pep      RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a608           RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
                130     140     150     160     170     180
                189
m608.pep      LERDIWIDX
a608           LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTG TGGCCGTATG
351 CCCCCTCTTT CATTCACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRVFV GLFGNVFFIG
51 AFEQAVELAA RLRFHIDNF LDTDFGIGSQ ADGNVRTLIM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTCTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTG TGGCCGTATG
351 CCCCCTCTTT GATTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRVFV GFFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

                10      20      30      40      50      60
m609.pep      MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRVFVGFVGNVFFIGAFEQAVELAA
                10      20      30      40      50      60
g609           MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRVFVGLFGNVFFIGAFEQAVELAA
                10      20      30      40      50      60
                70      80      90     100     110     120
m609.pep      RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTAKRGYGNHDLHTVAVCPVF
                70      80      90     100     110     120

```

```
a609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAATCTTTGA
51  TCGCTTTGTC GGCAACTCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTTTCTGA GGCTTTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCATAT TGGGAAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAT CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTTCGCCC GTGAGGCTGA CATCATAATC CAGTAA
```

a609.pep

1	MVVDRLLEILA	LDDETLDAFV	GNQRSSDIAH	HIFHEFRVFEV	GFFGNVFFIG
51	AFEQAVELAA	RLRLHIIDDF	LDTDFGIGSQ	ADGNVRTLVV	RAILGNFFGT
101	RAKRGYGNHD	LHTVAVCTVF	HFAREADIII	Q*	

		10	20	30	40	50	60
m609.pep		MVVDRL	EILALD	DETLD	AFVGNQR	SSDIAH	HFHEFRV
a609		MVVDRL	EILALD	DETLD	AFVGNQR	SSDIAH	HFHEFRV
		10	20	30	40	50	60
		70	80	90	100	110	120
m609.pep		RLRLHI	IDDFLD	TDFGIGS	QADGNV	RTL	VVRAVL
a609		RLRLHI	IDDFLD	TDFGIGS	QADGNV	RTL	VVRAVL
		70	80	90	100	110	120
		130					
m609.pep		DFARETD	IIIIQX				
a609		HFAREAD	IIIIQX				
		130					

```

g610.seq
1  ATGATTGGAG  GGCTTATGCA  ATTTCCCTTAC  CGCAATGTTC  CGGCTTCGCG
51  TATGCGCCGT  ATGCGCAGGG  TTGATTTTTC  ACGCGCGCTG  ATTCGCGGAG
101  ATATGCTGAC  CGCCGATGAT  ATGATTTATC  CGGTGTTCGT  ATTGGAGGGG
151  GCGGCGCGCG  AGGAGGATGT  GCCTTCTATG  CCGGCGGTGA  AGCGCTCAGAG
201  TTTGGACAGC  CTGCTGTTTA  CGGCGGAAGA  GCGCGGTGAAG  CTCGGTATTC
251  CGATGTTGGC  ACTCTTTCCC  TGGTGTTACG  CAAACAAAC  CGCGCGTGC
301  CAGGAGGCGT  ACAATCCCGA  AGGACTCGTG  CCGTCAACTG  tccgagccTT
351  CGCGAGGAGG  TttcCggaac  tggggattat  gacggatgtc  gcgctcgAtc
401  cttacacggt  gcacGGTCAG  GACGGACTGA  CGGACgaaa  cggttaCGTG
451  ATGaatgATg  aaaCCGTAGA  AGTCTTGGTG  AAACAGGCTT  TATGTcATGC
501  AGAGGCGGGC  ACGCAGGTCG  TTGCTCCTTC  CGATATGATG  GACGGGCGTA
551  TCGCGGCCAT  CCGCAGGGCT  TTGAGGATG  CCGGACATAT  CCATACGCGG
601  ATTATGGCAT  ATTCGCGCAA  ATATGCTTCT  GCATTCTACG  GCGCTTTCCG
651  TGATGCGGTA  GGCAGTTCGG  GCAATTGGG  AAAGCGAGAT  AAAAAGACTC
701  ATCAGATGGA  TCCTGCAAA  ACCGATGAGG  CGTGCATGA  AGTGGCGGCT
751  GATATTcAGG  AAGGTGCGGA  TATGGTGATG  GTGAAGCCCG  GTTTGCGGTA

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```

801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATCGCATGT TGCAGGCGGC GGTGCGCAAC
901 GCGTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

g610.pep

```

1  MIGGLMQFPY RNVFASRMRR MRRDDFSRRL MREHMLTADD LIYPVFLVLE
51  AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYYAI EAAKMLKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

m610.seq

```

1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTC CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTTATC CGGTGTTTCT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCCTTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTGGTTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GCGAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAAGCCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAAG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCGCAAC
901 GCGTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

m610.pep

```

1  MIGGLMQFPY RNVFASRMRR MRRDDFSRRL MREHMLTADD LIYPVFLVLE
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYYAI EAAKMLKR*

```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHMLTADDLIYPVFLVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNVFASRMRRMRRDDFSRRLMREHMLTADDLIYPVFLVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVVAPSDMM					
g610	FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGTQVVAPSDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN					

975

```

g610      DGRIGAIAREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAIAN
           |||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKragADGILTYAIEAAKMLKRX
           |||||
g610      GWLDGGKVVLESLLAFKragADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1   ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC CCGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCGCCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTGTTG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGCGGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTGT GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1   MIGGLMQFPY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTYAYQVSGE YAMLQAAVAN
301 GWLDGGKVVLE SLLAFKrag ADGILTYYAI EAAKMLKR*

m610/a610  99.4% identity in 338 aa overlap

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           |||||
a610      MIGGLMQFPYRNVSASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           |||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

```


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```

m610.pep      FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
|||||
a610          FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
|||||
a610          DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTAYAYQVSGEYAMLQAAIAN
|||||
a610          TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTAYAYQVSGEYAMLQAAVAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
|||||
a610          GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCGCGCG CGTCCGCATT Ctcgcgcagg ttgtGGctgt
201 tatcctTGGG CGGGCTGggt tgtttgcccg ccataaTTtc cagtacctgA
251 TcgcgGTCta tggtttcCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTCGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTgtc gCTCATgcCG TAGCGCGTTA
501 CCATTTTCGCG TGCCATTTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAYVGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAHFV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCGCGCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTGCACA TCGTTTCCAT
301 CTGTGTCGCG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCGTCTGGGT TTTCTCGGAA
401 ATGTTTTCGCG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTG GCTCATGCCG TAGCGCGTTA
501 CCATTTTCGCG CGCCATTTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGFH FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

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```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
g611          ADFRVDVLLGFLGNVLRRTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
g611          |
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1   ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTGCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTG TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTGTGTCGGG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTCC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCG AACGGGTTAC GTCGCTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GTCATGCCG TAGCGCGTTA
501 CCATTTTCGCG CGCCATTTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1   MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRRTGY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
a611          ADFRIDVLLGFLGNVLRRTGYAASQEDFAFVFRINHHAHFVAHAVARYHFARHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X

```

a611 |
 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
  1 ATGGGccttcg gcggaatata tgcAAAAAAG CTGGCcggGg taGATGAAAT
 51 AGCCTTtgac tttgacggca TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CGGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
  1 MGFGGNIAKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
 51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
  1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
 51 AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
  1 MGFGGNIAKK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
 51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIAKKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
  1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
 51 AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CGGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GGC GCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTT.AC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep     MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep     KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          KCAENVLFEVPAIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep     GHSNX
              ||||
a612          GHSNX
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGaggcagtc ggcaagggct tcgttgccgg
101  tgtttGcgGA CTCGGGTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTgtttGAt GCCGTGTCCG ATGTCGGTGG CACGgtgccc
201  gatgcCTGCC TGCCTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCG
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGCG GGAGAATGCC TGTTGTTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLLPL
201  ILQA*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101  TGTTTGCGGA CTCGGATTTC CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTTGTTGCT GTTGCCGCTT
  
```

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1 MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51 FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFFAESKPS SVMRPASFSP
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201 ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLSRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLPMPACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSPAPGSPPWRIFRIA					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
  1  ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
 51  GCGCAGTCTG  CTTATTTTCG  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101  TGTTTGCGGA  CTCGGGTTTC  CGGGAAATC   TGCCGATTTC  TTCGGCGATG
151  TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGCGCG  CACGGCTGCC
201  GATGTCTGCC  TCGGTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251  AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCT
301  CCTTCGAGCC  CGATGTCGCC  CGCCCCGGGT  TCGCCGCCCT  GGAGGATTTT
351  CTGTACCGCG  CTGTTGCCGA  AGGTGATTTC  GGTGTCTGCA  AAGCCGTTTC
401  CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451  GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGGCGGCAA  GTTCCGAGCG
501  GCTGTCCGGG  CTTTGCAGAA  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551  ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGTGCT  GTTGACGCTT
601  ATTTTACAGG  CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
  1  MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLPMFADSGS  RENLPICSAM
 51  FLPICLMPCP  MSAARLPMSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101  PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KPFPAESKPS  SVMRPASFNP
151  AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201  ILQA*

```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSGSRENLPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSPRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
a613	MSAARLPMSACVPKIRANSSDARERRLPSPRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSFAMFRVSVLPAAASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFNAMFRVSVLPAAASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

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```

g614.seq
1   AtggcTgcgt  tcAacgcttt  ggacggcaaa  aaagaagaca  acggggcaaat
51  cgaatATTCT  CAGTTCATCC  GACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGTT  ACCTGATTAA  AGGCGAGCGC
151 ACCGACAAAA  GCACCTTCTT  CACCAACGCG  CCCTTGGATG  ACAACCTGAT
201 TCAAACCCCTT  TTGAACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCGAGCGC  GCTGACTGCC  CTGTTTACA  GCCTGCTGCC  CGTCCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGGCGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCCT  TCGGCAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTTACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TGCAGGAAAT  CGTCGATTAC  CTCAAAGCAC  CGAACCCTa
501 tcaAAGcctc  ggcggccgtg  ttcCGCGCGG  CATCCTgCtg  gcgGgcagcc
551 CGGGAaccgg  taaAACACTC  TTGGCGAAAG  CCATTGCAGG  CGAGGCCGCG
601 GTGCCGTTCT  TCAGCATTTT  CGGTTCCGAT  TTTGTGAAA  TGTTGCTCGG
651 TGTCGGTGCA  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCA  AAGAAAAACG
701 CCCCATGCAT  TATCTTTATC  GACGAGATTG  ACGCGGTAGG  CCGCCAACGC
751 GCGCGAGgTT  TGGCGGCGCG  CAATGATGAG  CGCGAGCAAA  CATTAAACCA
801 ATTATTGGTT  GAAATGGACG  GTTTTGAGAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACCGCCCC  GACGTAATCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGCTTCG  ACCGCCAAGT  CGTCGTCCCC  CTGCCGGACA  TCCGGGGGCG
951 CGAACAGatn  ttGAACGTCC  ATTCTaaAAA  AGTGCcttTG  gacgaATCTg
1001 tggatTTTATT  GTCCCTCGCG  CGCGGCACGC  cgggtttTTc  cggcgcgat
1051 tTggcgaaac  tgggtcaacga  agccccctg  tttgccggcc  gccgcaacaa
1101 agtgaaagtc  gatcaaagcg  attTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGGAA  CGCCGCAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

```

g614.pep
1   MAAFNALDGK  KEDNGQIEYS  QFIRQVNNGE  VSGVNIIEGSV  VSGYLIKGER
51  TDKSTFFFTNA  PLDDNLIQTL  LNKNVVRVKVT  PEEKPSALTA  LFYSLLPVLL
101 LIGAWFYFMR  MQAGGGGKGG  AFSFGKSRAR  LLDKDANKVT  FADVAGCDEA
151 KEEVQEIVDY  LKAPNRYQSL  GGRVPRGILL  AGSPGTGKTL  LAKAIEAGEA
201 VPFFSISGSD  FVEMFVGVA  SRVRDMFEQA  KKNAPCIIFI  DEIDAVGRQR
251 GAGLGGGNDE  REQTLNQLLV  EMDGFESNQT  VIVIAATNRP  DVLDPALQRP
301 GRFDRQVVVP  LPDIRGREQX  LNVHSHKVPL  DESVDLLSLA  RGTGPFSGAD
351 LAKLVNEAPL  FAGRRNKVKV  DQSDLKTPKT  KSIWVRNAAV  W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

```

m614.seq
1   ATGGCTGCGT  TCAACGCTTT  AGACGGTAAA  AAAGAAGACA  ACGGGCAAAT
51  CGAATACTCT  CAGTTCATCC  AACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGCT  ACCTGATTAA  GGGCGAGCGC
151 ACCGACAAAA  GCACTTTCTT  CACCAACGCG  CCTTTGGACG  ACAACCTAAT
201 TAAACACTG  CTCGACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCGAGCGC  GCTGGCTGCC  CTGTTTACA  GCCTGCTGCC  CGTCCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGACGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCAT  TCGGTAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTGACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TACAGGAAAT  CGTCGATTAC  CTCAAAGCGC  CGAACCCTa
501 TCAAAGCCTG  GGCGGGCGCG  TGCCGCGCGG  CATCCTGCTG  GCGGGCAGCC
551 CGGGTACGGG  TAAGACGCTT  TTGGCGAAAG  CGATTGCAGG  CGAAGCCGCG
601 GTGCCGTTCT  TCAGCATTTT  AGGTTCGAC  TTTGTGAAA  TGTTGCTCGG
651 TGTCGGTGCG  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCG  AAGAAAAACG
701 CCCCTGCAT  CATCTTTATC  GACGAGATTG  ACGCAGTCGG  CCGCCAACGC
751 GGCGCAGGTT  TGGGCGGCGG  CAATGATGAG  CGCGAGCAAA  CATTAAACCA
801 ATTGTTGGTT  GAAATGGACG  GTTTTGAGAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACCGCCCC  GACGTAATCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGTTTCG  ACCGCCAAGT  GGTGTGTCCT  CTGCCGGACA  TCCGAGGGCG
951 CGAACAGATT  TTGAACGTCC  ATTCTAAAAA  AGTGCCTTTG  GACGAATCTG
1001 TGGATTTATT  GTCCCTCGCG  CGCGGCACGC  CGGGTTTTTC  CGGCGCGGAT
1051 TTGGCGAACT  TGGTCAACGA  AGCCGCCCTG  TTTGCCGGCC  GCCGAATAA
1101 AGTCAAAGTC  GATCAGAGCG  ATTTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGGAA  CGCCGCAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

```

m614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIEGSV VSGYLIKGER
51 TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND EREQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKVPL DESVDLLSLA RGTPGFSGAD
351 LANLVNEAAL FAGRRNKVKV QSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFTNA					
g614	MAAFNALDGKKEDNGQIEYSQFIRQVNNGEVSGVNIEGSVVSGYLIKERTDKSTFFTNA					
	10	20	30	40	50	60
m614.pep	70	80	90	100	110	120
	PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVTPEEKPSALTALFYSLLPVLL LIGAWFYFMR MQAGGGGKGG					
	70	80	90	100	110	120
m614.pep	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL					
g614	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
m614.pep	190	200	210	220	230	240
	AGSPGTGKTL LAKAIAGEAGVPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAGEAGVPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQT VIVIAATNRP DVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQT VIVIAATNRP DVLDPALQRP					
	250	260	270	280	290	300
m614.pep	310	320	330	340	350	360
	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL					
g614	GRFDRQVVVPLPDIRGREQILNVHSHKVPLDESVDLLSLARGTPGFSGADLAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	370	380	390			
	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201 TAAACACTG CTCGACAAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251 AACCAGAGCG GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG

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301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGGCGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCA
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTC AGGTTCCGAC TTTGTGCGAA TGTTCTGTCG
651 TGTCCGGTGA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGTCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTTCG ACCGCCAAGT GGTTGTCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGTCCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGKG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIIAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10          20          30          40          50          60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA
          10          20          30          40          50          60

          70          80          90          100         110         120
m614.pep  PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMRMQTGGGKGKG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      PLDDNLIKTL LDKNVRVKVTPEEKPSALAA LFYSLLPVLL LIGAWFYFMRMQTGGGKGKG
          70          80          90          100         110         120

          130         140         150         160         170         180
m614.pep  AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL
          130         140         150         160         170         180

          190         200         210         220         230         240
m614.pep  AGSPGTGKTL LAKAIIAGEAGVPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      AGSPGTGKTL LAKAIIAGEAGVPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
          190         200         210         220         230         240

          250         260         270         280         290         300
m614.pep  DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      DEIDAVGRQRGAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250         260         270         280         290         300

          310         320         330         340         350         360
m614.pep  GRFDRQVVVPLPDIRGREQI LNVHSHKKVPL DESVDLLSLARGT GPGFSGADLANLVNEAAL
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a614      GRFDRQVVVPLPDIRGREQI LNVHSHKKVPL DKSVDLLSLARGT GPGFSGADLANLVNEAAL

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	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1   ATGTGGA AAC GCGCGCGCG CCGTGtcggC AGCTTtgaag agcagcGaAT
51  agatgCCGCC GGCAAACAC AATGCGGAAa gcaggCtgaa gcGGTTgcgC
101 GGCagcTTca tGCCGCCTCC TcGTCCaGCC ACGtttGgca gattttggac
151 aggcgcAGGa ATTTGCGcCc gcgtgcggCA agtatgtcgc gcCAttgtgc
201 cacttcttcg gcggacggTG ctctgcgaT gctgCATTCG TACagcagga
251 aatcgagggT ttcttcgatg acggGgatgg AttccgTTTG GataAgCTgc
301 ttgagttcgt tcatgactGt TCgGATAcgg aaatcgggaa aatgccgtct
351 gAAagggctt CAGACGGCat tggATTATTT GCTGTGCAGG AAgcgcgttg
401 cctcttccca tttgcCGGAA AtgATGTCCg gtacggcctg cAGGGATttg
451 gCGACGGcat cgtcgatttg ccgGcggtgc ttCgcgcgtc ggtttGTTca
501 agacgtagcc gaCGACGagg ttgcggtcGC CGGGGtggcC GATGCCGAGG
551 CGCAGGCGGt aatagtctgC CGTGCCGAGT TTTGCctgAA TGTCTTTCAA
601 GCCGTTGTGT CgcCGttgc cgcCGCCGAG TTTGAATTTg ATCCGTCCGC
651 AAGGGATGTC GAGTTCGTCG TGGACGACGA GGATTCTTc GGGTTTGATT
701 TTGTAGAACT GTGCAAGCGC GGCAACCGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCCGGT TTGAGCAGCC AAACATCGCC GTCGGGCAGG GCGGCAGCGG
801 CAACTTCGCC GAAGAATTTT TTTTCTTCTT TAAACGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CAAAAGCCC GCATTGTGGC GGGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGttcg
951 acatgataTT TtccgtgTTT CTgTCGaatg cggTctgaAG GCTTCAGacg
1001 gcatggTtaT TCTTCTTgaT TTtgaACgcg tgtgcggCGC GCTTCTTTGG
1051 GGTGCATCAA CAGCGGGCGG TACACTTCGA TGCGGTCGCC GTCGCGCAGC
1101 GGCGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1   MWKRRRRGVG SFEEQRIDAA GKPQC GKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRH CATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSFMTVRIR KSGKCR LKGL QTA LDYLLCR KRVASSHLPE MMSGTACRDL
151 ATASSICRRR FRARFVQDVA DDEVAVAGVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAAAAAE FEFDP SARDV EFVVDDEDFE GFDFVELCKR GNRLSGTVHE
251 RGRFEQPNIA VGQGGAGNFA EEEFFFFFKRS LPFPRQFVEE PKARIVAGLF
301 VFFARVAQAD NHFDCVRHDI FRVSVECLGK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq Length: 1116
1   ATGCGGAAAA GCGGTGGCG CCGTTTCGGC AGCTTTGAAA AGCAGTGAGT
51  AAATGCTGCC TGCAAACAC AATGCCGAGA GCAGGATAAA GCGGTTGCGT
101 GGCAGATTCA TGCTTGTTCC TCTTCAAGCC ATGTCTGGCA TAGTTTGGAT
151 AGGCGCAGGA ATTTCCGCC GCGTGCGGCC AGCATATCGC GCCAAACGGC
201 AATTTCTTCG GCGGAGGGGG CATCGTCTAT GCTGCATTTC TAGAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTTCGTTTG GATAAGCTGC
301 TTGAGTTCCG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CTTCTTCCCA TTTGCCGCA AGGATGTCGG GTATGGCTTG CAGGGATTTC
451 GCGACGGCAT CGTCAATCTG TCGGCGGTGT .TCCGTACTG GGTTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGCC GATGCCAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCGCCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTCTTc GGGTTTGATT
701 TTGTAGAACT GTGCAAGCGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGCAGGT TTGAGCAGCC AAACGTCGCC GTCGGGCAGG GCGGCACGGG

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801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCTGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGCGG TACACTTCGA TGCGGTGCGC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNAA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFP PRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDP SAGNV EFVVDDEDF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTG DFA EEEEEFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVX HDI FRVSVECC LK ASDGMVILL DFERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAA	CKPQCREQDKAVAWQIHACS	SSSHVWHS	LD	RRRNFP	PRAA
g615	10	20	30	40	50	60
	MWKRRRRRGVGSFEEQRIDA	AGKPGQCGKQAEAVARQL	HA	SSSHVWQIL	DRRRNL	PPRAA
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLHS	XSRKSRVSSMTGMDSVWISC	LSSVMTVRIW	KSGTCRLKGL		
g615	70	80	90	100	110	120
	SMSRHCATSSADGASSMLHS	YSRKSRSVSSMTGMDSVWISC	LSSFM	TVIRKSGK	CRLKGL	
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHL	PARMSGMACRDLATASSICRRC	XRTGFVQDIA	DDEVAVARVA		
g615	130	140	150	160	170	180
	QTALDYLLCRKRVASSHL	PEMMSGTACRDLATASSICRRC	FRARFVQDVAD	DEVAVAGVA		
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQ	AVVSAVAAAEFEFDP	SAGNV	EFVVDDEDF	GFDFVELCKR	
g615	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQ	AVVSAVAAAEFEFDP	SARDVEFVVDDEDF	GFDFVELCKR		
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNV	AVGQGGTG DFA EEEEEFFKXS	LPFPRQFVEE	PKTRIVACLF		
g615	250	260	270	280	290	300
	GNRLSGTVHERGRFEQPN	IAVGQGGAGNFAEEEEFFKRS	LPFPRQFVEE	PKARIVAGLF		
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHFDCVX	HDIFRVSVECC LK ASDGMVILL	DFERVCGALLW	GRSTAGGTLR		
g615	310	320	330	340	350	360
	VFFARVAQADNHFDCVR	HDIFRVSVECC LK ASDGMVILL	DFERVCGALLW	GRSTAGGTLR		
m615.pep	370					
	CGRRRAAACRLX					
g615	370					
	CGRRRAAACRLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1   ATGCGGAAAC GGC GGCGGCGG CCGTGTTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGC GGCA AGTATGTGCG GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTG TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCAATT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG. TTCCGTACTG GGTGTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTTCTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTTCGG TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 GACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGTTGC CCAAGCCGAC AACCATTGTT ATTGTGTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTGATCAA CAGCGGGCGG TACTTCTCGA TGCGGTGCGC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1   MRKRRRRGVG SFEEQRIDAA GKPQCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCAATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPAGNV EFVVDDEDFG GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTGDEA EEEEEFFK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECLRK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS�DRRRNFPPRAA					
				:		
a615	MRKRRRRGVGSFEEQRIDAAAGKPQCGKQAEAVARQLHAASSSSHVWQILDRRRNLPRAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	: :					
a615	SMSRHCAATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXFRTGFVQDIADDEVAVARVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAAAEFEFDPAGNVFVVDDEDFGDFVELCKR					
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPAGNVFVVDDEDFGDFIKLRKG					
	190	200	210	220	230	240
	250	260	270	280	290	300

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFKXSLPFRQFVEEPKTRIVACLF
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615       GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFKXSLPFRQFVEEPKTRIVACLF
           250      260      270      280      290      300

           310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDVCVXHDFRVSVCECLKASDGMVILLDFERVCGALLWGRSTAGGTLR
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615       VFFARVAQADNHFDVCVXHDFRVSAECLKASDGMVILLDFERVCGALLWGRSTAGGTLR
           310      320      330      340      350      360

           370
m615.pep  CGRRRAAACRLX
           |||||
a615       CGRRRAAACRLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGGCGAC GGATCAAAAT CAAACTCGGC GcgggcaaCG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCCTCG CATCGgccac CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAACa aaccgagcgc gGaagcaccg Ccgggcaatc gacgatgCCG
501 TCGccaaATC CCTGcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gcTTCCTGCA CAGCAAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCaccgt ccgccgaaga
751 agtggcacaa TGcgcgacac tactTGccgc acgcgGcgGC AAATtCtTgc
801 gcctgtccaa aatctgcCaa aCGTGGcTGG ACgAGGAGGC GGCatgAAgc
851 tGCCGcgCAA CGcgttcaGc ctgctTCCG CATtGTGGTt TGCCGGCGGc
901 atctAtTcGc tgctcttcaa AGCTGccgaC ACCGCGCCGC CGCCGTtTCC
951 ACATtTcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGGAaAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

m616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEKKKFFGE
51  VARAALPDGD VWLLKPATFM NRSGQVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGy
151 VLNKPSAEAP PANRRCRRI PAGRTRHHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSRFPY PNSHRTQAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRROIAPVQ NLPNVAGRGG GMKLPRNRFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QILFLAKAFK TGKLPiPYRS
351 LIAFAFCFAV GSECAQWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 TCGGCCCGTG CGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGGCGAC GGATCAAAAT CAAACTCGGC GCGGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcAGG CAAACTCGG CACGGCAGAC TATTACGCC
401 TGCGCCCTCG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAACA .CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCTCTG TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGCGGGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

m616.pep

```

1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARAALPDGD VWLLKPATFM NRSGQAVAAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRCRRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPFPALRM QHRRCLRRR
251 NCRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPHFD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGS LGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
	VWLLKPATFMNRSGQAVAAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGNGGGHNLK					
g616	VWLLKPATFMNRSGQAVAAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGNGGGHNLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
	DIQAKLTADYYRLRLGIGHPGDRNLVVGVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
g616	DIQAKLTADYYRLRLGIGHPGDRNLVVGVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
	QMGRSNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRRNPRFPALRM					
g616	QMGRSNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRRNPRFPALRM					
	190	200	210	220	230	240
m616.pep	250	260	270	280	290	300
	QHRRCLRRRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRRCLRRRNCRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPRNRFILLSALWFAGS					
	250	260	270	280	290	300
m616.pep	310	320	330	340	350	360
	IYSLLFKAAETAPPPFPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAAETAPPPFPHFDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL					
	310	320	330	340	350	360
m616.pep	370	380	390	400		
	FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX					
g616	FSECAQAWFTATRTGSLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq
1 ATGTCAAACA CAATCAAAT GTTTGTGCGC TTGGGCAACC CGGGCAAAGA
51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCTCT GACGAACGG
101 CGTGGAATG GAAGGCTTCA TTTAAAGAAG AAAAAAATT CTTGCGCGAA
151 GTCGCCCGTG CTACCCGCGC CGACGCGGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCCG GACAGGAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TCGCCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCGGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCTC
701 GATTTCTGTC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACA TGGCGCGACA TACTTGCCGC ACGCGCGCGC AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGT TGCCGGCGGC
901 ATCTATTGCG TGCTCTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTGAC AAAGCAGCAC ACCTGCCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTCTCGCA CTCTTGCCG CCCGCGCCGC CGACCGCCCG
1201 GACTGA

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep
1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARATLPDGD VLLKPTTFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QMTRCRLKP
201 FQTACSRFFY PNSHRTQAA YPNRIHPRHR RNPRFPAVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMKLPRNRF LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QIWLLTKAFK TGKLPIPYRS
351 LMVFALCFAL FSECAQA*FT ATRTGS LGDV LADMAGTVLA LFAARAADRP
401 D*

m616/a616 90.0% identity in 401 aa overlap

m616.pep	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
m616.pep	70	80	90	100	110	120
m616.pep	VLLKPTTFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK					
a616	VLLKPTTFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK					
	70	80	90	100	110	120
m616.pep	130	140	150	160	170	180
m616.pep	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYVLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQMQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNRNPRFPALRM					
a616	QMXRGNPLPAQMQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNRNPRFPAVRM					
	190	200	210	220	230	240
	250	260	270	280	290	300

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m616.pep  QHRRCP LRRRNCRLARYAGRTRRKIPAPIQTMPD MAXRGTS MNLPNRNFILLSALWFAGS
          |||| :|||: :|||: ||||:||||:|:|:| || :|:||||| |||||:|
a616       QHRRRTIRRRSGT MARHTCRTRRQIPAPVQNL PNVAGRGGGMKLPNRNFSLLSALWFAGG
          250      260      270      280      290      300

          310      320      330      340      350      360
m616.pep  IYSLLFKAAETAPPPFP HFDKVAHLALFFAQI WLLTKAFRTDNRPI PYRSLMVFALCFAL
          |||||:|||||:|||||:|||||:|||||:| : |||||:|||||:|
a616       IYSLLFKAADTAPPPFP HFDKAAHLALFFAQI WLLTKAFKTGKLPI PYRSLMVFALCFAL
          310      320      330      340      350      360

          370      380      390      400
m616.pep  FSECAQAWFTATRTGSLG DVLADLTGAALAL FTARAACRPDX
          ||||| ||||| |||||:|:|:|:|:| |||| ||||
a616       FSECAQAXFTATRTGSLG DVLADMAGTVLALFAARAADRPDX
          370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

```

g619.seq
1  ATGCCGTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCTGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTGCTG GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGTtgcGC
301 GCGGTGGGCT ATAcatccct gccgttgacg ggCAAATTCG GCTTTGAACT
351 GGTTGTATAT ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTTGCCG CACATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GGCGCGCTGG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT TGTCGGCCCC
751 GTGAGCTTTT TCGGGCTTCT CGCCGCTCTG CTTGCCAACC ACTTTTCCcC
801 gtCCGTGCGC CATTCGCTCC GCCTGCcgt gacggtttGC gtcgGcgGCA
851 TCCTCTTGgt cggCggacaA ACCGTATTCG AACACTTCTT GGGCATGAag
901 gCggTATTAA GCGTGGTGGT cgAATTGCG ggcggactcG TTTTCTCTA
951 TCTCGTTTTA AAACACAAAA AATGA

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This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

```

g619.pep
1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSL YVF LQTLVFTFG
101 GVGYTSPLPT GKFGFELVVM MGSLLLFYT LIRQGGRLDLP HMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVRSELLGI GALVLLVSAA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCCGT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCGTCCTG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTTC TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTGCTG GTATGTGTTT TTGCAGACCT TGCTGGTGTG TACGTTCGGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAACT
351 GGTCGTCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGACG CGATTGTGCG CGCATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTTCG GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT GGTCGGCCCC
751 GTAAAGCTTTT TCGGGCTTCT CGCCGCTCTG CTTGCCAACC ACTTTTCCcC
801 GTCGGTCAAA CATTCGCTCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CCGGCGACAG ACCGTGTTCG AACACCTGCT CGGTATGCAG

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901 GCAGTGTGA GCGTAGTAGT AGAATTGGCC GGCGGACTCG TTTTCCTCTA
 951 TCTCGTTTAA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLLVETFG
 101 GVGYSASPLT GKFGFELVVM MGGSLLLFYT LIKQGGRDLS RMILIGVIFG
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMO
 301 AVLSVVVEFA GGLVFLYLVL KHKK*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
m619.pep	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
m619.pep	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLLVETFGGVGYASPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLLVETFGGVGYTSLPLTGKFGFELVVM					
m619.pep	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
m619.pep	MGGSLLLFYTLIKQGGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGGRDLPMLILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
m619.pep	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
m619.pep	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
m619.pep	VATATAVVGPPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMO					
g619	VATATAVVGPPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
m619.pep	250	260	270	280	290	300
m619.pep	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLKHKKX					
g619	AVLSVVVEFAGGLVFLYLVLKHKKX					
m619.pep	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
 1 ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGGTT CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTCG ATTTGGGTT
 251 TCGATTCCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGC
 301 GCGTGGGCT ATGCTTCCCT GCCGTGACG GGCAAATTCG GCTTTGAACT
 351 GGTCTGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
 401 AGGGCGGGCG CGATTGCGG CGTATGATTT TAATCGGCGT GATTTTCGGG
 451 ATTTTGTTC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCGA
 501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GGCGCGTGA TTCTGCTCGT CAGCGCGGCG
 601 GTCGTTTGGC GCGAACGTA CCGCTTGAC GTACACCTTT TGGGCGCGCA
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTCGGCCCC

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751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTATTCT AACACTTCTT GGGCATGAAG
901 GCGGTATTAA GCGTGGTGGT CGAATTGCG GCGGACTCG TTTTCTCTA
951 TCTCGTTTAA AGACACAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
  1 MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLYVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGGRLDP RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

      10      20      30      40      50      60
m619.pep MPSEKNIGFMAGSSRPLWVAFALLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA
a619      MPSEKNIGFMAGSSRPLWVAFALLVSCVLFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
      10      20      30      40      50      60

      70      80      90     100     110     120
m619.pep VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
a619      VGVSTQLFQTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
      70      80      90     100     110     120

      130     140     150     160     170     180
m619.pep MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
a619      MGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
      130     140     150     160     170     180

      190     200     210     220     230     240
m619.pep NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
a619      NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m619.pep VATATAVVGPFVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
a619      VATATAVVGPFVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
      250     260     270     280     290     300

      310     320
m619.pep AVLSVVVEFAGGLVFLYLVLKHKXX
a619      AVLSVVVEFAGGLVFLYLVLRHKKX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
  1 ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
 51 CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcgggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

g620.pep

```

1  MKKTLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

m620.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGTTCTC
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

m620.pep

```

1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVQMFGYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

a620.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGTTCTC
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

a620.pep

```

1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

995

m620/a620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAE	EGPPPLPRQISDRSVGHYCS	MNLTEHNGPKAQIFLNGKP			
a620						
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMF	GYTKLPPEEPKGI	RVIYVTDMG	NVTDW	TNP	ADTEWMDAKKAFYVIDS
a620						
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALP	FGNKEQAEKFAK	DKGGKVVG	FDDMPD	TYIFKX	
a620						
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta  cgcgtgtcgg  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAaaag  ctggCGTTTG  CCGCCGCCGC  CCTGCCAGAA  gccgTccgCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGCGAT  TCGGAAGaaa  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACACGCTGGA  TATGCAGGAA  ACCGTGCGCC  ACGCCTTCG  CGTGCCTGTC
301 GGCTTGGATT  CGATGGTTTT  GGGCGAGCCG  CAGATTTTGG  GGCAGATTAA
351 AGATGCGGTG  CGTGCGGCTC  AAGAACAGGA  AAGTATGGGG  GCAAACTCA
401 ATGCCCTGTT  CCAAAAAACC  TTTTCCGTTG  CTAAAGAAGT  CCGTACCGAT
451 ACCGCTGTCT  GCGAAAATTC  GGTTCGATG  GCTTCCGCGT  CCGTCAAGTT
501 GCGGAACAG  ATTTTCCCG  ACATCGGCGA  TTTGAACGTA  TTGTTTATCG
551 GCGCAGGCGA  AATGATTGAG  CTGGTTGCCA  CTTATTTTGC  CGCCAAAAAT
601 CCCCggCTGA  TGACGGTTGC  CAACCGGAGC  CTGGCGCGTG  CACAGGAGTT
651 GTGCGACAAG  CTCGGTGTTA  ACGCCGAACC  GTGCCTGCTG  TCCGATCTGC
701 CTGCCATTCT  GCACGATTAC  GACGTGGTGG  TTTCTTCAAC  GGCAGGCCAG
751 CTTCCGATAG  TCGCAAAGG  CATGGTCGAA  CGCGCATTGA  AACAGCGTCA
801 GAGTATGCCG  TTGTTTATGC  TTGACTTGCC  CGTGCCGCGC  GATATTGAAG
851 CGGAAGTCGG  CGATTGAAAC  GATGCGTATC  TTTATACGGT  GGACGATATG
901 GTCAACATCG  TCCAAAGCGg  caaggaggca  aggcagaaag  ccgccgcCgc
951 gcgcgaaacg  ctggTGTCGG  AAAAGGTTGC  CGAATTTGTG  AGGCAGCAGC
1001 AGGCGAGGCA  GagggttcCG  CTGATTAAGG  CCTTGC GGGA  CGAGGGCGAG
1051 AAAGCGCGCA  AGCAGGTGTT  GGAATATGCG  ATGAAACAGC  TTGCCAAAGG
1101 CGcaacCGCG  AAGGaggttt  TGgaacggct  gtccgtcCAA  CTGACCAACA
1151 AGCTGCTGCA  TTCGCCAACT  CAAACCTTGA  ATAAGGCGGG  GGAAGAAGAT
1201 AAAGatttGG  TTCATGCCgt  cGCGCAGATt  tatcatttGG  ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

g622.pep

```

1  MQLTAVGLNH  QTAPLSIREK  LAFAAAAALPE  AVRNLARSNA  ATEAVILSTC
51  NRTELYCVGD  SEEIIRWLAD  YHSLPIEEIR  PYLYTLDMQE  TVRHAFRVAC
101 GLDSMVLGEP  QILGOIKDAV  RAAQEQUESM  AKLNALFQKT  FSVAKEVRTD
151 TAVGENSVSM  ASASVKLAEQ  IFPDIGDLNV  LFIGAGEMIE  LVATYFAAKN
201 PRLMTVANRT  LARAQELCDK  LGVNAEPCLL  SDLFAILHDY  DVVVSSTASQ
251 LPIVGKGMVE  RALKQRQSMP  LFMLDLAVPR  DIEAEVGLDN  DAYLYTVDDM
301 VNIVQSGKEA  RQAAAAAET  LVSEKVAEFV  RQQGRQSV  LIKALRDEGE
351 KARKQVLENA  MKQLAKGATA  EEVLERLSVQ  LTNKLLHSPT  QTLNKAGEED
401 KDLVHVAQI  YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA  CCGCTGTCGG  ACTCAATCAT  CAAACCGCAC  CTTTAAGCAT
51  ACGGGAaaaG  CTGGCGTTTG  CCGCCGCCGC  CCTGCCTAAA  GCCGTCCGCA
101 ATCTTGCCCG  AAGCAATGCG  GCAACGGAGG  CGGTAATCCT  TTCTACCTGC
151 AACCGCACCG  AGCTTTACTG  CGTCGGTGAT  TCGGAAGAAA  TCATCCGATG
201 GCTTGCCGAT  TACCACAGTT  TGCCGATTGA  AGAAATCCGT  CCGTATCTGT
251 ACGCGCTGGA  TATGCAGGAG  ACTGTGCGCC  ATGCTTTCCG  CGTGCCTGTC

```

```

301 GGGCTGGATT CGATGGTGT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAATT
501 GGCGGAACAG ATTTTTCCTG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATGC TTGATTGGC AGTGCCTGCT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGCGCAG
1051 AAAGCGCGCA AACAGGTGTT GGAAAATGCC ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTTGG TTCATGCCGT CGCGCAGATT TATCATTTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQUESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGDIN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQMOTVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m622.pep	RVAQEQUESMGKKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQUESMGAKLNALFQKTFSSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPFLMLDLAVPRDIEAEVGDINDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQRQSMPFLMLDLAVPRDIEAEVGDINDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAGAA CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTTCCATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTTGG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSIQ LTNKLLHSPT QTLNKAGEED
401 KDLVHVAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

```

10      20      30      40      50      60
m622.pep MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD
|||||
a622     MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD
10      20      30      40      50      60

70      80      90      100     110     120
m622.pep SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
|||||
a622     SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
70      80      90      100     110     120

130     140     150     160     170     180
m622.pep RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
|||||
a622     RVAQEQESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
130     140     150     160     170     180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq

```

1  ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
51  GATAATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTAC
101 TCTCCGCCGC CTGCTGGGCA AAGGCAtccc cgcgcTTTCa ccgCTGGCTG
151 CACcgGCacc gCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTCCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
251 cctgcctcat gatcTTTgg CattTTCCCC aacnctggtg ggteGGGGCG
301 GTTTCATCGG TTTTTTGTTC CCTTGTcacc ATacggatgt gGcacAGacc
351 cgaatCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep

```

1  MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
101 VSSVFCSLVT IRMWHRPES*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq

```

1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TACTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
151 CACCGGCACC GCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTCCCG CGCAAAGCCA AAATATTTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTGGGGGCG
301 GTTTCATCGG TTTTTTGTTC CCTTGTGCGC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep

```

1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
g624	MIRYLLIACGGISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60

999

```

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g624           HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```

a624.seq
1   ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCTG TGCTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTAAGTC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTTCG CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCC AACGCTGGTG GGTGCGGGCG
301 GTTTCATCGG TTTTTTGTTC CTTGTCGCC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```

a624.pep
1   MIRYLLIACG CISLLGLIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*

```

m624/a624 99.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
m624.pep      MIRYLLIACGCISLLGLIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624           MIRYLLIACGCISLLGLIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV
              10      20      30      40      50      60

              70      80      90      100      110      120
m624.pep      HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a624           HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX
              70      80      90      100      110      120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```

a625.seq
1   ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```

g625.seq
1   atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtcTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtcgttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAAACC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGcc
351 gtAA

```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```

g625.pep
1   MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPmie ASAVPTASRA

```


1000

51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
1 ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51 ACGGTTTGG TTGGCTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTCGTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRSWLAFFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTkmppEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTkmppEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTkmppEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTkmppEMVYRASSSRMKG IYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTGAAA TCCTCGGCAG
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTATCCTG ATTACATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCTATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
201 CATCACCATC TTCCCCGTCC TGAGCATCTT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCCGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTAATGAC GGGTCCCTGT TTTTCAATAT TGCTGGCGGT TTCTAtgggT
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

```

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc
551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CATcgTACAT
601 ACCCTcgtCT TTTTCgTttt cAAACTACTg taa

```

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

```

g627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH
201 TLVFFVFKLL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

```

m627.seq
  1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCACATCGC CGAAGTGGGC AAACCTCTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATCTT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTACCCTG TTTTCATTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

```

m627.pep
  1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGTL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	IALTAVSMAITPKQVRAGNEFNFEPIAEVG				
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVIL	ITLTAVSMAITPKQVRAGNEFNFEPIAEVG				
	10	20	30	40	50	60

1002

	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINTMYFWMMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627.seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCGGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GCGGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTTG TTTTCATTCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAGGCC ATTGCCGAAC AGCGCGCGCT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627.pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHP
101 NVMYFWMSSI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627.pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627.pep	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVVSLVHDTAGHPINVMYFWMMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627.pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVPMP					
	130	140	150	160	170	180
	190	200	210			
m627.pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

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a627 TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX
 190 200 210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628.seq
 1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT
 51 TTCGATATTG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC
 101 ACACATGGAT TTTACGTTTCG GTCAGGCGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT
 301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC
 351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628.pep
 1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRRLLNTNRPR
 51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
 101 D*IRLRRTFS LLNFASASGT *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628.seq
 1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC
 101 AACATGGAT TTTGCGTTTCG GTCAAACGGC TCAATACCAA CAGGCCGCGT
 151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA
 251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG
 301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC
 351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628.pep
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRPR
 51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVAVHKP
 101 DWIRLRRTSS PLKFASASGA *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	SDGTSAPAAALQ	TWILRSVKRLNTNRPR	LKSSAASLIM		
g628	MCVPLKPAGCGPPNSCVSILA	AFSDGTSAPAAALHTWILRSV	RRLNTNRPR	LKSSAASLMM		
	10	20	30	40	50	60
m628.pep	TVGSAASGLVSIALTKMANGS	ASTAGILLNGR	VRSAVHKPDWIRLRRTSS	PLKFASASGA		
g628	TVGSAASGLVSIALTKMANGS	ASTAGILLNGR	VRSAVHKPD	XIRLRRTFSL	LN	FASASGT
	70	80	90	100	110	120
m628.pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

```

a628.seq
1  ATGTGCGTGC  CACTCAAACC  GGCCGGATGC  GGGCCGCCGA  ATTCATGTGT
51  TTCGATGTTG  GCAGCATTTC  CAGACGGCAC  GTCTGCGCCA  GCTGCCTTAC
101 ACACATGGAT  TTTACGCTCG  GTCAAACGGC  TCAATACCAG  CAAACCTCGT
151 CTGAAATCCT  CGGCGGCTTC  TTTGATCACA  ACCACAGGGT  CTGCCGCCAG
201 CGGATTGGTG  TCCATCGCAT  TGACGAAGAT  GCGGAACGGC  TCGGCATCGA
251 CGGCAGGGAT  TTTGCTGAAC  GGACGGGTAC  GCAGCGCAGT  CCACAAACCG
301 GATTGGATCA  GATTGCGGCG  CACTTCTTCG  CCGCTTAAGT  TTGCCAACGC
351 TTCGGGCGCG  TAG

```

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

```

a628.pep
1  MCVPLKPAGC  GPPNSCVSML  AAFSDGTSAP  AALHTWILRS  VKRLNTSKPR
51  LKSSAASLIT  TTGSAASGLV  SIALTKMANG  SASTAGILLN  GRVRSVHKP
101 DWIRLRRTSS  PLKFANASGA  *

```

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAA	LQTWILRSVKRLNTNR	PRLKSSAASLIM		
a628	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAA	LHTWILRSVKRLNTSKPRLKSSAASLIT			
	10	20	30	40	50	60
	70	80	90	100	110	120
m628.pep	TVGSAASGLVSI	ALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSS	PLKFASASGA		
a628	TTGSAASGLVSI	ALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSS	PLKFANASGA		
	70	80	90	100	110	120

```

m628.pep  X
          |
a628      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

```

g629.seq
1  ATGACTGCca  aacCTTTTTC  CCTCAACCTG  GCcaaCCTCC  TGCTGCCggc
51  ggtatTGTTT  GCCGTCAGcc  tGtcggTCGG  cattgccgaT  TTCCGCTGGT
101 CGGATGTGTT  TTCGCTGTCC  GACAGCCAGC  AAGTGATGTT  CATCAGCCGC
151 CTGCCGCGCA  CGTTTGcgaT  TGTGTTGACG  GGCgcgtcga  tagcgGtggc
201 gGGAtgatt  atgcagATTC  TGATGCGCAA  CcgtTTGTGTC  GAGCCTtcta
251 tggcgGGTGC  GGGCCAAAGt  gcgGCTTTGG  GTttgcttct  gAtgtccctg
301 ctgctgcctg  CgcgGccgct  gccggtcaAA  ATGTCGGtag  Cgcgccgttgc
351 CGCGCTGATC  GGGATGTTGG  tctTtatgct  gctaataccgC  Cgcctgccac
401 cgacggcgca  gctgatgGTg  ccgCTGGTGG  Gg.ttatTTT  CGGCGGCGTG
451 GttgaGGCGG  TGGCGACGTT  TGTCGCGTAT  GAGTTTGAGA  TGCTGCAAAT
501 GTTGGGCGTG  TGGCAGCAGG  GCGACTTTTC  AAGCGTGCTG  CTGGGGCGGT
551 ACGAGCTGCT  TTGGATTACG  GCGGTTTGG  CCGTGTTTGC  CTACCTGATT
601 GCCGACCGGC  TGACGATTTT  GGGGCTGGGC  GAGACGGTGA  GCGTGAATTT
651 GGGTTTGAAC  CGGACGGCGG  TGTGTGGTC  GGGTTTGATT  ATTGTGGCAC
701 TGATTACATC  GCTGGTCATT  GTAACGGTCG  GCAATATTCC  GTTTATCGGG
751 CTGGTCGTGC  CGAATATCGT  CAGCCGCCTG  ATGGGCGACA  GGCTGCGCCA
801 AAGCTGCCT  GCGGTCGCCC  TCTTGGGCGC  GTCTTTGGTT  TTATTGTGCG
851 ACATTATCGG  ACGCATGATT  GTGTTTCCGT  TTGAAATTCC  GGTCTCCACG
901 GTTTTGGTG  TGTGGGTAC  GGCTTTGTTT  TTGTGGCTTT  TGTTGAGGAA
951 ACCCGCTAT  GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

```

g629.pep
1  MTAKPFSLNL  ANLLLPAVL  AVSLSVGIAD  FRWSDVFSLS  DSQQVMFISR
51  LPRTFAIVLT  GASIAVAGMI  MQILMRNRFV  EPSMAGAGQS  AALGLLLMSL
101 LLPAAPLPVK  MSVAAVAALI  GMLVFMLLIR  RLPPTAQLMV  PLVGXIFGGV

```

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151 VEAVATFVAY EFEMLQMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
 251 LVVPNIIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRMI VFPFEIPVST
 301 VFGVLGTALF LWLLLRKPAY AV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2023>:

m629.seq
 1 ATGACTGCCA AACCTTTTTC CCTCAACCTG ACCAACCTGC TGCTGCTGGC
 51 GGTGTTGTTT GCCGTGAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
 101 CTGATGTGTT TTTACTGTCC GACAGCCAGC AGGTCATGTT CATCAGCCGC
 151 CTGCCGCGCA CGTTTTCGAT TGTGCTGACG GCGCGCTCGA TGGCGGTGGC
 201 CGGCATGATT ATGCAGATT TGTGCGCAA CCGTTTGTG GAACCGTCGA
 251 TGGTGGGCGC AAGCCAAAGC GCGGCTTTAG GTTTGCTGCT GATGACCCTG
 301 CTGCTGCCCG CCGCGCCGCT GCCGGCGAAA ATGTCGGTTG CCGCCGTTGC
 351 CGCGCTGATC GGGATGTTGG TCTTTATGCT GCTGATCCGC CGCCTGCCGC
 401 CGACCGCGCA ACTGATGGTG CTTTGGTTCG GGATTATTTT CGGCGGTGTG
 451 ATTGAGGCGG TAGCCACCTT TATCGCGTAT GAAAACGAAA TGCTGCAAAT
 501 GCTCGGCGTG TGGCAGCAGG GCGATTTTTC GAGCGTGCTG CTGGGCGGGT
 551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CCGTGTGTTG CTATCTGATT
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAAACGGTAA GCGTGAATTT
 651 GGGTTTGAAC CGGACGCGG TGTTGTGGTC GGGTTTGATT ATTGTGGCTT
 701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
 751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATGGGCGACA GGTGCGCCA
 801 AAGCCTGCCT GCGGTGGCCT TGCTGGGCGC ATCTTTGGTG TTGCTGTGCG
 851 ACATTATCGG ACGCGTGATT GTGTTTCCGT TTGAAATTCC GGTCTCTACG
 901 GTTTTGGTG TATTGGGTAC GGCTTTGTTT TTGTGGCTTT TGTTGAGGAA
 951 ACCCGCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2024; ORF 629>:

m629.pep
 1 MTAKPFSNLN TNLLLLAVLF AVSLSVGVAD FRWSDVFSLS DSQQVMFISR
 51 LPRTFAIVLT GASMAVAGMI MQILMRNRFV EPSMVGASQS AALGLLMTL
 101 LLPAAPLPAK MSVAAVAALI GMLVFMLLIR RLPPTAQLMV PLVGIIFGGV
 151 IEAVATFIAY ENEMLQMLGV WQQGDFSSVL LGRYELLWIT GGLAVFAYLI
 201 ADRLTILGLG ETVSVNLGLN RTAVLWSGLI IVALITSLVI VTVGNIPFIG
 251 LVVPNIIVSRL MGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
 301 VFGVLGTALF LWLLLRKPAY AV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m629/g629 95.7% identity in 322 aa overlap

	10	20	30	40	50	60
m629.pep	MTAKPFSNLNLTNLLLLAVLFAVSLSVGVADFRWSDVFSLSDSQQVMFISR					
	: : : : : :					
g629	MTAKPFSNLNLANLLPAVLFAVSLSVGIADFRWSDVFSLSDSQQVMFISR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m629.pep	GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLLPAAPLPAKMSVAAVAALI					
	: : : : : :					
g629	GASIAVAGMIMQILMRNRFVEPSMAGAQSAALGLLMSLLLPAAPLPVKMSVAAVAALI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m629.pep	GMLVFMLLIRRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMLQMLGVWQQGDFSSVL					
	: : : : : :					
g629	GMLVFMLLIRRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEFEMLQMLGVWQQGDFSSVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m629.pep	LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
	: : : : : :					

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g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300
           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629.seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GGC CGCGTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTGTG GAGCCTTCTA
251 TGGCGGCGCG GGGTCAGAGT GCGGCTTTGG GTTGCTTCT GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTTTATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTTGGTCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTTG CTCGGACGGT
551 ATGAACTGTT GTGGGCAACG GGGATTTTGG CTTTGTGTTG CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACTT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCGCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GCGTGTGTTT TTATGGCTTT TGTTAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629.pep
1  MTAKPFSLNL TNLLLLAVLF AVSLSVGVD FRWSDVFSLS DSQQVMFISR
51  LPRTFAIVLT GASMAGMI MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLLR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMLQMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCIDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

m629/a629  95.7% identity in 322 aa overlap

           10      20      30      40      50      60
m629.pep  MTAKPFSLNLTNLLLLAVLFAVSLSVGVD FRWSDVFSLS DSQQVMFISR LPRTFAIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSLNLTNLLLLAVLFAVSLSVGVD FRWSDVFSLS DSQQVMFISR LPRTFAIVLT
           10      20      30      40      50      60
           70      80      90      100     110     120
m629.pep  GASMAGMIMQILMRNRFVEPSMVGASQAALGLLMTLLLPAAPLPKMSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAGMIMQILMRNRFVEPSMAGAGQAALGLLMSLLLPAAPLPVKMSVAAVAALI
           70      80      90      100     110     120
           130     140     150     160     170     180
m629.pep  GMLVFMLLRRLPPTAQLMVPLVGIIFGGVIEAVATFIAYENEMLQMLGVWQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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a629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAZENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180

           190      200      210      220      230      240
m629.pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629.pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629.pep  VFGVLGTALFLWLLLRKPAYAVX
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATT  TGGTGTGGCT  ggctttgttt  ccccccattgt  tttacggcat
51  gtacaacgtc  GCGGCACAGG  CATTCGGTGC  CTTAACGCCCC  GAtttgctgc
101 aacaaagcat  cgcccacgac  ggcaattacg  ccctcgccaa  cgctttgggc
151 atcaatatgt  cccccgaaGc  ggcggtgtTg  ggcaaaatgc  tgctcgGCGC
201 GATttacttc  ctgcccattt  acgcgaccgt  aTTTATTGTG  GGcggcttct
251 ggGaagtCTT  GTTCGCATCc  gtACGCAAAC  ACGAAATCAA  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCCGCCCA  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAA  AACTTCATGA  ACCCTGCGCT  GGCAGGCCGC
451 GCCTTCCTGT  TCTTCGCCTA  CCCCGCCAAC  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAC  CGCGCTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCC  GGCTCCATCG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTTT  GCCCGCATCG
701 CTtcttgGCG  CATTATTGcC  ggCGTGATGA  TCGGTatGat  tGcgatgTCT
751 tcgctgatta  acctcatCGg  ttctgacacc  aaagctatgt  ttgctatgca
801 cttggtacat  ggcacttggt  GGAaagatGa  ttAtcactca  ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF  PPMFYGMYNV  GAQAFGALTP  DLLQOSIAHD  GNYALANALG
51  INMSPEAGVL  GKMLFGAIYF  LPIYATVFIV  GGFWEVLFA  VRKHEINEGF
101 FVTSILFALI  VPPTLPLWQA  ALGISFGVVV  AKEVFGGTGK  NFMNPALAGR
151 AFLFFAYPAN  LSGDAVWTAV  DGYSGATALA  QWAAHGADGL  KNAVTGQTIT
201 WMDAFIGKLP  GSIgevSTLA  LLIGGAFIVF  ARIASWRIIA  GVMIGMIAMS
251 SLINFIGSDT  KAMFAMHLVH  GTWWKDDYHS  LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT  TGGTGTGGCT  GGCTTTGTTC  CCTGCCATGT  TCTACGGTAT
51  GTACAACGTC  GCGCGCGCAGG  CATTCGGTGC  GTTAACGCCCT  GATTtGCTGC
101 AACAAAACAT  CGCCAACGAC  TGGCATTACG  CCTTTGCCAA  CGCTTTGGGC
151 ATCAATATGT  CGTCTGAAGC  GGGCGTGTCT  GACAAAATGC  TGTtTGCGCG
201 GATTTACTTC  CTGCCGATTT  ACGCGACTGT  ATTTGTTGTG  GGCGGTTTCT
251 GGGAAAGTTT  GTTCGCCACC  GTGCGCAAAC  ACGAAATCAA  CGAAGGTTTC
301 TTCGTTACTT  CGATTCTGTT  TGCCTTAATC  GTTCCGCCCA  CGCTGCCGCT
351 GTGGCAGGCG  GCTTTGGGTA  TTTCTTTCGG  CGTTGTGGTT  GCGAAAGAAG
401 TATTCGGCGG  TACAGGTAAA  AACTTCATGA  ACCCTGCGCT  GGCAGGCCGT
451 GCTTTCCTGT  TCTTCGCCTA  CCCTGCCAAC  TTGAGCGGCG  ATGCGGTTTG
501 GACGGCGGTT  GACGGCTATT  CCGGCGCAAC  CGCACTGGCG  CAATGGGCGG
551 CACACGGTGC  AGACGGCCTG  AAAAACGCCG  TAACCGGTCA  AACCATCACT
601 TGGATGGACG  CGTTTATCGG  CAAACTGCCC  GGCTCCATTG  GCGAAGTCTC
651 CACTTTGGCA  CTCTTAATCG  GCGGCGCGTT  TATCGTGTTT  GCCCGCATCG
701 CTCTTTGGCG  CATTATTGCC  GCGGTGATGA  TCGGTATGAT  TGCGATGTCT
751 TCGCTGTTC  ACTTCATCGG  TTCGGACACC  AACGCTATGT  TTGCTATGCC

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801 TTGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
 851 TGGCGACCGA CCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
 901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
 951 GGCTTACCCC GAAGGCATGA TGTGCGCAT TCTGTTTGCC AACCTGTTTG
 1001 CCCCATTTC GACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep
 1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG
 51 INMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF
 101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
 151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
 251 SLNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
 301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
 351 ARSNG*

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALF	PAMFYGMYNV	GAQAFGALTP	DDLQONIAND	WHYAFANALG	INMSSEAGVS
g630	MMILVWLALF	PPMFYGMYNV	GAQAFGALTP	DDLQSIHNDG	NYALANALG	INMSPEAGVL
	10	20	30	40	50	60
m630.pep	DKMLFGAIYF	LPIYATVFVV	GGFWEVLFAT	VRKHEINEGF	FVTSILFALI	VPPTLPLWQA
g630	GKMLFGAIYF	LPIYATVFIV	GGFWEVLFAS	VRKHEINEGF	FVTSILFALI	VPPTLPLWQA
	70	80	90	100	110	120
m630.pep	ALGISFGVVV	AKEVFGGTG	KNFMNPALAG	RAFLFFAYPAN	LSGDAVWTAV	DGYSGATALA
g630	ALGISFGVVV	AKEVFGGTG	KNFMNPALAG	RAFLFFAYPAN	LSGDAVWTAV	DGYSGATALA
	130	140	150	160	170	180
m630.pep	QWAAHGADGL	KNAVGTQTIT	WMDAFIGKLP	GSIGEVSTLA	LLIGGAFIVF	ARIASWRIIA
g630	QWAAHGADGL	KNAVGTQTIT	WMDAFIGKLP	GSIGEVSTLA	LLIGGAFIVF	ARIASWRIIA
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSS	LNFIGSDTN	NAMFAMPWYW	HLVVGGFAIG	MLFMATDPVS	ASFTNVGKWW
g630	GVMIGMIAMSS	LNFIGSDTK	AMFAM----	HLVHGTWKK	DDYHSLYIK.	
	250	260	270	280		
m630.pep	YGALIGVMCV	LIRVVNPAYP	EGMMLAILFA	NLFAPIFDYF	VAQANIKRRK	ARSNGX
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq
 1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
 51 GTACAACGTC GGCGCACAGG CATTGCGTGC GTTAACGCCC GATTTGCTGC
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GGCAAAATGC TGTTCCGCGC
 201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT
 251 GGAAGTTTT GTTCGCCACC GTGCGCAAAC ATGAAATCAA CGAAGGTTTC
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
 351 GTGCGAGGCA GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
 401 TATTCGGCGG TACAGGTAAA AACTTCATGA ACCCTGCGCT GGCAGGCCGT
 451 GCCTTCCTGT TCTTCGCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG
 501 GACGGCGGTT GACGGCTATT CCGCGCAAC CGCGCTGGCG CAATGGGCGG
 551 CACACGGTGC AGACGGCTG AAAAACGCCA TAACCGGTCA AACCATCACT
 601 TGATGGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
 651 CACTTTGGCA CTCTTAATCG GCGGCGGCTT TATCGTGTTC GCCCGCATCG

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTTGGTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGTCGAT TCTGTTTGCC AACCTGTTTG
1001 CCCCATTTCG GACTATTTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG
1051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

```

a630.pep
1  MMILVWLALF PAMFYGMYNV GAQAFGALT PDLLQQSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQQNIANDWHYAFANALGINMSSEAGVS				
a630	MMILVWLALFPAMFYGMYNVGAQAFGALT	PDLLQQSIANDWHYALANALGINMSSEAGVL				
	10	20	30	40	50	60
m630.pep	DKMLFGAIYFLPIYATVFVVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
a630	GKMLFGAIYFLPIYATVFIVG	GFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA				
	70	80	90	100	110	120
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTA	VDGYSGATALA				
a630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTA	VDGYSGATALA				
	130	140	150	160	170	180
m630.pep	QWAAHGADGLKNAVTGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP	GSIGEVSTLALLIGGAFIVFARIASWRIIA				
	190	200	210	220	230	240
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVS	ASFTNVGKWW				
a630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVS	ASFTNVGKWW				
	250	260	270	280	290	300
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
a630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANL	FAPIFDYFVAQANIKRRKARSNGX				
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

g635.seq

```

1  ATGACCCGGC GACGGGTCGG CAAGCAAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTTGCGGT ATTCAGATA CACGATGACG
101 GGGATTTTCA ACTGCGCGAG CTGTTGCGAA GACAGGGCAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCCG CATATCCTCA AACGACGCGC
201 GCATCTGTTT CTTACCCAGT TTTTCCAACA CTTCTTCTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGAGGA

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301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCCGCCGC GCTTTCCAAC
351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AAACATCGGT
401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

q635 . pep

1 MTRRRVGKQN RIAIHSAYR KMVVFAVFQI HDDGDFQLRE LFERQGIAGR
51 LKTQIGHNAP HILKRRAHLF LTQFFQHFFF RQLLPVKIVQ KRRHRSRPAG
101 KIQILLYNIE IPPREPTLOF DESVNNRIIV KHRCSIOTIR QGSVPD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq

1	ATGACCCAGC	GACGGGTCGG	CAAGCAAAC	CGTATTGCCG	TCTATACCGC
51	GGAATACCGA	GAAATGTATCA	TCCTTGGCGT	ATTTCAGATA	CACGATTGACG
101	GGCATTTGCA	ACTGTGCAAG	CTGCTCGAA	GACAGGCGAT	AGCCTTTTCGC
151	TTCAAACCC	AAATCAGGCA	TAATGCGCCG	CATATCCCTA	AACGACGCGG
201	GCATCTGCTC	CTTATCCAGT	TTTTTAAAC	CGTCTCTTTC	CGTCAGCTTT
251	TGCGCGTAAA	AATTGTTCAA	AAGCGTCACC	ACCGAAGCCG	CCCCGCAAGGA
301	AAAATCCAAA	TCCTGCTTTA	CAATATTGAA	ATCGCGCTTT	TCTTTCCAAC
351	TCTGCAGCTT	GATTTTTCCT	GAAGCAACAG	GATTATATGT	GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635 . pep

1 MTQRRVKGQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAGR
51 FKTQIRHNAP HILKRRGHLI LIQFF*HVLQ RQLLPVKIVQ KRHHRSRPAG
101 KIOILLYNIE IAPFEPTLHF DESISNRIIV D*

m635/g635 80.0% identity in 130 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq

1	ATGACCCAGC	GACGGGTCGG	CAAGCAAAC	CGTATTGCCG	TCTATACCGC
51	GCAATACCGA	GAAATGATCA	TCCTTGCGGT	ATTTCAGATA	CACGATGACG
101	GGGATTTTGCA	ACTGTGCAAG	CTGCTCGAAA	GACAGGGCAT	AGCCTTTTCG
151	CTCAAAACCC	AAATCAGGCA	TGATGCGCCG	CATATCTCTA	AACAGCGCGC
201	GCATCTGCTC	CTTATCCAGC	TTTTTCAACA	CGTCCTCTTC	CGTCAGCTTT
251	TGCCCGTGAA	AATTGTTCAA	AAGCTGCGCC	ACCGAAGCCG	CCCCCGCAGGA
301	AAATCCCAA	TCCTGCTTTA	CAATATTGAA	ATCGCGCCTT	TCTTTCCAAC
351	TCTGCACATT	GATTTTTCCA	TAAGCAACAG	GATTATAGTG	GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pcp

1 MTQRRVGKQN RIAVYTAQYR EMII LAVFQI HDDGDLQLCK LLERQGI AFR
51 LKTQIRHDAP HILKRR A HLL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG
101 KIOILLYNIE IAPFEPTLHE DFSISNRIIV D*

m635/a635 95.4% identity in 131 aa overlap

10 20 30 40 50 60

1011

```

m635.pep    MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHNAP
a635        MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHDA
              10      20      30      40      50      60

              70      80      90      100     110     120
m635.pep    HILKRRGHLLLIQFFXHVLFRLQLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
a635        HILKRRGHLLLIQFFXHVLFRLQLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
              70      80      90      100     110     120

              130
m635.pep    DFSISNRRIIVDX
a635        DFSISNRRIIVDX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  ATGATTGGCG GACAGTTTAT CGTAGttgGc atTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 TTAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 TTTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 AAATATTGCC GCTGacttcg ctgtcgTTGG TGTACATATA GTGGACGGCG
251 AAACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 GCGCgcccgg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 CGCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 CAACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 GCTGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG GTACGGGCTA TGGTACGCC GCTCTTGTC CTTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTCAATCG TAATCGGTTT GTCGATATAA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCG
751 GCGCGCGGCA AAAATTTTCG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 CCGCTGCCGA TGCCGTCTGA AAAATGCTGC CGGCGGCAAG TATCAGCAGC
851 GCCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 CGTTCGGTAT GCGCGAACAA AATAAGCAT CATCAAAATG TGCCTGTTTT
951 TATAGCGAAA CCGCTGAAA CCGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDAI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 IGNAVPPFG NVVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 TRMKVYAERI IKNIVVFNQG ARGGFFEINT GIHCWQAHTG TGNGQVAERY
201 VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFGLIYA GSQFDRIARP
251 GAGKNFGKV VLRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 RSVWPNKIKH HSNVPVFIK PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTTGGC ATTATAGGCA AATACGCACT
51  TGCTGCCTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACGG
201 AAATATTGCC GCTGATTTTC CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 GCGCACCGGG TGCGTTCCAA ACGGTAACGC CGTTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 AGAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG GTACGGGCTA TGGTACGCC GCTCTGTGCG CTTTCGATGG
651 TTGCGGAACG GTCGGCAGGC CCTCAATCG TAATCGGTTT GTCAATGTGA
701 AGTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep

```

1  MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFGVVRAG
101 IGKNAVPPFG NVVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIVVFNOG ARGSF FEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVAFDGGCT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

```

m638/g638 88.2% identity in 254 aa overlap

m638.pep	10	20	30	40	50	60
	MIGEKFIVVG IIGKYALACL VDNVVVNIGI VDIVEHNALI AAADGDIVEY FEPLGKHQHI					
g638	MIGGQFIVVG IIVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH FEPFGKHQHI					
m638.pep	70	80	90	100	110	120
	AHIVAHGNIA ADFAVVG VHI VDGETQIAE AVVFGVVRAG IGKNAVPPFG NVVADDLRTG					
g638	AHIVAHGNIA ADFAVVG VHI VDGETQVAE AVVFIGVVRAG IGKNAVPPFG NVVADDLRTG					
m638.pep	130	140	150	160	170	180
	CVPNGNAVAA LVHAQSRVAD DFILAHHRIG RTMQIYADRI IQNIVVFNOG ARGSF FEINT					
g638	RVPNGNAIAA LIHAQGR IADDFILAHHRIG RTMKVYAERI IKNIVVFNOG ARGSG FFEINT					
m638.pep	190	200	210	220	230	240
	GIHCGQAHTG TGNGQVAERY VRRVYGYGTP APVAFDGGCT VGRPFNRNRF VNVKFGFIYA					
g638	GIHCWQAHTG TGNGQVAERY VRRVYGYGTP ALVPFDGCGT VGRPFNRNRF VDIKFGLIYA					
m638.pep	250	260				
	GSQFERIARP GAGKCGIPISIIGSX					
g638	GSQFDRIARP GAGKNFGKVVL RGNVDDGCRCLKNAAGGKYQHGLQPYTERGC VHSVPLF					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq

```

1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAAT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 ATTGAAAAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTACG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTTCCTTCA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 TTCCGGCGCG TGTACGGCTA TGGTACGCCC GTCCTGTCTC CCTTCGATGG
651 TTGCAGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep

```

1  MIGGQFIVVG IIVGKNALARF VDNVVVNIGI VDIVEHDALV AAADGDIVKH
51  FEPLGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRTG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIIIVFNQ ARGSF FEINT GIHCGQAHTG TGNGQVAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGFIYA GSQFERIARP

```

1013

251 GAGKCGIPIS IIDSW*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIVVGIIGKYALACLV	DNVNVNIGIVDIVEH	NALIAAADGDIVEY	FEPLGKHQHI		
a638	MIGGQFIVVGIVGKNALARF	VDNVVNIGIVDIVEH	DALVAAADGDIVKH	FEPLGKHQHI		

	70	80	90	100	110	120
m638.pep	AHIVAHGNIAADFAVVG	VHIVDGETQIAEAVV	FVGVVRAGIGKNA	VPPFGNVVADDL	RTG	
a638	AHIVAHGNIAADFAVVG	VHIVDGETQIAEAVV	FIGVVRAGIGKNA	VPPFGNIVADDL	RRAG	

	130	140	150	160	170	180
m638.pep	CVPNGNAVAALVHAQSR	VADDFILAHHRIGR	TMQIYADRIIQNI	VFNQGARGSF	FEINT	
a638	RVPNGNAIAALVHAQSR	VADDFILPHHRIGR	TMQIDADRIIQNI	IVFNQGARGSF	FEINT	

	190	200	210	220	230	240
m638.pep	GIHCGQAHTGTGNGQVA	ERYVRRVYGYGTPAP	VAFDGCGTVGRPF	NRNRFVNVKFG	FIYA	
a638	GIHCGQAHTGTGNGQVA	ERYVRRVYGYGTPAP	VSFDGCRTVGRPF	NRNRFVDVKFG	LIIYA	

	250	260
m638.pep	GSQFERIARPGAGKCGIP	SISIIGSX
a638	GSQFERIARPGAGKCGIP	SIDIISWX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTCCCAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACACA CCTATAAAA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAATGGGC GCAGGCGCAG TTTCCCGCCG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAG GCGGAAAAC GGTCTTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2046; ORF 639-1.ng>:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSVSGN ISVGNMGGYV LMFSERLKVF DNIavgSRD*
151 GIMLNyVNYS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201 AIEGTSLHDN SFINNGSQVK YVSTRELDWS EGGHGNYSWD NSPFDLNGDG
251 FGDSAYRPDG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLEAET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

1014

m639-1.seq

```

1   ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAAGTGGCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCTGG GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACACA CCTACAAAA CAACCGCTTC
301 AGCGATTTCG GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCG GATATTCACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCTTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTCT CGATTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC GCAGGCGCAG TTCCCGCCG TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAC CGCTGATGAA GCCTTATGCC CCCAAATTC AAACCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGCGAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

m639-1.pep

```

1   MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFNTS THNTYKNNRF
101 SDLRFVHYM YTNDSISGN ISVGNMGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNYYNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRENG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDELLKEVET RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

	10	20	30	40	50	60
g639-1.pep	MSLPAMDAGIYLEKAAPRALVEHNNIFDNSFGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
	10	20	30	40	50	60
g639-1.pep	NGVTVWNAPGAQVVGNDISKGRDGIFNTSTHNTYKNNRFSDLRFVHYMYTNDSEVSGN					
m639-1	NGVTVWNAPGAQVVGNDISKGRDGIFNTSTHNTYKNNRFSDLRFVHYMYTNDSEISGN					
	70	80	90	100	110	120
g639-1.pep	ISVGNMGYVLMFSERLKVFNDIAGVSRDXGIMLNYYNYS DIHDNIINKAGKCVFAYNAN					
m639-1	ISVGNMGYVLMFSERLKVFNDIAGVSRDQGIMLNYYNYS DIHDNIINKAGKCVFAYNAN					
	130	140	150	160	170	180
g639-1.pep	YDKLSANHFENCQIGMHFTAIEGTSLHDNSFINNGSQVKYVSTRFLDWSEGGHGNYSW					
m639-1	YDKLFANHFENCQIGIHFTAIEGTSLHDNSFINNESQVKYVSTRFLDWSEGGHGNYSW					
	190	200	210	220	230	240
g639-1.pep	NSPFDLNGDGFSDSAYRDPGIIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
m639-1	NSAFDLNGDGFSDSAYRPNGIIDQIIWRAPVSRLLMNSPAISIVKWAQAFPAVLPGGVV					
	250	260	270	280	290	300
g639-1.pep	DSKPLMKPYAPKIQTRYQAMKDELLKEAETRQSERGRAENGSLNX					
m639-1	DSKPLMKPYAPKIQTRYQAMKDELLKEVETRQSEWGRAENGSLNX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

a639-1.seq

```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AAACTGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGGCGTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGGA
201 CGCGCCCGGC GCGCAGGTGC TCGGCAACGA TATTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACACA CCTATAAAA CAACCGCTTC
301 AGCGATTGTC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACG ACAACATTAT
501 CAACAAAGCG GCGAAGTGC TTTTGCCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GGCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGGC CAGGCGCAA TTTCCCGCGC TTTGCGCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCCGTTA
951 TCAGGCGATG AAGGACGGGC TGCTCAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGGAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNMGMV LMFSERLKVF DNIAVGSRDQ
151 GIMLNYVNS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLDN SFINNESQVK YVSTRFLDWS EGGHGNYSW NSAFDLNGDG
251 FGDSAYRPN IIDIWRAPV SRLLMNSPA ISIVKWAQAF PAVLPGGVV
301 DSKPLMKPYA PKIOTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 .98.8% identity in 344 aa overlap

a639-1.pep	10	20	30	40	50	60
m639-1	10	20	30	40	50	60
a639-1.pep	70	80	90	100	110	120
m639-1	70	80	90	100	110	120
a639-1.pep	130	140	150	160	170	180
m639-1	130	140	150	160	170	180
a639-1.pep	190	200	210	220	230	240
m639-1	190	200	210	220	230	240
a639-1.pep	250	260	270	280	290	300
m639-1	250	260	270	280	290	300
a639-1.pep	310	320	330	340		
m639-1	310	320	330	340		

1016

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
  1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
 51  TATGTCCTGT TTTTCAATCC GGCGTATGTC TCGGTTTCGG GCGCGGATAA
101  CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151  GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201  TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251  GCgtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301  GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351  TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401  AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTCGA TAAGTTCATC
451  GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCGAGCGT
501  GCGCGCGGGC GACATCATCA GcggTGCGAC TgttaCACTG ATGGTGGTTA
551  ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601  GGTTCCGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651  CCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701  AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751  CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801  GGCCGGCGTG GCCGATCAGC CCGAACAGGG CGATCCTGAC GATACCTTTA
851  TTGATTTGTA TGTTCCTTGG GTCAGCCAGC CTTCCATCGG TAAAAGCCTG
901  CTGGGTGAGG ACGGCTGGGC GCATCTGCAA AAACGGCTGA AACCCTGGCA
951  GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAAGT TTCTTGTTT ACCATCCCTG
1151 AAGGCGTAGC GTTTGACGGT GCGGAGCCGT GGCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
  1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAF VFLTAALPAY
 51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101  AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151  DKYIGLNFIF NPPTPSVAPG DIISGATVTL MVVNDISIQR YKVIANQYRL
201  GSDKALQTAS ASDVREAAPA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251  LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301  LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGYVVRGGI FDRIEMIQGE
351  NSFRFTDAQH ERVELSAAD APRFKEVSF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
  1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
 51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101  CGGCGTTTTT TGCCGCTTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151  GCGGAGCGTC TGCTGATTTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201  TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251  GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301  GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351  GTTGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401  AACCATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
  1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
 51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGDE QLGLVYITTD
101  AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

```

          10      20      30      40      50      60
m640.pep  MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAAFVFLTAALPAYAERLPDFLAK
          |||||:|||||:|||||:|||||:|||||:|||||
g640      MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK
          10      20      30      40      50      60
          70      80      90     100     110     120

```

1017

```

m640.pep    IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
g640        IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAN
              70      80      90      100     110     120

              130     140
m640.pep    DGTIAGAKLVDHHEPIMLIGIPH
g640        DGTIAGAKLVDHHEPIMLIGIPQSRVDKFIDKYIGLNFINKPPTPSVAPGDIISGATVTL
              130     140     150     160     170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a640.seq (partial)
  1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
 51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101  CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151  GCGGAGCGTC TGCCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201  TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCCC
251  GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301  GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351  GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401  AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a640.pep (partial) Length: 143
  1  MIHIISILKS IGISGIVMSC FSIKRMSAFR ARITAFFAAF VFLTAALPAY
 51  AERLPDFLAK IQPSEIVPGA DRYSKPEGKPMVARVYKGDE QLGLVYITTD
101  AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

              10      20      30      40      50      60
m640.pep    MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFFVFLTAALPAYAERLPDFLAK
g640        MIHIISILKSIGISGIVMSCFSIKRMSAFRARITAFFAAFFVFLTAALPAYAERLPDFLAK
              10      20      30      40      50      60

              70      80      90      100     110     120
m640.pep    IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMVLAN
g640        IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVAVNTRGYSSKPIDTLMALAK
              70      80      90      100     110     120

              130     140
m640.pep    DGTIAGAKLVDHHEPIMLIGIPH
g640        DGTIAGAKLVDHHEPIMLIGIPH
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g642.seq
  1  ATGCGGTATC CGCCGCAATC GGCGGTTTTG CAGAATGCCG CGCGTTGCCT
 51  TTTGCGCCGC CCGAAATCTG CCTGCCGCCG TATTTGCCCG CTATCCGCAA
101  TATCGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151  GGTGCTTCG TGTTCTCCTT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201  TGCCGATGAA GACTTTTTGC AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251  TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgtCgc gGGCAACGGC
301  GGcaaagcgG ACatcggtTT Gcacggcgtc gagCAGGGtt tggTTTTTGT
351  CCAACTTAAT GCCTGCTTCT TTTTCTTCGG CGGTGGCGCG GACGAACCTG
401  TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451  GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501  CCTTCGCGCC CAAGAGTTT TGCAACATT GCGCGGCGGc gTAAGTGTAT
551  TCCGTGGCGa ggGTTTTGAc gatgTTCGCC TCCATCAATT GATGGGCGAc
601  ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCCG
651  AAACCTGATG GCGGCGTTGG ATTTGCGGCG GTTCGTAATC GACGAATCTG

```

1018

```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCGAGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAAGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTTCGAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC CgtttttgCG ctcctttgCG
1001 gcaacgaggA GGAAGTCGCT TTGCGAATG CCCTGCCAGT ATTTTCGCGC
1051 GttgACGTAA ATGGTTgtt cgtcggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAt cgCcgcgccg gaggtTtcgg gttcggtaAc gcccaaacgg
1151 cggctttcgc ctTTGAAAAT CATGTCCAAA CCTTGTGCGA CTTGCgcttc
1201 gccgccgaac tCTTGCAAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

```

g642.pep
  1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVVOQEGC
 51 GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVVFQLN ACFFFFGGGA DELVNVFGIK HIVRAFKNRE
151 GADIDGDIAG WVSFAKTLRA QEFLQHLRGG VSVFRGEGFD DVRLHQLMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFNH
251 AVRHADQLQA AADKDVLEA QTGSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFCGEGFAA DVCFGDEQV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLEFVGI FVAGLHFAFN RRAGGFGFGN AQTAFAFEN HVQTLCDLRF
401 AAELLQLQLH QRAFDAGTQR NGHVMPRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

```

m642.seq (partial)
  1 GCCTGCCGCC GTATTTGCCC GCTACCCGCA ATATCGGCAG TCCAATATAT
 51 CTTTGCGGAT GTCGTTGAGC AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACCTCA TGCCTGCTTC
301 TTTTCTCTCG GCGGTGGCGC GGACAACTG GTCGTAAAT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATACCG
401 ATATTGCCGG CCGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCCG CTCCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGCGGCGCG
601 GATTTCCGGG CGTTCGTAAT CGACGAATTT GATGTCGTTG CGGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATACGGC GGTGTCAGGC ATTTCCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTTGAAAA
1101 TCATCTCCAA ACCTTGCGCG ACTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

```

m642.pep (partial)
  1 ACRRICPLPA ISAVQYIFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
 51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFVGIKHV RAFKNREGAD VDSIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVFSQI FKDVFNHNAVR HADQLQAAAD KDVLEAQTG
251 SVALGEFHGG GCRHFGIDAV DGVTDGAQAF GCEGFAADV C FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFVV GLHFACNRRR
351 GGFGFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

1019

m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30	
				ACRRICPLPAISAVQYIFADV	VVQEGCGVFVRLYED		
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VVQEGCGVFVFLLYED					
	10	20	30	40	50	60	
m642.pep	40	50	60	70	80	90	
	KESGDDFADKDFLQGAGIGQGVFLQEAA	DVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH				
g642	KKSGDDFADEDFLQGAGVGQGVFLQEAA	DVFGQSVVAGNGGKADIGLHGVEQGLV	FVQLN				
	70	80	90	100	110	120	
m642.pep	100	110	120	130	140	150	
	ACFFFFGGGADKL	VVNFGIKHIVRAFKNREGADV	SDIAGGVSAFKTLRTQEF	LQHLRGG			
g642	ACFFFFGGGADEL	VVNFGIKHIVRAFKNREGADIDG	DIAGVWSAFKTLRAQEF	LQHLRGG			
	130	140	150	160	170	180	
m642.pep	160	170	180	190	200	210	
	VSVFRGEGFDDVRLHQLMGDGGNRRNGMAD	VAVKNLGNLMAAPDFAAFVIDE	FDVVADVS				
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMAD	VAVKDFGNLMAALDFAAFVIDES	DIVADIS				
	190	200	210	220	230	240	
m642.pep	220	230	240	250	260	270	
	FQIFKDVFNHNAVRHADQLQAAADK	DVLERAQTSVALGEFHHGGCRHFGID	AVDGVTDGA				
g642	VQVVKDVFNHNAVRHADQLQAAADK	DVLERAQTSVAPGEFHHGGCRHFGID	AVDGVTDGA				
	250	260	270	280	290	300	
m642.pep	280	290	300	310	320	330	
	QAFGCEGFAADV	CFGDEQQVDDFGEFAVFALFGGNEEE	VALRVALPVFRGVDV	NGLSVDI			
g642	QAFGCEGFAADV	CFGDEQQVDDFGEFAVFALFGGNEEE	VALRIALPVFRGVDV	NGLFVGI			
	310	320	330	340	350	360	
m642.pep	340	350	360	370	380	390	
	FVVGLHFACNRRAGGFG	FGNTQTAAALAFENHLQTLRDLRFIAELLQWLQHQ	RAFDAGTQR				
g642	FVAGLHFACNRRAGGFG	FGNAQTAAAFENHVQTLCDLRFIAELLQRLQHQ	RAFDAGTQR				
	370	380	390	400	410	420	
m642.pep	400						
	NGHAVMPRNP						
g642	NGHAVMPRNPX						
	430						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1  GCCTGCCGCC GTATTTGCCG GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGC GGAT GTCGTT CAGC AGGAAGGCTG CGGTGTCCTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTC CTGCAGGAAG CTGCGGATGT
201 CTTCCGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACTTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCGCGGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTCCG CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCCG
601 GATTTCCGGG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTTCCAGGTT TTCAAGGGTG TATTCCATAA TGCCGTGCGT CATGCCGATC

```

1020

```

701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCCGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGCG CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCGTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a642.pep Length: 407
  1 ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
 51 QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VDSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVVSFQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFV RLFHSGNRRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

              10      20      30      40      50      60
m642.pep      ACRRICPLPAISAVQYIFADV VVQQEGCGVFVFRLYEDKESGDDFADKDFLQGAGIGQGVF
              ||||| |||||:|||||
a642           ACRRICPLSAISAVQYVFADV VVQQEGCGVFVFRLYEDKESGDDFADKDFLQGAGIGQGVF
              10      20      30      40      50      60

              70      80      90      100     110     120
m642.pep      LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFFGGGADKL VVNFGIKHIV
              ||||| |||||:|||||
a642           LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFFGGGADKL VVNFGIKHIV
              70      80      90      100     110     120

              130     140     150     160     170     180
m642.pep      RAFKNREGADVDSDIAGGVSAFKTLRTQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
              ||||| |||||:|||||
a642           RAFKNREGADVDSDIAGGVSAFKTLRAQEF LQHLRGGVSVFRGEGFDDVRLHQLMGDGCN
              130     140     150     160     170     180

              190     200     210     220     230     240
m642.pep      RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADV SFQIFKDV FHNVRHADQLQAAAD
              ||||| |||||:|| |||||
a642           GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADV SFQVFKGV FHNVRHADQLQAAAD
              190     200     210     220     230     240

              250     260     270     280     290     300
m642.pep      KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAF GCEGFAADVC FGDEQQVDDF
              ||||| |||||:|||||
a642           KDVLERAQTG SVALGEFHHGGCRHFGIDAVDGVTDGAQAF GCEGFAADVC FGDEQQVDDF
              250     260     270     280     290     300

              310     320     330     340     350     360
m642.pep      GFAVFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFV VRLHFACNRRAGGFGFGNTQT
              ||||| |||||: |||||
a642           GFAVFALFGGNEEEVALRV ALPVFRGVDV NGLSVGIFV VRLHFSGNRRAGGFGFGNAXT
              310     320     330     340     350     360

              370     380     390     400
m642.pep      AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
              |||||: |||||
a642           AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP

```

1021

370 380 390 400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

g643.seq

```

1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAc
51  gttgtancGt TTGGcaATGt tGaaCAgggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagatGGTT TCTTCAGCCT GCCGGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAt
351 GACCTGCGCg aGTGtTGCGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTG a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

g643.pep

```

1   MVLPLMLLAT IRSATLTLXR LAMLN RVSPS TTRWMLAWSG EVSASPSAAL
51  ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVWVSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

m643.seq

```

1   ATGGTGTTCG CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTTCGG CTTCCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTGCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

m643.pep

```

1   MVLPLMLLAT IRSATLTL*R LAMLN RVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
g643	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR					
	10	20	30	40	50	60
m643.pep	70	80	90	100	110	120
	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
g643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFGGMTCA					
	70	80	90	100	110	120
m643.pep	130					
	SVAVWVSDGMAVCFSVX					
g643	SVAVWVSDGMAVCFSVX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

```

a643.seq
  1  ATGGTGTTC  CTTTGATGTT  GTTGGCGACA  ATCAGGTCGG  CTACACTGAC
 51  GTTGTAGCGT  TTGGCAATGT  TGAACAGGGT  GTCGCCTTCT  ACAACGCGGT
101  GGATGCTGGC  ATGGAGCGGG  GAGATTTCCG  CTTCCGCGTC  GGCAGCTTTG
151  GCTACGCGCG  TTTCCAAACG  TACCCGCGCT  TTGCCGTCGG  CGGCAACGGT
201  ATGTTGCGGA  GATGAGGAAA  TGTGTGTGTC  GGCAACTGTG  TCAGGCGTGC
251  CGATGACGGC  AGAGATGGTT  TCTTCAGCCT  GTCGGCGCAG  GTTGTTCGG
301  GCAACAAGCT  GCATGAGTTC  GTCTGCCGCC  TGCATGTCGT  TTTGGGGGAC
351  GATCTGCGCG  AGTGTGCGG  TTTGGGTTTC  AGACGGCATG  GCGGTCTGTT
401  TTTGCGTTTG  A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
  1  MVLPLMLLAT  IRSATLTL*R  LAMLN RVSPS  TTRWMLAWSG  EISASPSAAL
 51  ATRVSKRTRR  LPSAATVCCG  DEEMLCSATV  SGVPMTAEMV  SSACRRRLFR
101  ATSCMSSSAA  CMSFWGTICA  SVAVWVSDGM  AVCFSV*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
a643	MVLPLMLLATIRSATLTLXRLAMLN RVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR					
	10	20	30	40	50	60
m643.pep	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGTICA					
	70	80	90	100	110	120
m643.pep	LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAAACMSFWGTICA					
	70	80	90	100	110	120
	130					
m643.pep	SVAVWVSDGMVAVCFVSX					
a643	SVAVWVSDGMVAVCFVSX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
  1  ATGCCGTCTG  AAAGGccgc  GGATTGTTC  CCGGTGCACT  TTGTGGTAAA
 51  GTTTAGAAAA  TTAACCTCTA  ACTGTGGCAG  GCGGTTTGAC  CGGCCGCCGA
101  TTAATGGGAA  CCGACAGAGG  AAGCCGATGA  TACACACCGA  ACCGAGCGCG
151  CAGCCGTCAA  CCATGGACAC  GGCTGCTTTT  TTAAagcaca  tcgaatCCGC
201  ATTcCCCCGC  ATTTTTTCAG  ACGGCATCGA  CCTGATGCGA  TACCTGCCCG
251  AAGACAAATG  GCTTGCCCTG  AAGCAGGCGG  GTTGTCTGTT  GCCCTTCCTC
301  GACAAAAAAC  ACGGCGGGCG  CAAGGGCAGT  CAGTTTGAAA  TCCAAGAAGT
351  CCTAAGGATT  GCGGGGCATT  ACGGCGTGCC  CGTTACGCTG  CGTACCGGCA
401  TCGAAGGCGC  GCTGGTGTTC  CAGCCTCTGC  AAGagttcgg  cggcgaagcG
451  CAAGTCGCAC  AAGGTTTGGA  CATGATTTTC  AAagggcaaa  gccgcggttt
501  gggcgTtacc  gaaccgaAa  cctccggcgc  gGcgaTTGCA  CGCGAAAtgc
551  agtcctgcta  cgaatatacc  gacgaacaAA  CCATTTACGT  caaCGCCGCG
601  AAATACTGGC  AGGGCAATTC  GCAAAGCGAC  TTCTCctcg  ttgccgcaaa
651  agagcgcaaa  aacGGcaaac  tcgcaaaagt  CATCGACCTG  CTGCTCGTCC
701  CCAAAACATA  CATCCGCTGC  GAAACCCTCG  CATCCGAAGG  CCTGCGCGCC
751  GTCCGTTACG  CCGTCAACCG  CATCGATGCC  GAAATGCGTG  CAACCGCCGT
801  GATGAACTC  TCCCGGGGCG  ACGCTGCCGG  TTTGCGCGCG  TTCCAAAACA
851  TCTTTATCCG  CAGCCGCCTG  CAACTGATCG  GCATGACGCA  CGGCATTATG
901  GAATACATCC  TTGACAACCT  GAACCGATAT  GTCCGCAACG  ATATCAGATT
951  CCGCGATTAC  GAACGCCGCG  AAATCCAACG  CCGCCATCAG  GTTCCGAAA
1001  TCCTTTACCG  CTACGTCTGC  CATTCCGTTT  CGcccgtcgC  GCccgTCGCC
1051  CATCAATGTA  TGGAGGCGAA  catcgTCAAA  ACcctCGCCA  CGGAATACAC
1101  TTAcgcCGCC  GCGCAAAATG  TGCAAAAAC  CTGGGCGCG  AAGGGTTTG
1151  AACGCGGACA  CCCAGCCGGC  AATATCGCCA  TCGATATCCG  CCCCTTCACG
1201  ATTTTGTGAG  GCCCGAACGA  TATGCTTTAT  GCCGAAATTT  ACGACCAGTT
1251  CGTCCGCGCC  ACCGCCGAAG  AAAAGAAGC  AGGCATTAAAG  TTGGACAAAA
1301  accaaaCCCT  Gctcgacgcc  gtgCAaaccg  atGTCcgctt  tgCCGCGGTT
1351  GCCcgcGacT  ACGCTTTGCC  CGAAGACATC  CGCAGCTTCC  TGCAGGAACA
1401  CACCCTGACC  GACGCCTGCG  CCCTGCAAAA  AGTCTTCATC  GGCAAAATCA

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1023

1451 TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

1 MPSERPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA
51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMLR YLPEDKWLAL KQAGLLLPFL
101 DKKHGGRRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGGEA
151 QVAQGLDMIF KGESRRLGVT EPETSGAAIA REMQSCYEYI DEQTIYVNAA
201 KYWQGNQSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSRL QLIGMTHGIM
301 EYILDNLNRY VRNDIRFVDY ERREIQRHQQ VSEILYRYVC HSVSPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHPAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGIK LDKNQTL LDA VQTDVRF AAV
451 ARDYALPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQEEHEDTTA
501 FLLNDIRKDI LDCRYCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAA
51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TAAAGCACA TCGAATCCGC
201 ATTCCGCGCG ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCCTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TCCAAGAAGT
351 CcTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAGTCGCGC AAGGTTTGA GATGATTTTC AAAGGCGAGG GCGGCGGTTT
501 GGGTGTTACC GAACCCGAAA CCTCCGCGCG GCGGATTGCA CGCGAAATGC
551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTGCGCGGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAACTC TCCAGAGCG ACGCTGCCGG TTGCGCGCG TTCCAAACA
851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT
951 CGTCGATTAC GAACGCCGCG AAATCCGCG CCGCCATCAG GTTCCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCGCTT CGCCTGTGCG CCCCCTGCGC
1051 CATCAGCTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGTGCG AAGGGTTTTG
1151 AACCGCGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCCGCGCC ACGGCCGAAG AAAAAAGAG AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACCTTGCC TGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCTGACC GATGCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTGTCTTTC GTACAGGCGA AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG
1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

1 MPSERSADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMLR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRRKGS QFEIQEVLRI AGHYGVPVTL RTGIEGALVL QPLQEFGDEA
151 QVAQGLEMIF KEGGGGLGVT EPETSGAAIA REMQSYEYI DGQTIYVNAA
201 KYWQGNQSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSRL QLIGMTHGIM
301 EYILENLERV VRNDIKFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAKHEDTAA
501 FLLNDIRKDI LDCRYCG*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSERPADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					

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	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
g644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
g644	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMI FKGE GGLGVTEPETS GAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
g644	REMQSYEYIDQGTIYVNAAKYWQGSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
g644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
	310	320	330	340	350	360
m644.pep	370	380	390	400	410	420
g644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644.pep	430	440	450	460	470	480
g644	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLQEHTLT DACALQKVFI					
	430	440	450	460	470	480
m644.pep	490	500	510			
g644	GKIIARLFVQAKHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

a644.seq

```

1  ATGCCGTCCTG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCCGC
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCGAG ACGGTATCGA CCTGATGCGA TACCTGCCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTTGCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGGTTTGGG CATGGTTTTC AAAGGCGAGG GCGGCGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTTACGT CAACGCCGCG
601 AAATACTGGC AGGGCAATC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACGCCGCT
801 GATGAAATC TCCAGAGCG ACGCTGCCG TTTGCGCGCG TTCCAAAACA

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1025

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851 TCTTTATCCG CAGCCGCCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCGGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAACT CTTGGGCGCG AAGGGTTTGT
1151 AACGCGGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTTGAAG GCGCAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCCT GCTCGACCGC CTGCAAACCG ATGCCCGCTT TGCCGCCGTC
1351 GCGCCGCGACT ACACTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCGTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCTGTCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644.pep
1  MPSERSADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYTDGQTIYVNA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNI FIRSRL QLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEEAGMK LDKNQTLDDR LQTDARFAAV
451 ARDYTLPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

m644/a644 97.3% identity in 517 aa overlap

          10          20          30          40          50          60
m644.pep  MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
          |||
a644      MPSERSADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
          10          20          30          40          50          60

          70          80          90          100         110         120
m644.pep  LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
          |||
a644      LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
          70          80          90          100         110         120

          130         140         150         160         170         180
m644.pep  AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMI FKEGGGGLGVTEPETSGAAIA
          |||
a644      AGHYGVPVXXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKEGGGGLGVTEPETSGAAIA
          130         140         150         160         170         180

          190         200         210         220         230         240
m644.pep  REMQSYEYIDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC
          |||
a644      REMQSYEYTDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC
          190         200         210         220         230         240

          250         260         270         280         290         300
m644.pep  ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
          |||
a644      ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM
          250         260         270         280         290         300

          310         320         330         340         350         360
m644.pep  EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK
          ||
a644      EYTLENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK

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1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a 644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLDRQLTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
a 644	TAEKEAGMKLDKNQTLDRQLTDARFAAVARDYTLPEDIRSFLQEHTLTDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
a 644	GKIIARLFVVFQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645 . seq

```

1  ATGATGATGG TGTGCGGCTT GGGGATGTCG ATGCCGGTTT CGATGATGGT
51  GGAACAGAGC AACACATTGA ATCTTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCACGC AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata cCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CCGCTTCGCG CACGCTGCCT TCGCTGAACG GTTGACAAA GGTTTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TCGCGGAAT CCGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGTCGCACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTCGGGGCG AGTACGGCGA
701 CCTGTTTGCC GCCATCACC GCCACAAACG CGGCGCGAAG GCGGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTAATCA CGGcggcgat ggcgcgcgc TGGTCTTCGG
851 TTCTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645 . pep

```

1  MMVLALGMS MPVSMVEQS NTLNLCKKS RMTSSSRSR SCPCATPIRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPRLS SRNTASRLP SLNGLTKVFT
101 ARRLGAVVI SEKSRRPSSA MLRVRGIVA VMVRMSTLAR RRLSCSFCRT
151 PKRCSSTIN PKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLLK
201 RERLATFTGK SAKRSKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPTH SRSIGFACVK SLITAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645 . seq

```

1  ATGATGATGG TGTGCGGCTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCGTCTCTCC GCGTTTGAGT TCGCGCAACA
251 CCGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CCGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCGAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAAGCGT GGTCGGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCATCACC GCCACAAACG CGGCGCGCAG GCGGACTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTAATCA CGGCGCGGAT GCGGCGGCC TGGTCTTCGG

```

1027

851 TTTCTTCGTA G

This corresponds to the amino acid sequence <SEQ ID 2078; ORF 645>:

m645.pep

```

1  MMMVLALGIS IPVSMMEQSN TLNRCCKKS RMTCSSRSR SCPCATPMRA
51  SGRVSSRSR IFSIVSTSLC RKNTCPPLS SRNTASRTL SLKGLTKVLT
101 ARRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF*RT
151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCF CCSTKSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMMEQSN	TLNRCCKKS	RMTCSSRSR	SCPCATPMRA	SGRVSSRSR	
g645	MMMVLALGMSMPVSMMEQSN	TLNRCCKKS	RMTCSSRSR	SCPCATPIRA	SGRVSSRSR	
	10	20	30	40	50	60
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPL	SSRNTASRTLPSL	KGLTKVLTARRRL	GAVVISEKSR	SPSNA	
g645	IFSIVSTSLCRKNTCPPL	SSRNTASRTLPSL	NGLTKVFTARRRL	GAVVISEKSR	RPSSA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRIST	LARRRLSCSFXRTP	PKRCSSSIITKPKFL	NLMSSCTSLCVP	ITI	
g645	MLRVRGIGVAVMVRIST	LARRRLSCSFCRTP	PKRCSSSIINKPKFL	NLMSSCTNLCVP	ITI	
	130	140	150	160	170	180
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALL	LLKRERLATFTGK	SAKRSKFCACCSTK	SVVGASTATCL	PPIT	
g645	STVPSAMPSSVALVALL	LLKRERLATFTGK	SAKRSKFCACCSTR	SVVGASTATCL	PPIT	
	190	200	210	220	230	240
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPT	SPHTRRSIGFACVK	SLITAAMAAWSSV	SSX		
g645	ATNAARRATSVLPKPT	SPHTRRSIGFACVK	SLITAAMAAWSSV	SSX		
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq

```

1  ATGATGATGG TGTTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC
201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA
251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG
301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT
501 TATGTCGTCC TGCACCAAGT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAGC GGTGCGCAAA
651 ATTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTCGGTGCG AGTACGGCAA
701 CTTGTTTGCC ACCATTACC GCCACAAACG CGGCGCGCAG GGCGACTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGCGCGCAT GCGGCTGCG TGGTCTTCGC
851 TTTCTTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2080; ORF 645.a>:

a645.pep

```

1  MMMVLALGMS IPVSMMEQSN TLNRCCKKS RMTCSSRSR SCPCATPMRA

```

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```

51  SGSRVSSRSR MFSMVSTSLC RKNTCPPLRL SRNTASRTLPL SLNGLTKVLT
101 ARRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLLK
201 RERLATFTGK SAKRSKFCF CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

              10      20      30      40      50      60
m645.pep      MMMVLALGISIPVSMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           MMMVLALGMSIPVSMVEQSNTLNRCCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
              10      20      30      40      50      60

              70      80      90     100     110     120
m645.pep      IFSIVSTSLCRKNTCPPLRLSSRNTASRTLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
              :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           MFSMVSTSLCRKNTCPPLRLSSRNTASRTLPSLNGLTKVLTARRRLGAVVISEKSRSPSSA
              70      80      90     100     110     120

              130     140     150     160     170     180
m645.pep      ILKVRGIGVAVMVRISTLARRRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           ILKVRGIGVAVMVRMSTLARRRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
              130     140     150     160     170     180

              190     200     210     220     230     240
m645.pep      STVPSAMPSSAALVALLLLKRELRATFTGKSAKRSKFCACCSTKSVVGASTATCLPPIT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           STVPSAMPSSAALVALLLLKRELRATFTGKSAKRSKFCACCSTRSVVGASTATCLPPIT
              190     200     210     220     230     240

              250     260     270     280
m645.pep      ATNAARRATSVLPKPTSPHTRRSIGFACVKS LITAAMAAWSSVSSX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a645           ATNAARRATSVLPKPTSPHTRRSIGFACVKS LITAAMAAWSSVSSX
              250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2082; ORF 647.ng>:

```

g647.pep
1  MQRLAADGIQ IFFVGVGDQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51 GFKGTVGQTE RGTVAVADTV FRQIVGVVDD TDAERTAVHS RGTRGFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGCACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence <SEQ ID 2084; ORF 647>:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

	10	20	30	40	50	60
m647 . pep	MQRLAADGIQIFFVSV	DGQFALRINGLVKER	ARTVF	FFGKVCRCFEQVILY	GFGKT	VVGQTE
g647	MQRLAADGIQIFFVSV	DGQFALRINGLVKER	AARSVFFGKVCRCFEQVILY	GFGKT	VVGQTE	
	10	20	30	40	50	60
	70	80	90	100		
m647 . pep	RGTVA	ADTVFRQII	SIVNHADAERTAAH	SRGRGFYRISLIIX		
g647	RGTVA	ADTVFRQIVGVDDTDAERTAVHSRGRGFYRISLIIX				
	70	80	90	100		

```
a647.seq
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTTTG TAGGTGTCGA
51 TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CAGTCACGCA
101 CCGTATCTCT TGGCAAGGTT TGCCGATGCT TTGACGAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGTGTAGC
201 GGACACCGTT TTTCGCCAAA TAATACGCAT AGTTGATCAC GCCGATACCG
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA
```

```
a647.pcp .
      1  VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY
     51  GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAAHS GGTRGFYRIS
    101  LII*
```

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSV	DGQFALRINGLVKERARTVF	FGKVCRCFEQVILYGFKGT	VQGTE		
a647	VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVF	FGKVCRCFEQVILYGFKGT	VQGTE			
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTVA	AVADTVFRQIISIVNHADAERTAAHSRGTRGFYRISLIIX				
a647	RGAVAVADTVFRQII	RIVDHADTERTAASGGTRGFYRISLIIX				
	70	80	90	100		

```
g948.seq
1  ATGAACAGGC  GCAACGCGCG  GATCGAACGG  GCTGTGCGTA  TTGCAGTGTAT
51  CGACGTTTTG  AATGTAGATG  GCCCCGGTCC  CGGCACGCTC  TCGCATCAGC
101 TGGGAAAACA  GGTGCGCAGC  CGGAATGATA  CGCTTGCCTA  TGTTCGGGTC
151 TTGCTCGTAT  TTCGTATAGA  GCCGCTCAA  TTCGTCTTGG  TCGGCAAAAA
201 ACGCTTCGTA  CAACCCCGAA  ACCTCGTTGG  CGGAAAAACG  CGTAATGTGT
251 CGCCCTTAA  TACGGCGGGT  GTACAGCAG  CGGTTGATT  GCACGCATCA
301 ATCAAGCTGG  CGGATACGGT  TGTCTTCCAC  GCCCGGGTTG  TTTTCAACA
351 CCAGCAGGCT  TTCGGCTTCA  ATATGCCACA  AGGGGTAGAA  CRAAGTTGCC
401 GCGCGCGCG  GCACGCCATC  TTGCGAATC  GATTTGACC  CGCCTGAAA
451 CATCTTAAAG  AAGGGAATGC  AGCCGGATG  CCGGGCTTCA  CGCCCCCGGA
501 TTTCGCTGTC  CAGCCCGCGG  ATACGTCGG  CATGTATGCC  GATGCCCGCG
551 CGTTGGGAAA  CGTATTTCAC  AATCGCGCTG  GTAGTGGCAT  TGATGGAATC
601 CAAACTATCG  TCGATTTCAA  TCAGCACACA  GCTTGA
```

q648 . pep

1030

```

1  MNRRNARIER AVRIAVIDVL NVDPAPGPTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAALNQAG VQQAVDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV E QGCRAAAHAT LRTFRDRRLK
151 HKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1  ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC ACCCGGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCGCC TTGCGAACAG GATTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCCGGA
501 TTTCGCTGTC CAAACGCGG ATACGTCGG CATTGATGCC GATGCCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1  MNRRDARIER AVRIAVIDVL NVDPAPSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVDLHAV
101 IKLTDTVVFH TAVVFQHQQA FGFDMPPQGV E QGCRAAAHAA LRTGFDRRLK
151 HKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDPAPSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
g648	MNRRNARIERAVRIAVIDVLNVDPAPGPTLLHQRGKQVGS	RNDTLAYVRVLLVFRIEPLK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQA	VDLHAVIKLTDTVVFHTAVVFQHQQA				
g648	FVLVGKKRFVQPRNLVGRKQRNVAALNQAGVQQA	VDLHAIKLTADTVVFHAPVVFQHQQA				
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPPQGVQGCRAAAHAALRTGFDRLKHFK	EGNAAGMPRFAAPDFAVQTADTSGIDA				
g648	FGFNMPPQGVQGCRAAAHATLRTFRDRRLKHL	KEGNAAGMPGFTAPDFAVQPADTSGIDA				
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHN	NRAGSGIDGIQTIVAFNQHTAX				
g648	DARALGNVFHN	NRAGSGIDGIQTIVAFNQHTAX				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1  ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTTG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCGGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTGATTT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTTCCAC GCGCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCGCG GCACGCCACC TTGCGAACAG GATTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTGCTTCG CCGCCCCGGA

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1031

501 TTTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCCGA
 551 CGCTGGGAAA CGTATTTTAC AATCGCGCTG GTAGTGGCGT TGATGGAATC
 601 CAGGCTGTCG TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648.pep
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV
 101 IKLTDTVVFH APVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCRLK
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI
 201 QAVVAFDQYA A*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
a648	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648						
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPQGV E QGCRAAAHAALRTGFDRRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
a648						
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIIVAFNQHTAX					
a648	: : : :					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGA CTGGTAT CAACAACTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCACCG ACATACCAA CATATCAGCA
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCTT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649.pep
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECRKYLER
 51 RAAWYRSQGN VQELRENNKA RKAFTLPYA EQKIQCAAAY EAFDDFDGGR
 101 FRR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649.seq
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGA CTGGTAT CGACAACTGC
 51 CGCTGCCGGT ACGTCAGAAC CCGCCACCG CGATACCAA CATATCCGCA
 101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
 151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGC GCGAAAA
 201 CAAAAAGGCG CGCAAAGCAT TCCGTCCCTT GCCTTATGCG GAACAGAAAA
 251 TCCAATGCCG GCGGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649.pep

1032

```

1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCRAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649           MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
g649           VQELRENKKARKAFRTLPHYAEQKIQCRAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTTGTC TGCAATATTG GGACTGGTAT CGACAACCTGC
51 CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
151 CGTGCCGCGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA
201 CAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51 RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCRAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649           MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCRAAYEAFDDFDGGSFRRX
              |||||
a649           VQELRENKKARKAFRSLPYKEQKTQCRAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCGAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCGCAG CTATTTCGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGAAAA AAACaccgGT TTACGacggc aggcacGacg TTtacgcaGc
501 taccgatgcc gcactCAACT AtctGcAATA TCTCTAtgga CTGTTCCGCG
551 ACTGGCCGCT CGCCTTTGCC GCCTACAACT GGGGTGAAGG CAACGTCGGA
601 CGCGCCGTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

```

1033

```

751 ATAGACAACA AACCCCTATTT TCAGGCAGTC GAACCGGGGCC GTCCGCTCGA
801 caacGAagcC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTGAATCC TGCATTCAAC GTCCCCGcgt tcatCCCCAA AAAcaaacgc
901 aaacTGCTGC TTCCTGTGCG GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCTGTTT CATCGACATC GACAATACGC CcgacacCTa ccgttccaaT
1201 ATGCcggcag gcaCGGTGAA CGTCAGCATt gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatcccct tgtccgcaTt accgaaccog ccctTGCGAC
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pep
1 MSKLTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGRFMGEV NPFLVRRHES KFIASRSYFD RVVNRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAVNRARDQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYPQAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVSI ARIQPAQAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCGGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGGC CTTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAAACA
151 TATTTCGAAT CCGGCAGCCT GTGGGCGGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACACG
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGCTACCGG CAGGCATTAC
451 GGCCTGGAAG AAAACACCGT TTACGACGGC AGGCACGACG TTTACGCCCG
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT TGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTGGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCCCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTC AAC GTCCCCGCGT TTATCCCCAA AAGCAAACGC
901 AAATGCTGCT TTCCTGTGCG GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTCa ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1 MSKLTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGRFMGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWEGENVG
201 RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAT PQSFGMNISD
251 IDNKPYPQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVGI ARIRPAAQAQT ADITVAPLPQ KTVRTXTRSP CPYCRTPCPD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLKTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	10	20	30	40	50	60
	MSKLKTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWDE					
m650.pep	70	80	90	100	110	120
	LRQGFRMGVEVNPVLRHESKFIAHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
g650	70	80	90	100	110	120
	LRQGFRMGVEVNPVLRHESKFIAHSYFDRVVRNRSRPYMYHIANEVKKRNMPAEAAALLP					
m650.pep	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	130	140	150	160	170	180
	FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEGNVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
g650	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEGNVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
m650.pep	250	260	270	280	290	300
	PQSFGMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	250	260	270	280	290	300
	PQSFGMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVSIDIIDNTPDTPYRSNMPAGTVNVGIARIQPAQAQT					
g650	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLHTASESVSIDIIDNTPDTPYRSNMPAGTVNVSIARIQPAQAQT					
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCPYCRTPCDSRSATSNRKTDRAVX					
g650	430	440	450	460		
	ADITVAPLPQETVRTGTTRSPCPHYRTRPCDSRSATSNRKTDCHAVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

a650.seq

1	ATGTCCAAAC	TCAAAACCAT	CGCCCTGACC	GCGTCAGGTC	TGTCCGTTTG
51	TCCGGGTTTC	CTATACGCCC	AAAACACCTC	ATCACACCAA	ATCGGTTTGG
101	CGATTATGCG	CTTAACTCT	TCAATACTCG	ACCTGCCACC	GACAAAACAA
151	TATTTCCAAT	CCGGCAGCCT	GTGGAGCGAG	CTGCGCCAAG	GCTTCCGGAT
201	GGGCGAAGTC	AATCCCGAAC	TGGTACGCCG	CCACGAAAGC	AAATTCATCG
251	CAAGCCACAG	CTATTTCAAC	AGGGTCATCA	ACCGGAGTAG	ACCCTATATG
301	TACCATATCG	CCAACGAAGT	CAAAAAACGC	AATATGCCCG	CCGAAGCCGC
351	CCTGCTTCCC	TTCATCGAAA	GCGCGTTCGT	CACCAAAGCC	AAATCACACG
401	TCGGCGCATC	GGCCTGTGG	CAGTTCATGC	CCGTACCCGG	CAGGCATTAC
451	GGCCTGGAAA	AAACACCGGT	TTACGACGGC	AGGCACGACA	TTTACGCCGC
501	CACCGATGCC	GCACTCAACT	ATCTGCAATA	CCTCTATGGA	CTGTTCCGGC
551	ACTGGCCGCT	CGCCTTTGCC	GCCTACAAC	GGGGTGAAGG	CAACGTCGGA
601	CGCGCCATCA	ACCGCGCCCG	CGCCCAAGGG	CTCGAACC	CCTACGAAAA
651	CCTGCGTATG	CCCAACGAAA	CGCGCAACTA	TGTTCCCAAG	CTGCTCGCCG
701	TGCGCAACAT	CATTGCCGCC	CCCCAATCTT	TCGGCATGAA	TATCAGCGAC
751	ATAGACAACA	AACCGTATTT	TCAGGCAGTC	GAACCGGACC	GTCCGCTCGA
801	CAACGAAGCC	ATCGCCCGGC	TTGCCGGCAT	CACGCAAAGC	GAGCTGCTCG
851	CCCTAAACCC	CGCATTCAAC	GTCCCCGCGT	TCATCCCCAA	AAGCAAACGC

```
901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTGTGTCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTGTGCA ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGCGAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTTGCCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCGGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```
a650.pep
  1  MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
 51  YFQSGSLWSE LRQGRMGEV NPVLRRHES KFIASHSYFN RVINRSRPFY
101  YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151  GLEKTPVYDG RHDIIYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201  RAINRARAQG LEPTYENLRM PNETRNYVPK LLAVRNIIAA PQSFGMNISD
251  IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301  KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351  DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTNYSRN
401  MPAGTVNVGI ARIRPAAQQT ADITVAPLPQ KTVRTXTRSP CPYCRCTPCPD
451  SRSATSNRKT DRHAV*

m650/a650  99.1% identity in 465 aa overlap

          10          20          30          40          50          60
m650.pep  MSKLKTIALTASGLSVCPGFLYAQTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
          |||||||
a650       MSKLKTIALTASGLSVCPGFLYAQTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
          10          20          30          40          50          60

          70          80          90          100         110         120
m650.pep  LRQGRMGEVNPVLRRHESKFIASHSYFNRVINRSRPFYHIANEVKKRNMPAEAALLP
          |||||||
a650       LRQGRMGEVNPVLRRHESKFIASHSYFNRVINRSRPFYHIANEVKKRNMPAEAALLP
          70          80          90          100         110         120

          130         140         150         160         170         180
m650.pep  FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
          |||||||
a650       FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG
          130         140         150         160         170         180

          190         200         210         220         230         240
m650.pep  LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAT
          |||||||
a650       LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIIAA
          190         200         210         220         230         240

          250         260         270         280         290         300
m650.pep  PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
          |||||||
a650       PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPFIPKSKR
          250         260         270         280         290         300

          310         320         330         340         350         360
m650.pep  KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          |||||||
a650       KLLLPVASVQTFQSNYLNAA PDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          310         320         330         340         350         360

          370         380         390         400         410         420
m650.pep  NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQQT
          |||||||
a650       NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTNYSNMPAGTVNVGIARIRPAAQQT
```

	370	380	390	400	410	420
	430	440	450	460		
m650.pep	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD
a650	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTD
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

g652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51 GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGGCG GGCGAAGACG TATTATTCCG ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATACTTGGAA GGCTTGGTTA
551 ACGAATTCCC GATTATTTCC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATTG GGCAAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCTGTA CCAATCCGAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGc cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCAccgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTA AAAAccgG TTCTTTGAGC
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCcgccctACT ACCCCGGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

g652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMNVINGG EHANN SLNIQ EFMIMPV GAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKD GK YHLEA EGRSY TNAEFAEYLE GLVNEFP IIS IEDGMDENDW
201 EGWLLTEKL GK KVLV GDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAYNQ LLRIEEELAE AAYYPGKA AF YQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

m652.seq

```

1 ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTGG GTGCGAATGC
51 GACTTTGGCG GTTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAGGCG GGCGAAGACG TATTATTCCG ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGAA GGCTTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAACTG GGCGGTAGAG TTCAATTGGT
651 TTGGCGACGAC TTGTTCTGTA CCAATCCAAA AATCTTGCC GAAGGCATCG
701 AAAAAGGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

m652.pep

```

1 MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51 VPMNVINGG EHANN SLNIQ EFMIMPV GAK SFREALRCGA EIFHALKKLC

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1037

```

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
201 EGWKKLLTEKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEEELAE AADYPSKAAF YQLGK*

```

m652/g652 98.2% identity in 335 aa overlap

```

          10      20      30      40      50      60
m652.pep  MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
          |||
g652      MIELDGTENKGNLGNATLAVSMAVARAAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG
          10      20      30      40      50      60

          70      80      90     100     110     120
m652.pep  EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPPTTVGDEGGFAPNLN
          |||
g652      EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPPTTVGDEGGFAPNLN
          70      80      90     100     110     120

          130     140     150     160     170     180
m652.pep  SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
          |||
g652      SHKEALQLMVEAAEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE
          130     140     150     160     170     180

          190     200     210     220     230     240
m652.pep  GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA
          |||
g652      GLVNEFPPIISIEDGMDENDWEGWKLLTEKLGKKVQLVGDDLFVTNPKILAEGIEKGVANA
          190     200     210     220     230     240

          250     260     270     280     290     300
m652.pep  LLVKVNQIGTILSETLKAVDLAKRNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
          |||
g652      LLVKVNQIGTILSETLKAVDLAKCNRYASVMSHRSGETEDSTIADLAVATNCMQIKTGSLS
          250     260     270     280     290     300

          310     320     330
m652.pep  RSDRMAKYNQLLRIEEELAEAAADYPSKAAFYQLGKX
          |||
g652      RSDRMAKYNQLLRIEEELAEAAAYYPGKAAFYQLGKX
          310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

```

a652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGCGGCG CAGGCCCGAT GTCCTGCCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGGC GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAAGCG GCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTGCCGA ATATCTGGAA GGCTTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GGATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAACTG GCGGCGAAAG TCCAACCTCGT
651 TGGCGACGAC CTCTTCGTTA CCAACCCGAA AATCCTTGCC GAAGGCATTG
701 AAAAAGGCGT GGCAAACGCA CTATTGGTCA AAGTCAACCA AATCGGTACT
751 TTGAGTGAAG CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCGACC GCATGGCGAA ATACAACCAA CTGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCCGCGGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

```

a652.pep
1  MIELDGTENK GN LGANATLA VSM AVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC

```

1038

151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFPPIIS IEDGMDENDW
 201 EGWKLLETKL GQKVLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT
 251 LSETLKAVDL AKRNRYSVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
 301 RSDRMAKYNQ LLRIEELAE AADYPSKAAF YQLGK*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
a652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
a652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFPPIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFPPIISIEDGMDENDWEGWKLLETKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTSLSETLKAVDLAKRNRYSVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNQIGTSLSETLKAVDLAKRNRYSVMSHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAKYNQLLRIEELAEAADYPSKAAFYQLGKX					
a652	RSDRMAKYNQLLRIEELAEAADYPSKAAFYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCGGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGCTATTCC GGCAAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAA GCAATTTGGG TCGGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTTGCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGCGC AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCCGC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TGCGGTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGTAAAGG CTCCCGACC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAA ACCACTTGGG AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGTTAA CGAATTCCCG ATTATTTCCA
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GCGGACGACT TGTTCTGAAC
951 CAATCCGAAA ATTCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 TCGCATCTGG CAAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGCGGAAACC GAAGACGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCGGT TCTTTAGGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCTACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGAGPM SLPVPMNVI
151 NGGEHANNS L NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAAEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKQVL V GDDLFTVNP K ILAEGIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKCNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

m652-1.seq

```

1  ATGAGCGCAA TCCTTGATAT TTTGCGCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTATTTCG GGCAAGGGCG TATTGAAGGC
201 GGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACGC GCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGGCG AGGCCGATG TCCCTGCCG TACCGATGAT GAACGTCATC
451 AACGGCGGGC AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GGGCAGAAAT CTTTCCGCGA AGCGTTGCGC TGCAGGTGCG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCG ACAGCAAAGG CTTCCTGACC
601 ACAGTCGGCG ACGAAGGCGG TTTGCGCCCG AACCTGAACA GCCACAAAGA
651 AGCCTGCGAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGGCAAA T ACCACTTGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAAATGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGCGAGAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CCGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCGAGCAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGA NA TLAVSMAVAR AAAEDSGLPL YRYLGAGPM SLPVPMNVI
151 NGGEHANNS L NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKQVL V GDDLFTVNP K ILAEGIEKGV ANALLVKVNQ IGTLSSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLLES GVMGRAAVPSGASTGQKEALELRDGDKSRY S					
	10	20	30	40	50	60
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGA NATLAVSMAVAR					
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGAGGPM SLPVPMNVI NGGEHANNS LNIQEFMIMPV GAKSFREALR					
g652-1	AAAEDSGLPLYRYLGAGGPM SLPVPMNVI NGGEHANNS LNIQEFMIMPV GAKSFREALR					
	130	140	150	160	170	180

1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKL	CDSKGFPTTV	GDDEGGFAP	NLNSHKEAL	QLMVEATEA	AAGYKAGEDV
g652-1	CGAEIFHALKKL	CDSKGFPTTV	GDDEGGFAP	NLNSHKEAL	QLMVEAAEA	AAGYKAGEDV
	190	200	210	220	230	240
	250	260	270	280	290	300
m652-1	LDCASSEFYK	DGKYHLEA	EGRSYTNA	EFAEYLEGL	VNEFPIIS	IEDGMDEND
g652-1	LDCASSEFYK	DGKYHLEA	EGRSYTNA	EFAEYLEGL	VNEFPIIS	IEDGMDEND
	250	260	270	280	290	300
	310	320	330	340	350	360
m652-1	EKLGGVRVQ	LVGDDLFV	TNPKILA	EGIEKGVAN	ALLVKVNQ	IGTLSETLK
g652-1	EKLGGKVVQ	LVGDDLFV	TNPKILA	EGIEKGVAN	ALLVKVNQ	IGTLSETLK
	310	320	330	340	350	360
	370	380	390	400	410	420
m652-1	SVMSHRSGE	TEDSTIAD	LAVATNCM	QIKTGSLS	RSRDRMAK	YNQLLRIEE
g652-1	SVMSHRSGE	TEDSTIAD	LAVATNCM	QIKTGSLS	RSRDRMAK	YNQLLRIEE
	370	380	390	400	410	420
	429					
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCCG GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGCG GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGTTATTCG GGCAAGGGCG TATTGAAGGC
201 GGTGCAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTGTCACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCGAAAAT CTTTCCGCGA AGCGTTGCCG TCGGGTGGCG
551 AAATTTTCCA CGCCTTGAAA AACTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAAGCGG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGCAAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDEVLES G VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRY S GKVLKAVEH VNNQIAQAL I GIDANEQSYI DQIMIELDGT
101 ENKGNLGAN A TLAVSMAVAR AAAEDSGLPL YRYLGAGGPM SLPVPMNVI
151 NGGEHANN S NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCD SKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLF A LDCASSEFYK
251 DGKYHLEAE G RSYTNAEFAE YLEGLVNEFP IISIEDGMD E NDWEGWKLLT
301 EKLGGKVVQ L GDDLFVTNPK ILAEGIEKGV ANALLVKVNQ IGTLS ETLKA
351 VDLAKRNRY A SVMSHRSGE T EDSTIADLAV ATNCMQIKTG SLSRSRDMAK
401 YNQLLRIEE E LAEAADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRYs
a652-1      MSAIVDIFAREILDSRGNPTVECDVLLESGVMGRAAVPSGASTGQKEALELRDGDKSRYs
              10      20      30      40      50      60

m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

m652-1      AAAEDSGPLPYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGPLPYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

m652-1      CGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

m652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLRSRDRMAKYNQLLRIEEELAEAADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLRSRDRMAKYNQLLRIEEELAEAADYPSK
              370     380     390     400     410     420

m652-1      AAFYQLGKX
a652-1      AAFYQLGKX
              429

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcgg aaccgatgcg gAtgccggag gtaAcgtaCG GTTTTCCGG
51 ATCGTTCGGG ATGGCGTTT TGTgacggT GATGTGCGCt ttgcccAAG
101 CGGCTtcggc ggcctttgcCg gtgaTTTCA TCGGTTGCAG GtcgacgaGG
151 AAaacgTGGC TTTCGGTGCG GCCGGAaAcg atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTTCACTTGT FTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGGCG
301 ATAACGTgca tcaACGGAcc gCCTTGCAGG CTTGGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTTGTGG GTGGTAGTGg ttACgaaGtc GCAGAtggc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtcgcGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRMPE VTYGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51 KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGKMEEFSAF SWVLSRHKIT PPRGPRRVLW VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51 ATCGTTCGGA ATGGCGTTT TGTGACGGT GATGTGCGCT TTGCCCAAAG
101 CGGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```

151 AAAACGTGGC TTTCCGGTGGC GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAAG CTTGGGAAGA TGGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m553.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m553/g653 96.9% identity in 163 aa overlap

```

              10      20      30      40      50      60
m553.pep    MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
g653        MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m553.pep    MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
g653        MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
              70      80      90      100     110     120

              130     140     150     160
m553.pep    SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX
              |||||
g653        SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATSPAX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGGCGCGCG AACCAGTGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCGGG ATGGCGTTTT TGTTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTTGCCG GTAATTTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTCCGGTGGC GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAACTC GGGTTGCAAT GCTTCTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAAG CTTGGGAAGA TGGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRRLW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m553/a653 100.0% identity in 163 aa overlap

```

              10      20      30      40      50      60
m553.pep    MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              |||||
a653        MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
              10      20      30      40      50      60

              70      80      90      100     110     120
m553.pep    MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              |||||
a653        MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
              70      80      90      100     110     120

              130     140     150     160
m553.pep    SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX
              |||||
a653        SWVLSRHKITPPRGPRRLWVVVVTKSQNGTGLGYSPPATRPAX

```

1043

130 140 150 160

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2123>:

```
g656.seq
1   ATGCCGCGTT TCTCCGGTTC GATTTCCTCG ATGATTTCCTCA TCGCGCGGAC
51  TTTtggcGCG CCGGAGAGTG TGCcggcagg gAAGGTGGCG GCGAGGATGT
101 CCATATTGGT AACGCCCTCT TTCAAACAGc ctTCGACGTT GGAAACGATG
151 TGCATCACAT GGGAGTATTT TTCAATCACC ATTTTGTCTCG TGACTTTGAC
201 TTCGCCTGTT TTGCTGATGC GTCCGACATC GTTGCGCCCC AAATCGATAA
251 GCATAACGTG TTCGGCgatt TCTTTGGCGT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGT'TTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACGTcat CGCGTTCGCG GCGGACGAGG ATTTCGGGCG
401 AGGAACCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2124; ORF 656.ng>:

```
g656.pep
1   MPRFSGSISS MISIARTFGA PESVPAGKVA ARMSILVTPS FKQPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSIISITCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRT R ISGEEPTMWK SPKS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2125>:

```
m656.seq
1   ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTCA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTCGACGTT GGAAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTCTCG TAACTTTGAC
201 TTCGCCGTT TACTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTTCG
301 TTGGCAAGGT CTTCGGCGGG GGT'TTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATAACGTCGT TCGGTCGCG TCGGACGAGG ATTTCGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2126; ORF 656>:

```
m656.pep
1   MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPS FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT ITSLSRRT R ISGEEPTMWK SPKS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m656/g656 91.0% identity in 144 aa overlap

```

10      20      30      40      50      60
m656.pep  MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPSFRRPSTLETMCITWEYFSIT
          |||: || ||||:||||:||||:||||:||||:||||:||||:||||:||||:
g656      MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPSFKQPSTLETMCITWEYFSIT
          10      20      30      40      50      60

70      80      90      100     110     120
m656.pep  ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT
          ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
g656      ILSVTLTSPVLLMRPTSLRPKSIISITCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT
          70      80      90      100     110     120

130      140
m656.pep  ITSLSRRTTRISGEEPTMWKSPKSX
          :|| ||||:||||:||||:||||:||||:||||:||||:||||:||||:
g656      MTSSRSRRTTRISGEEPTMWKSPKSX
          130      140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCGCGTT TGCTCGGTTC GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TTTGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGTT GGAACGATG
151 TGCATTACAT GGGAGTATTT TTCAATCACC ATTTTGTGCG TAACTTTGAC
201 TTCGCCGGTT TTACTGATGC GGCCGACGTC GTTGCCTCCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTGGCGGG GGTTTTGCCG CGCAGGCGCG TGCCGGCGAT
351 GGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTCGGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRTR ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ITSLRSRTRISGEEPTMWKSPKSX					
a656	MTSSRSRTRISGEEPTMWKSPKSX					
	130	140				
m656.pep	ITSLRSRTRISGEEPTMWKSPKSX					
a656	MTSSRSRTRISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCGCGT TGGACGAATT
201 GCCAAAATGC GCGGCGGTTa cgACCGAATT TGAAAcgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATAACACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTGAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCCGTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattc ATCGTCcccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GCGCAACgc tTGGCGGACG AATTGGATTA TGTCGGCgta
751 TTGGCGGTAG AAATGTTTGT TGTGCGCGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGCAGA CCAGTTCCAA CAGCAGGTAC GCATTATGTG CAACcTGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTGGGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGGCCGAA TGCACACCTG CACCTATACG GAAAAAAAAC CGCACAGAAA
1051 GGTGCGAAAA TGGGACACTT TaccgTTTTG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657.ppep

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	CTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYVGV

1046

251 LAVEMFVVG D THELLVNETA PRTHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSPC CMANILGDVW QEDGGEPDWL PLQSRPNAHL HLYGKKTAQK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657.seq
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGGCA TCCTCGGCGG
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTTGCC
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCCTAG CGGCGATTGT
 301 GTGGCGATTG CACAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAGC
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA
 401 CTGAAGCAAG CGCGCAATTT TTGCCCAGCA TCCTGAAAAC GGCTACGTTG
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACTCAA
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
 551 TGGATTGCGC CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC
 601 AACGTGCAAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT
 651 GGCTTATTCC ATCGTCCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG
 701 CGCGGCAGAT GCGCGAACGC TTGGCGGACG AATTGGATTA TGTCGGCGTA
 751 TTGGCGGTAG AAATGTTTGT TGTCGGTGAC ACGCATGAAT TGGTCGTCAA
 801 GCAAAATCGCC CCGCGCCCGC ACAATTCCGG ACACCATACG ATAGATGCCT
 851 GCGCAGCAGA CCAGTTCCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG
 901 CCTGCCGATA CCAAATTACT GAGTTCTTGC TGTATGGCAA ATATTTTGGG
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTTA ACCACCGATT CGGACACCGC
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657.pep
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAPAAEFA
 51 DRHLCAPFND QAALDELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVCKA EDITEASAQF LPGILKTATL
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADEL DYVGV
 251 LAVEMFVVG D THELVVNEIA PRPHNSGHHT IDACAADQFQ QQVRIMCNLP
 301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSHPNAL HLYGKKTAHK
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAM	LGILGGGQLGR	MFTVAAKTM	GYKVTVLDP	DPDAPAAEF	ADRHLCAPFND
	::	:				
g657	MNTPPILPPAM	LGILGGGQLGR	MFVAAKTM	GYKVTVLDP	DPNAPAAEF	ADRHLCAPFDD
	10	20	30	40	50	60
	70	80	90	100	110	120
m657.pep	QAALDELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
	:					
g657	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	70	80	90	100	110	120
	130	140	150	160	170	180
m657.pep	TAPYQVCKA	EDITEASAQF	LPGLIKTATL	GYDGKGQIR	VKTLDLKA	FAEHGGVDCVL
g657	TAPYQAVCKA	EDITEASAQF	LPGLIKTATL	GYDGKGQIR	VKTLDLKA	FAEHGGVDCVL
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657.pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657.pep	LADEL DYVGV LAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657.pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNHLHLHYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNHLHLHYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657.pep	TTDSDTAFQEAKKLHQSLX					
g657	TTDSDTAFQEAKKLHQSLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

```

a657.seq
1  ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTCGGCA TTCTTGGCGG
51  CGGACAATTA GGCAGAAATG TTACTGTTGC TGCCAAAACC ATGGGCTACA
101 AAGTAACCGT ACTCGATCCC AACCCGAATG CGCCGGCAGC GGAATTTGCC
151 GACCGCCATT TGTGTGCGCC GTTTGACAAC CAAACCGCTT TGGAAGAATT
201 GGCAAAATGT GCGGCTGTTA CGACCGAGTT CGAAAACGTC AATGCCGATG
251 CGATGCGTTT TCTCGCCAAA CATAACCAATG TTTCCCCCAG CGGCGACTGC
301 GTTGCCATCG CGCAAAACCG CATTACAGGAA AAGGCATGGA TACGCAAAGC
351 AGGCCTGCAA ACCGCGCCGT ATCAAGCAAT TTGCAAAGCC GAAGACATCA
401 CTGAAGAAAG CATACAATTT CTGCCCGGCA TCCTGAAAAC CGCTACATTG
451 GGCTATGACG GCAAAGGCCA AATCCGCGTC AAAACGGTGG ATGAACTCAA
501 AGCCGCGTTT GCCGAACACC GCGGCGTGGA TTGCGTTTTG GAAAAAATGG
551 TGGACTTGCG CGGCGAAATT TCCGTTATCG TATGCCGTCT GAACAATGAC
601 AACGTGCAAA CTTTCGATCC TGCCGAAAAC ATTCACGAAA ACGGTATCCT
651 CGCCTACTCC ATCGTCCCAG CCCGACTGAG TGCCGACATT CAGCAACAGG
701 CGCGACAAAT GGCGCAGCGT TTGGCCGATG AATTGAACTA CGTCGGCGTA
751 TTGGCGGTAG AAATGTTTGT TGTCGGCGAC ACGCATGAAT TGGTCGTCAA
801 CGAAATCGCG CCGCGTCCG ACATATCCGG CCACCATACC GTCGACGCCT
851 GCGCGGCAGA CCAATTCCAG CAACAGGTCC GCCTGATGTG CAACCTGCCA
901 CCTGTGACA CCAATTGCT GAGTTCCTGC TGTATGGCGA ATATTTTGGG
951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGTTT CCCCTGCAAA
1001 GCGGCGCGGA CGCGCACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA
1051 GGGCGGAAAA TGGGACACTT TACCATTTTA AGCACCGATT CGGACACCGC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

```

a657.pep
1  MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP NPNAPAAEFA
51  DRHLCAPFDN QTALEELAKC AAVTTEFENV NADAMRFLAK HTNVSPSGDC
101 VAIAQNRIQE KAWIRKAGLQ TAPYQAICKA EDITEESIQF LPGILKTATL
151 GYDGGQIRV KTVDELKAAF AEHRGVDCVL EKMVDLRGEI SVIVCRLNND
201 NVQTFDPAEN IHENGILAYS IVPARLSADI QQARQMAQR LADELNYVGV
251 LAVEMFVVGDTHELVVNEIA PRPHNSGHHT VDACAADQFQ QQVRLMCNLP
301 PADTKLLSSC CMANILGDVW QEDGGEPDWF PLQSRPDAHL HLYGKKTAKH
351 GRKMGHFTIL STDSDTAFQE AKKLHQSL*

```

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657.pep	MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPDPDAPAAEFADRHLCAFPND					

1048

```

a657      |||||
          MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAFPDN
          10      20      30      40      50      60

          70      80      90      100     110     120
m657.pep  QAALDELAkCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
          |||||
a657      QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
          70      80      90      100     110     120

          130     140     150     160     170     180
m657.pep  TAPYQVVCKAEDITEASAQFLPGILKTATLGyDGKGQIRVKTLDelKAAFAEHGGVDCVL
          |||||
a657      TAPYQAICKAEDITEESIQLPGILKTATLGyDGKGQIRVKTVDelKAAFAEHRGVDCVL
          130     140     150     160     170     180

          190     200     210     220     230     240
m657.pep  EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR
          |||||
a657      EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQARQMAQR
          190     200     210     220     230     240

          250     260     270     280     290     300
m657.pep  LADELdYVGVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
          |||||
a657      LADELNYVGVLAVEMFVVGDTHELVVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP
          250     260     270     280     290     300

          310     320     330     340     350     360
m657.pep  PADTKLLSSCCMANILGDVWQEDGGEpDWLPLQSHPNahlhLYGKkTAHKGRKMghFTVL
          |||||
a657      PADTKLLSSCCMANILGDVWQEDGGEpDWFLQSRPDAHLhLYGKkTAHKGRKMghFTIL
          310     320     330     340     350     360

          370     379
m657.pep  TTDSDTAFQEAKKLHQSLX
          :|||
a657      STDSDTAFQEAKKLHQSLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2135>:

```

g658.seq
1  ATGGTGGCCG GAATTGTGCG TGC GCGGGGC GGTTCATTG ACGAGCAATT
51 CATGTGTGTC GCCGACAACA AACATTCTA CCGCCAAtac GCCGACATAA
101 TCCAATTTCGT CCGCCAagcG TTGCGCCGTC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGCCGCGcgg gGACGATGga atAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCGGGG TCGAAGGTTT GCACGTTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAT CTCGCCGCGC AAGTCCACCA TTTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCGTCCA
351 ACGTTTTGAC GCGGATTGTA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTGCAAAACC GCCTGATACG GCGCGTTTG CAAGCCTGCT TTGCGTATCC
501 ACGCTTTTTT CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gtTTTCAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCGGTC GTCAAACGGC GCGCACAAAT GGCGGTCGGC AAATTCGCC
701 GCCGGCGCAT TCGGGTCGGG ATCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTAGCGGCA ACGGCAACA TTctgcctAA

```

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

```

g658.pep
1  MVAGIVRARG GFIDEQFMCV ADNKHfYRQY ADIIQfVRQA LRRLPRLLLL
51 VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

```

1049

```

101 NAIHAAVFGK RGFEFVQRFADLTFVAVQA RSRFQDAGQK LRACFSNVFG
151 LANRLIRRGL QACFAYPRFF LNAVLCNGHA VAAGGNVGM LQRAHRVIGD
201 VFKFGRNRRR FCQFVQRPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG
251 FSGNGKHSAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

```

m658.seq
1 ATGGTGTCCG GAATTGTGCG GCGCGGGGCG GATTTCGTTG ACGACCAATT
51 CATGCGTGTC ACCGACAACA AACATTTCTA CCGCCAATAC GCCGACATAA
101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT
201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTTGTC ATTGTTCAAA
251 CGGCATAACG TTACGGAAAT TCACTGCGC AAATCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA
351 ATGTTTTTAC GCGGATTTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC
451 CTTACAAACC ACTTGATACG GCGCGGTTT CAATCCCGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA
551 GGGGAAACAT TGGTATGTTT TGCCAAAAAG CGCATCGCAT CGGCATTGAC
601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAAG
651 CAGCTTGGTC GTTAAACGGC GCGCACAAAT GCGGTCGGC AAATTCTGCT
701 GCCGGCGCGT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT
751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

```

m658.pep
1 MVSGIVRARG DFVDDQFMRV TDNKHFYRQY ADIIQFVRQA LRHLPRLLLH
51 VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG NFTAQIHHFFQ
101 NAIHAAVFGK RGFEFIQCFY ADLTFVAVQA RSRFQDAGQK LRACFSDVFS
151 LTNHLIRRGL QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID
201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENGYFVAHG
251 FGGNGKHSAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

```

m658.pep      10      20      30      40      50      60
MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTQSRGDDG
||:||||| |:|:| |:|||||:|||||:|||||:|||||:|||||
g658          10      20      30      40      50      60
MVAGIVRARGGFIDEQFMCVADNKHFYRQYADIIQFVRQALRRLPRLLLHVGTQPRGDDG

m658.pep      70      80      90      100     110     120
ISQDAVFVDVFGRVESLHVIVQTAYDYG NFTAQIHHFFQNAIHAAVFGKRGFEFIQCFY
|||||:| |:|:| |:|||||:|||||:|||||:|||||:|||||
g658          70      80      90      100     110     120
ISQDAVFVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHAAVFGKRGFEFVQRFD

m658.pep      130     140     150     160     170     180
ADLTFVAVQA RSRFQDAGQKLRACFSDVFS LTNHLIRRGLQSRFAYPCLF LNAVLCNRHT
|||||:| |:|:| |:|||||:|||||:|||||:|||||:|||||
g658          130     140     150     160     170     180
ADLTFVAVQA RSRFQDAGQKLRACFSNVFGLANRLIRRGLQACFAYPRFF LNAVLCNGHA

m658.pep      190     200     210     220     230     240
IAARGNIGMF CQKAHRIGIDVFKFSGHRRR AFCQFVQSSLVVKRRAQMAVGKFCCRRVRIG
:| |:|:| |:|:| |:|||||:|||||:|||||:|||||:|||||
g658          190     200     210     220     230     240
VAAGGNVGM LQRAHRVIGIDVFKFGRNRRR AFCQFVQRPVVKRRAQMAVGKFRRRRIRVG

m658.pep      250     260
VENGYFVAHGFGGNGKHSAX

```

1:050

```

          :|||||||:|||||||
g658      IENGYFVAHGFSGNGKHSAX
          250      260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2139>:

```

a658.seq
1  ATGGTGGCCG GAATTGTGCG GACGCGGCGC GATTTCGTTG ACGACCAATT
51  CATGCGTGTG GCCGACAACA AACATTCTA CCGCCAATAC GCCGACGTAG
101 TTCAATTCAT CGGCCAAACG CTGCGCCATT TGTCGCGCCT GTTGCTGAAT
151 GTCGGCACTC AGTCGGGCTG GGACGATGGA GTAGGCGAGG ATACCGTTTT
201 CGTGAATGTT TTCGGCAGGA TCGAAAGTTT GCACGTGTG ATTGTTTCAGA
251 CGGCATACGA TAACGGAAAT TTCGCGCGC AAGTCCACCA TTTTTCCAA
301 AACGCAATCC ACGCGCGGT GTTCGGCAA CGCGCTTTG AGTTCATCCA
351 CCGTTTTGAC GCGGATTTGG CCTTGCCTG CATAGCCCAA TGTAGCGGTT
401 TTCAGGATGC CGGCAGAAA TTGTATGCTT TCTTCAGTGA TGTCTTCGGC
451 TTTGCAAATT GCTTGATACG GCGCGTTT CAGGCTGCT TTGCGTATCC
501 ATGCCTTTTC CTGAATGCGG TTTTGCGCGA TGGCAACGCA GTCGCCGCTG
551 GGGGAAACAT TGGTATGTTT GGCGAGAAA CGCATCGCAT CGGCATTGAC
601 GTTTTCGAAC TCGGTCGTAA CAGCCGCACA TTTTGCCAAT TCTTCAAAG
651 CGGTTTGGTT GTCAAACGGC GCACACAAAT GGCGGTCGGC AAATCCGCT
701 GCCGGCGCAT TCGGTTGGG ATCGAGTACG GTTACTTTGT AGCCCATGGT
751 TTTGGCAGCA ACAGTAAACA TTCTGCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2140; ORF 658.a>:

```

a658.pep
1  MVAGIVRTRR DFVDDQFMRV ADNKHFYRQY ADVVQFIGQT LRHLSRLLLN
51  VGTQSGWDDG VGEDTVFVNV FGRIESLHV IVQTAYDNGN FAAQVHHFFQ
101 NAIHAAVFGK RGFEFIHRFD ADLAFAVIAQ CSGFQDAGQK LYAFFSDVFG
151 FANCLIRRLG QACFAYPCLF LNAVLRDUNA VAAGGNIGMF GEKTHRIGID
201 VFELGRNSRT FCQFFQSGLV VKRRTQMAVG KFCRRRIRVG IEYGYFVAHG
251 FGSNSKHSAX*

```

m658/a658 75.3% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFMRVTDNKHFYRQYADIIQFVRQALRHLPRLLLHVGTQSRGDDG					
a658	MVAGIVRTRRDFVDDQFMRVADNKHFYRQYADVQFIGQTLRHLSRLLLNVTQSGWDDG					
	10	20	30	40	50	60
m658.pep	ISQDAVFVDVFGRVESLHVIVIVQTAYDYGNTAQIHFFQNAIHAAVFGKRGFEFIQCFY					
a658	VGEDTVFVNVFGRIESLHVIVIVQTAYDNGNFAAQVHHFFQNAIHAAVFGKRGFEFIHRFD					
	70	80	90	100	110	120
m658.pep	ADLTFVAVQSRFQDAGQKLRACFSDVFSLTNHLIRRLGQSRFAYPCLFLNAVLCNRHT					
a658	ADLAFAVIAQCSGFQDAGQKLYAFFSDVFGFANCLIRRLGQACFAYPCLFLNAVLRDUNA					
	130	140	150	160	170	180
m658.pep	IAARGNIGMFCQKAHRIGIDVFKFSGHRRACQFVQSSLVVKRRAQMAVGKFCRRVRIG					
a658	VAAGGNIGMFGEKTHRIGIDVFELGRNSRTFCQFFQSGLVVKRRTQMAVGKFCRRRIRVG					
	190	200	210	220	230	240
m658.pep	VENGYFVAHGFSGNGKHSAX					
a658	IEYGYFVAHGFSGNSKHSAX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2141>:

1051

```

g661.seq
  1  ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51  GGCGGGCATT GCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG
101  CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT
151  ACCGGA AAAA CCctgcaccg cagtgaTTt gccgatgaag gCGGCATCGT
201  TGCCGTGCAG ATTGCCGGCA GCGACCcga acaGATGGCG Gatgcggcgc
251  gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC
301  cccgccaaga AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA
351  CGAGccgctg gttgcCgcca tTTtgaggc ggtggtcAAG GCGGCGGgcg
401  TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac
451  ctgcCcgccg tcgcaaaaat cgccgaagat tgcggcattg ccgccCttgc
501  cgttccacgg gcgCGCgcgC ACGCAAATGT ACAAAGGCGA GGCgcGTTAC
551  Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCGG cctGggtCAA
601  CGGCGACATC actTCgccc AAAAAGCCGC CGccgTCCTC AAACAAACCG
651  CCGCCGACGG CATCATGATA GGGCGCGCGC CGCAAGGCAG GCCGTGGTTT
701  TTCCGCGATT TGAAGCATTA TGCCGAACAC GCGGTTTTAC CGCCTGCCTT
751  GAGTTTGGCA GAATGCAGAG CCGCCATTTT GAACCACATC CGCGCCATGC
801  ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA
851  GGCTGGTACA TCGGCGAAAT GCCCGACGGC GAACAGGCGC GCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

```

g661.pep
  1  MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN
 51  TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC
101  PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDDQDN
151  LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ
201  RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFPRFEAL CRTRRFTACL
251  EFGRMQSRHF EPHPRHARVL WXDRCARHRT QTHRLVHRRN ARRRTGAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

```

m661.seq
  1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
 51  GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101  CAGTTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151  ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201  TGCCGTGCAG ATTGCCGGA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251  GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301  CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351  CGAGCCGCTG GTTGCCGCCA TTTTGGAAGC CGTCGTCCGT GCGGCAGGCG
401  TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451  CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATCG CCGCCCTTGC
501  CGTCC.AC GG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC
551  GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601  CGGCGACATT ACTTCGCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651  CCGCCGACGG CATTATGATA GGGCGCGCGC CGCAAGGCAG GCCGTGGTTC
701  TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT
751  GAGTTTGGCA GAATGCGCCG CCGCTATTTT GAACCACATC CGCGCCATAC
801  ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851  GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

```

m661.pep
  1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
 51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101  PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDDHQN
151  LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ
201  RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFAACL
251  EFGRMRRRYF EPHPRHTRVL RRHRCARHRT QTHRLVHRRN ARRRTDTS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNP	IAPMAGITDK	PFRRLCRDF	GAGWAVCEML	TSDPTLRN	TRKTLHRSDF
g661	MHIGGYFIDNP	IAPMAGIADK	PFRRLCRAFG	AGWAVCEML	ASDPTLRNTG	KTLHRSDF
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQI	AGSDPQOMAD	AARYNVSLGA	QLIDINMGCP	AKKVCNVQAG	SALMQNEPL
g661	ADEGGIVAVQI	AGSDPEQMA	DARYNVGLGA	QVIDINMGCP	AKKVCNVQAG	SALMQDEPL
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRA	AGVPVTLKTR	LGWHDDHQNL	PVIAKIAEDC	GIAALAVXR	THAYANVQRR
g661	VAAILEAVVKA	AGVPVTLKTR	LGWHDDQNL	PAVAKIAEDC	GIAALAVPR	ARAHANVQRR
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQ	MPSEHPGLQ	RRHYFAAKSP	SRPQTNR	RRRHDRARR	ARQAVVLP
g661	GALRTHRRDQ	KPSEHPGLQ	RRHHFAAKS	RRRPQTN	RRRRHHR	ARRARQAV
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAAC	LEFGRMRRR	YFEPHPRH	TRVLR	RRHRC	CAHRTQTH
g661	CRTRRFTAC	LEFGRMQSR	HFEPHPRH	ARVLWXD	RRCAHRTQ	THRLVHRR
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1   ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATTT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCGGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCACGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGCTCG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACCTCGCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGCGC CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCACATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGCG GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1   MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMG
101 PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDDHQ
151 LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201 RRHYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPFRFETL RRTRCFTACL
251 EFGMRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNP	IAPMAGITDK	PFRRLCRDF	GAGWAVCEML	TSDPTLRN	TRKTLHRSDF

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60
           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           |||||
a661      ADEGGIVAVQIAGSDPQQMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL
           70      80      90      100     110     120
           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180
           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPFRFETL
           |::|
a661      SGLRPDCRNQMPSEHPGLQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPFRFETL
           190     200     210     220     230     240
           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||
a661      RRTRCFACLEFGRMYRHYFEPHPSHARVLRRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTTCGCTT
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAAACCG TGTTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTGGACG ACGCGCTGGC GGCGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTTCAGA TGCGGTGTA CGCGCTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTTCGGAC GCAACAATTC GGTTTTGTG
601 GATTTTTTCG GCATtcagac GGCAACGATT ACCGGCTTGA GCCGATTGTC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTTGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCCTTTA TCGAAGAACG
801 CGTGCGCGAA CACCCGGAAC AATATTTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLOFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNNSVFE
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPIV READNTVTLO FYPAWSFSPS
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTTGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAAACCG TGTTGAAACA

```

1054

```

201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TGCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCGCGATCAG GATTTCGGAC GCAACGATTC GGTTTTGTG
601 GATTTTTTCG GTATTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTTG GCTGCACAAG CGTTTTAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
  1 MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
  51 KCFSEWSEEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
 101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
 151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
 201 DFFGIQTATI TGLSRIAALA NAKVIPAIPIV READNTVTILH FYPAWSFSPG
 251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEEK				
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP	RRRIGEINLAKCFPEWDEEK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m663.pep	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
g663	RKTVLKQHFHMAKLMLEYGLYWYASAKCLKSLVRYRNKH	YLDDALAAGEKVIILYPHFT				
	70	80	90	100	110	120
	130	140	150	160	170	180
m663.pep	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
g663	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
	130	140	150	160	170	180
	190	200	210	220	230	240
m663.pep	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPIV	READNTVTILH				
g663	SAPFLYLPDQDFGRNNSVFVDFFGIQTATITGLSRIAALANAKVIPAIPIV	READNTVTILQ				
	190	200	210	220	230	240
	250	260	270	280	290	
m663.pep	FYPAWSFSPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKR	FKTRPEGSPDFYX				
g663	FYPAWSFSPSEDAQADAQRMNRFIEERVREHPEQYFWLHKR	FKTRPEGSPDFYX				
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
  1 ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
  51 TCTGCCGTTT GCGCTGCTGC ACAAACTTGC TGATCTGACA GGCTTGCTCG
 101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA

```

1055

```

151 AAATGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAAACCG TGTGAAACA
201 GCATTTTCAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCCGC CGGGCGTTTG AAATCACTGG TGCCTACCG CAACAAACAT
301 TATTTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTC
401 CGCTGATCAG TATGTATTC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCGATCAG GATTTCGGAC GCAACGATTC GGTTTTTGTC
601 GATTTCCTCG GTATTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGGAATC CTTCCGAGT
751 GAAGATGCGC AGGCCGACGC GCAGCGCATG AACCGTTTGA TCGAGGAACG
801 CGTGC GCGAA CATCCGAGC AGTATTTTGG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHET AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFE
201 DFFGIRTATI TGLSRIAALA NAKVIPAIPIV READNTVTLH FYPAWESFSP
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

	10	20	30	40	50	60
m663.pep	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFSEWSEEK				
a663	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKP	RRRIGEINLAKCFPEWDGKK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m663.pep	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDALAAGEKVIILYPHET				
a663	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKH	YLDALAAGEKVIILYPHET				
	70	80	90	100	110	120
	130	140	150	160	170	180
m663.pep	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
a663	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN	VFLIGRTEGLRALVKQFRKS				
	130	140	150	160	170	180
	190	200	210	220	230	240
m663.pep	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAIPIV	READNTVTLH				
a663	SAPFLYLPDQDFGRNDSVFVDFFGIRTATITGLSRIAALANAKVIPAIPIV	READNTVTLH				
	190	200	210	220	230	240
	250	260	270	280	290	
m663.pep	FYPAWKSPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
a663	FYPAWESFSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGCTGAcgg gCGCACCCGG ATGGCGGGTC
101 GGGCCTGCGT CTTCGGGGAA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGGAAA TATTCGTGTC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGGCGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTTCCAT CGCGCCCAT
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCaa
451 cCgaagcgc gtttcgtcCc acttcatcgC gtTTTTTCAA cgaTTCCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAaa ACTCGATTTT

```


1056

551 GA

This corresponds to the amino acid sequence <SEQ ID 2154; ORF 664.ng>:

```

g664.pep
  1  MIHPHHFRAF  FINGHGVEIV  HLLIADGAHR  MGGRACVFGE  LVLAQQADVL
 51  DAAHGAAGAV  AGKLLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEIFVSDHG
101  FNAFEIGIGG  GAAVGEDELG  VKNVQTLVFH  RAHIEIAYGD  DHENIQVIFQ
151  PEARFVPLHR  VFSTIPRQSR  PWVCPLRWCK  TRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

```

m664.seq
  1  GTGATACATC  CGCACTACTT  CCGCGCCTTT  TTCATAAACG  GTCATGGTGT
 51  AGAAATTGTT  CATCTCCTCA  TAGCTGGCGG  GGCGCACCGG  ATGGGCGGTC
101  GGGCCTGCGT  CTTCGGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTC
151  GATCGCGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTCGC
201  GGAACACGGT  CAGCCCTTCC  TTCAGCGAAA  GCTGGAACCA  GTCGCGGCAG
251  GTTACGCGGT  TGCCCGTCCA  GTTGTGAAAA  TACTCGTGTC  CGACCACGGA
301  TTCGATGCCT  TCGAAATCGG  TATCGGTGGC  GGTGCGGCTG  TCGGCAAGGA
351  CGAACTTGGT  GTTAAAGATG  TTCAAACCTT  TGTTTTCCAT  CGCGCCCAT
401  TTGAAATCGC  CCACGGCGAC  GACCATGAAA  ATATCCAAGT  CGTATTCCAA
451  ACCGAAGCGC  GTTTCGTCCC  ATTTTCATCG  GTTTTT.CAA  CGATTCCACG
501  CCAAAGCCGA  CCTTGGGCTT  GTCCGCTTCG  GTGGTGTAAG  ACTCGATTTT
551  GA

```

This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:

```

m664.pep
  1  VIHPHYFRAF  FINGHGVEIV  HLLIAGGAHR  MGGRACVFGE  LVLAQQADVF
 51  DAAHGAAGAV  AGKFLVAEHG  QPFLQRKLEP  VAAGYAVARP  VVEILVSDHG
101  FDAFEIGIGG  GAAVGKDELG  VKDVQTLVFH  RAHIEIAHGD  DHENIQVVFQ
151  TEARFVPFHR  VFXTIPRQSR  PWACPLRWCK  TRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m664/g664 91.8% identity in 183 aa overlap

	10	20	30	40	50	60
m664.pep	VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRACVFGEVLVAQQADVFDAHGAAGAV					
	: : : : : : :					
g664	MIHPHHFRAFFINGHGVEIVHLLIADGAHRMGGRACVFGEVLVAQQADVLDAHGAAGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m664.pep	AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVGKDELG					
	: : : : : :					
g664	AGKLLVAEHGQPFLQRKLEPVAAGYAVARPVVEIFVSDHGFNAFEIGIGGGAAVGEDELG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m664.pep	VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVFXTIPRQSRPWACPLRWCK					
	: : : : : :					
g664	VKNVQTLVFHRAHIEIAYGDDHENIQVIFQPEARFVPLHRVFSTIPRQSRPWACPLRWCK					
	130	140	150	160	170	180
m664.pep	TRFX					
g664	TRFX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

```

a664.seq
  1  GTGATACATC  CGCACCCTTT  CCGCGCCTTT  TTCATAAACG  GTCATGGTGT
 51  AGAAATTGTT  CATCTCCTCA  TATCGGCGCG  GGCGCACCGG  ATGTGCGGTC
101  GGACCTGCGT  CTTCGGGGAA  CTGGTGCTGG  CGCAGCAGGC  GGATGTTTTC
151  GATACGGCGC  ACGGCGCGGC  TGGCGCGGTC  GCCGGAAAAT  TCTTGGTCGC

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1057

```

201 GGAACACGGT CAACCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTCACGCGGT TGCCCGTCCA GTTGTGAAA TATTCGTGTC CGACCACGGA
301 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
351 CGAACTTGGT GTTAAAGATG TTCAAACCTT TGTTTTCCAT CGCACCATA
401 TTGAAATCGC CCACGCGGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
451 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
501 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGAAA ACTCGATTTT
551 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
  1 VIHPHHFRAF FINGHGVEIV HLLISGGAHR MCGRTCVEGE LVLAQQADV
51 DTAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

              10      20      30      40      50      60
m664.pep    VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGGRAVFGELVLAQQADVDAHGAAGAV
              ||||:|||||:|||||:||||| ||:|||||:|||||:|||||
a664         VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTCVEGELVLAQQADVDTAHGAAGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m664.pep    AGKFLVAEHGQPFLQRKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAVKGDELG
              |||||:|||||:|||||:|||||:|||||:|||||
a664         AGKFLVAEHGQPFLQRKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG
              70      80      90      100     110     120

              130     140     150     160     170     180
m664.pep    VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVEXTIPRQSRPWACPLRWCK
              |||||:|||||:|||||:|||||:|||||:|||||
a664         VKDVQTLVFHRTTHIEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK
              130     140     150     160     170     180

m664.pep    TRFX
              |||
a664         TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
  1 atgaagtGg acgaaacgcg cttcgGgttg GAAatgact tggatatTT
51 CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTCTGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGGCGCGAAG TGGTGCGGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTCCaacy CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCAGTTCG CCTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGGAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTCGA GTTAACCATT AAACAAACCG
701 TGCCGCCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCTGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAACGC GCAACCGAAG CCGTGTGCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACGC TTTCACGTGC TGGGAAGCCG

```

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1001 CCCAAACGCT CTACCGTCGC GCCGTCGCCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCATCG GGTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCGTC CGAAGCCGAa ctGTGGGACG GCACGAAAAA CATcgaCCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtCCG
1251 CttcctgcCG AAATGGCACG AATTGGaccg tcaggcggcg aagCAggaaa
1301 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
1351 AACGTCTGCC GCGCCTcgt cctGCGCGCC GACCCGCGC acatcgAAAC
1401 TGTTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCTGTGC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
1501 CTGGCGCAGT TTGCCGAcAA gTtttcAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTTATCGGCT CAAGccggcg cagCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
1651 GCCCGTTTCGC TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTTTCACGC
1701 ACAAGACGGC AGCGGCTACC GCTTCAATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA cCCGCAggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTgGTGAAAC AAGAATTGCA
1851 GTGCATTTCG GCGCAGGAAG GATTGTGCAA AGacGTGGGC GAaatcgtCG
1901 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
51 TDTFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNVFELTI KQTVPPTPDM ADKQPMPIPV
251 KVGLLNRNGE AVAFDYQKGR ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLN YPSDDDLLLL LAHSDAFTC WEAAQTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDRAQA KQENQSYEYS PETADWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNM HEWGILSAVN GNESDTRNCL
501 LAQFADKFSD DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLNPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTTCCGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGCACCGCC
151 ACCGATACCG ATTTTCAAGG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCAAGTC CCCGAAGACG CAGGCCGAC CGCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TAGTGCGGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCCGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAAGTTC CTTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCCCA GCCCGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCCTGCT CGAAGGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTCGCG
901 GGGTTCAGCG CGCCGGTGCA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CCCAAACGCT CTACCGCCGC GCCGTCGCCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTCA GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCGG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

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1059

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1351 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
1401 CGTTGCCGAA AAATACGGCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTGCC CTCGTCGGCT CAAGCCGCGC CAGCGACACC CTGCAACAGG
1601 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
1651 GCCCGTTTCG TCATCGGCAG CTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTCAA CCCGAGGTC GCCGCCCGCT TAGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTTCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFIMVV AVGDFNMGM ENKGLNIFNT KFVLADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAEGR LKNNIFELTV KQTVPTPDM TDKQPMIPV
251 KVGLLNRNGE AVAFDYQGKR ATEAVLLLTE AEQTFLLLEGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLATLS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNQAA KQENQSYEYS PEAAGWRTL
451 NVCRAFLVRA DPAHIETVAE KYGEMAQNMT HEWGILSAVN GNESDTRNRL
501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

```

              10      20      30      40      50      60
m665.pep      MKWDETRFGL EYDLDFIMVVAVGDFNMGMENKGLNIFNTKFVLADSRATDTDFEGIES
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           MKWDETRFGL EYDLDFIMVVAVGDFNMGMENKGLNIFNTKFVLADSRATDTDFEGIES
              10      20      30      40      50      60

              70      80      90      100     110     120
m665.pep      VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRR IENIRLLRQHOF
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           VVGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRR IENIRLLRQHOF
              70      80      90      100     110     120

              130     140     150     160     170     180
m665.pep      PEDAGPTAHPVRPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           PEDAGPTAHPVRPVSYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
              130     140     150     160     170     180

              190     200     210     220     230     240
m665.pep      QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPTPDM
              190     200     210     220     230     240

              250     260     270     280     290     300
m665.pep      TDKQPMIPVKVGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLR
              : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g665           ADKQPMIPVKVGLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR
              250     260     270     280     290     300

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1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRVAANLATLSDGVELPKHEK					
g665	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEEAAQTLYRRVAANLAALSDGIGLPKHEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
g665	KWHELDROAAKQENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVVRTALQH					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	PKFSLENPNKARSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILDX					
g665	CNKLEPHRKNLVKQELQCIRAQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG ACGAAACGCG CTTGCGTTTG GAATACGACT TGGATATTTT
51  CATGTCGTC  GCCGTGGGCG ATTTCAATAT GGGTGGCATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGTACCGCC
151 ACCGATACCG ATTTTGAAGG CATCGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTGACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGTTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCCGTGCG CCGTATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGTCGGAC CGCACATCCG GTGCGCCCCG
401 CCCGATATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGCGGAT GTATCACACC TTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGT ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCTGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGTGG ACGCGAACGG CATCAACCTC
601 GACCAATTCG CTTTGTGTA CAGCCAAGCA GGTACGCCGG TTTTAGATGC
651 TCAAGGGCGT CTGAAAAACA ATGTGTTCGA GTTAACCATC AAACAAACCG
701 TGCCGCCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAATCGGCG TGCTGAACTG CAACGGCGAA GCGGTGGCAT TTGATTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCCAGTT CGAAAGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAACTAT CCGTACAGCG ACGACGACCT
951 GCTGCTTCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CACAAACGCT CTACCGCCGT GCCGTGCGCG CCAACCTTGC CGCGCTTTCA
1051 GACGGCGTCG AGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTCA GACGACTCT TAGACAACGC TTCAAAGCC CTGCTTTTGG
1151 GTGTGCCGTC TGAAGCCGAG CTGTGGGACG GCGCGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATATAC TTGCCGTCCG
1251 CTTTCTGCCG AAATGGCACG AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACTAAAGCTA CGAGTACAGC CCCGAAGCCG CCGGTTGGCG CACGCTGCGC
1351 AATGTCTGCC GCGCCTTCGT CCTGCGCGCC GATCCGCGC ACATCGAAAC

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1061

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG
1451 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
1551 ATATTTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG
1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA
1651 GCCCGCTCGC TCATCGGCAG CTTCAGCCGC AACGTCCCGC ATTTCCACGC
1701 AGAAGACGCG AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
1751 ACCGCTTTAA CCCGCAGGTC GCCGCCCGCC TGGTGCAGGC GTTCAACCTC
1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
1851 GCGCATTTCG GCGCAGGAAG GATTGTGCGA AGACGTGGGC GAAATCGTCG
1901 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:

a665.pep

```

1 MKWDETRFGL EYDLDFIMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMVDANGINL
201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMIIPV
251 KIGLLNCNGE AVAFDYQGKR ATEAVLLLTE AEQTFQFESV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAAQTLYRR AVAANLAALS
351 DGVELPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDILAVRFLP KWHELNQAA KQENQSYEYS PEAGWRTLRL
451 NVCRAFLRA DPAHIETVAE KYAEMAQNMW HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD*

```

m665/a665 97.3% identity in 638 aa overlap

	10	20	30	40	50	60
m665.pep	MKWDETRFGLEYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES					
a665	MKWDETRFGLEYDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATDTDFEGIES					
	10	20	30	40	50	60
	70	80	90	100	110	120
m665.pep	VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
a665	VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m665.pep	PEDAGPTAHPVRPASYEEMNFFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG					
a665	PEDAGPTAHPVRPARYEEMNFFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m665.pep	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM					
a665	QAVTCDDFRAAMVDANGINLDQFALWYSQAGTPVLDAQGRKNNVFELTIKQTVPTPDM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m665.pep	TDKQPMIIPVKVGLLNRRNGEAVAFDYQGKRATEAVLLLTEAEQTFLEGVTEAVVPSLLR					
a665	ADKQPMIIPVKIGLLNCNGEAVAFDYQGKRATEAVLLLTEAEQTFQFESVTEAVVPSLLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLATLSDGVELPKHEK					
a665	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVAANLAALS DGVELPKHEK					
	310	320	330	340	350	360

1062

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNRQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMT					
a665	KWHELNRQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYAEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
a665	HEWGILSAVNGNESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPFHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFSRNVPFHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQRIRAQEGLSKDVGEIVGKILDX					
a665	CNKLEPHRKNLVKQALQRIRAQEGLSKDVGEIVGKILDX					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAACGC CTGCCTACCG
51  CATTCTTGAA ACCGAACTGC ATTTTCGACAT TGCCGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTC GAGCCGCAGA GGGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAACT CTGTCCGTC AAAATCAACG GCGCGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAG GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGCAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTG
551 CTTTGGTGGC GGGCGATTG GCGGTAACGG AAGACCGTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAACC
651 CAAGGTCGGC TTGCGCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGGTTGGAA TATGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTAGGCCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CGGCGACCGC GCCGGCCGCG
1001 CCGTGCGCCG CATCGAGAAC ATCCGCCTGC TCGCCAGAA CCAGTTCCCC
1051 GAAGACGCG GCGGACCGC CCATCCGGTG CGCCCCGTC GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAAAAGGC GCGGAAGTGG
1151 TCGGGATGTA TCATACCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG CGAGTGACCT GCGACGATTT
1251 CCGCGCGCG ATGGCGGATG CGAACCGCAT CAATCTCGAC CAGTTTCGCT
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGGAAGCCGA AGGCCGTCTG
1351 AAAAAACATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAA GTCCGGGCTC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGTATCT GAACATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCACGACA GCGACGCTT CACGTGCTGG GAAGCCGCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCGCCA ACCTGCGCG GCTTTCAGAC GGCATCGGGT

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1063

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCTT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAACTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTGT GATACGCTTG CCGTCCGCTT CCTGCCGAAA
1951 TGGCAGCAAT TGGACCGTCA GCGGCGAAG CAGGAAAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACCGCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTCCGCCCTT
2251 ATCGGCTCAA GCCGCCGAG CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCCGC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG AATTGCAGTG CATTCCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGCGGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pep

```

1  MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EFQRAGEPLV
51  LDGSAKLLSV KINGAAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS YLFALVAGDL AVTEDRETTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETFRGLE YDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTDPEGIESV VGHEYFHNWT
301 GNRVTCRWF QLSLKEGLTV FRDQEFSGDR AGRVRRRIEN IRLLRQNQFP
351 EDAGPTAHPV RVSYSYEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNVFELTIK QTVPPTPDMA DKQPMMPVK VGLLNRRNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLNYP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LIGVPSEAEI WGTENIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLNR VCRAFLVRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSSRRSDTL QQVQTAHQHP KFSLENPNKA RSLIGSFSRN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVGE IVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTATC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCCGG TTTGACGGTT GAGCCGCAGA GGGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCGG
251 AACGCTTCAC CGTGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAAACAA
301 TCCTGTATGG GGTGTATGCT TTCCGGCGGC AATTTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACCACCACC ATCGTCGCGC AAAAAAACG CTATCCCGTT
451 TTGCTTTTCA ACGGCAACAA AATCGACGGC GGCGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTTG
551 CTTTGGTCGC GGGCGATTG GCGGTAACGG AAGACTATT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCGTCGCC
751 GTGGCGGATT TCAATATGGG CGCGATGGAA AACAAGGTT TGAACATCTT
801 TAACACCAGG TTCGTCTTGG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACTGGACG
901 GCGCAACCGC TAACCTGCCG CCACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAAC ATCCGCCTGC TGCGCCAGCA CCAGTTCCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCCGCCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGGCG GCGGAAGTAG
1151 TGCGGATGTA TCACACCCTG CTCGGCGAAG AGGGCTTCCA GAAAGGCATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCCGTTACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCTT
1301 TTGCGTACAG CAGGCGGGC ACGCCCGTTT TGAAGCGGGA AGGTCGCTCG
1351 AAAAACAATA TTTTCGAGTT GACCGTCAAA CAAACCGTGC CGCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGCGGAAGCG GTGGCATTCC ACTATCAGGG CAAACCGCGC

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1064

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1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGATCAT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTCGCCGCCA ACCTTGCCAC GCTTTCAGAC GCGGTTGAGC
1751 TGCCGAAACA CGAAAACTG CTGCGCGCG TCGAAAAAGT CATTTAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTTG CCGTCCACTT CCTGCCGAAA
1951 TGGCACGAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 ATACAGCCCG GAAGCCGCGG GCTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTTGTCCT GCGCGCGGAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAATA TTTTGCCCTC
2251 GTCGGCTCAA GCCCGCGCAG CGACACCCTG CAACAGGTTT GAACCGCCTT
2301 GCAGCATCCG AAATTCAGCC TCGAAAACCC CAACAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCCGCATT TCCACGAGA AGACGGCAGC
2401 GGCTACCGCT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCACCG CAAAACTTG GTGAAACAAG CATTGCAGCG CATTGCGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

```

1  MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51  LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSERFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTETYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL YLDIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLLRQHQP
351 EDAGPTAHPV RPASYEEMNN FYTMTVYEKG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPTPDMT DKQPMIPVK VGLLRNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFLLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVELPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAEI WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNQAAK QENQSYEYSP EAAGWRTLRLN VCRAFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AOFADKFSDD ALVMDKYFAL
751 VYSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGFSRN VPHFAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

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m665-1/g665-1 96.1% identity in 866 aa overlap

```

          10      20      30      40      50      60
m665-1.pep MSKTVHYLKDYQTPAYHILKTDLHFDINEPQTVVKSRLTVEPQRVGEPLVLDGSAKLLSV
          |||:::|||||:||||:||||| |||:|||||:|||||:|||||
g665-1      MSKTVRYLKYQTPAYRIETELHFDIAEPQTVVKSRLTVEPQRAGEPLVLDGSAKLLSV
          10      20      30      40      50      60

          70      80      90      100     110     120
m665-1.pep KINGAAADYVLEGETLTIAGVPSERFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
          |||:|||||:|||||:||||| |||:|||||:|||||:|||||
g665-1      KINGAAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASGGNLFTQCEPEG
          70      80      90      100     110     120

          130     140     150     160     170     180
m665-1.pep FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFSDGRHWVKWEDPFSKPS
          |||:|||||:|||||:||||| |||:|||||:|||||:|||||
g665-1      FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEFSDGRHWVKWEDPFAKPS
          130     140     150     160     170     180

          190     200     210     220     230     240
m665-1.pep YLFALVAGDLAVTETYFTTMSGRNVKIEFYTTEADKPKVGFIVESLKNAMKWDETRFGL
          |||:|||||:|||||:||||| |||:|||||:|||||:|||||
g665-1      YLFALVAGDLAVTEDRFTTMSGRNVKIEFYTTEADKPKVGFIVESLKNAMKWDETRFGL
          190     200     210     220     230     240

          250     260     270     280     290     300
m665-1.pep YLDIFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRATDTDFEGIESVVGHEYFHNWT
          |||:|||||:|||||:||||| |||:|||||:|||||:|||||
g665-1      YLDIFMVVAVGDFNMGAMENKGLNIFNTKFLVADSRATDTDFEGIESVVGHEYFHNWT

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1065

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHQFPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHGDQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHGDQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMTDKQPMPIPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPDMADKQPMPIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRNGEAVAFDYQGKRATEAVLLLTEAEQTFLLLEGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRNGEAVAFDYQGKRATEAVLLMTEAEQAFPLEGVTEAVVPSLLRGFSAPVYLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDLLLLLAHDSDAFTRWEAAQTLYRRAVANLATLSDGVELPKHEKLLAAVEKVISD					
g665-1	YSDDDLLLLLAHDSDAFTCWEAAQTLYRRAVANLAALSDGIGLPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFKALLLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNQRAAK					
g665-1	DLLDNAFKALLLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDQRAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPAAAGWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRNVCRAFVLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPHFAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSRNVPHFAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRIAQEGLSKDVGEIVGKILDX					
g665-1	VKQELQCIRIAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTAC ATTTTGATAT TAACGAACCG CAAACCATTG
101 TGAAGTCGCG TTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTGTCCGTC AAAATCAACG GCGTGGCGGC
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCGG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAAACAAA
301 TCGCTGATGG GCGTGTATGC GTCCGCCGGT AACCTGTTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA TATCGACCGT CCGGATGTCA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACAAAAAACG CTATCCCGTT
451 TTGCTCTCCA ACGGCAACAA AATCGACGGC GCGGAGTATT CAGACGGCCG

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a665-1.pwp

a665-1/m665-1 97.2% identity in 867 aa overlap

a665-1.pep	10	20	30	40	50	60
	MSKTVHYLKDYQTPAYHILKTDLHFDINEPQTIVKSRLTVEPKRVGEPLVLDGSAKLLSV					
m665-1	10	20	30	40	50	60
	MSKTVHYLKDYQTPAYHILKTDLHFDINEPQTVVKSRLTVEPQRVGEPLVLDGSAKLLSV					
	70	80	90	100	110	120

1067

a665-1.pep	KINGVAADYVLEGETLTIADVPSEFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
m665-1	KINGAAADYVLEGETLTIAGVPSEFTVEVETEILPAENKSLMGLYASAGNLFTQCEPEG
	70 80 90 100 110 120
a665-1.pep	130 140 150 160 170 180
m665-1	FRKITFYIDRPDVMSKFTTTIVADKKRYPVLLSNGNKIDGGEYS DGRHWVKWEDPFAKPS
	130 140 150 160 170 180
a665-1.pep	190 200 210 220 230 240
m665-1	YLFALVAGDLAVTEDYFTTMSGRNVKIEFYTTEADKPKVGF AVESLKNAMKWDETRFGLE
	190 200 210 220 230 240
a665-1.pep	250 260 270 280 290 300
m665-1	YDLDFIMVVAVGDFNMGAMENKGLNIFNTKFVLADSR TATDTDFEGIESVVGHEYFHNWT
	250 260 270 280 290 300
a665-1.pep	310 320 330 340 350 360
m665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQP PEDAGPTAHPV
	310 320 330 340 350 360
a665-1.pep	370 380 390 400 410 420
m665-1	RPARYEEMNFFYTM TVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRH DQAVTCDDFRAA
	370 380 390 400 410 420
a665-1.pep	430 440 450 460 470 480
m665-1	MVDANGINLDQFALWYSQAGTPVLDAQGR LKNNVFELTIKQTVPTPD MADKQPMMPVK
	430 440 450 460 470 480
a665-1.pep	490 500 510 520 530 540
m665-1	IGLLNCNGEAVAFDYQ GKRATEAVLLLTEAEQTFQFESVTEAVVPSLLRGFSAPVHLNYP
	490 500 510 520 530 540
a665-1.pep	550 560 570 580 590 600
m665-1	YSDDDLLLLLAHDSDAFTRWEAAQ TLYRRAVAANLAALSDGVELPKHEKLLAAVEKVISD
	550 560 570 580 590 600
a665-1.pep	610 620 630 640 650 660
m665-1	DLLDNAFKALLGVPSEAELWDGAENIDPLRYHQAREALLDILAVRFLPKWHELN RQAAK
	610 620 630 640 650 660
a665-1.pep	670 680 690 700 710 720
m665-1	QENQSYEYSPEAAGWRTL RNVCRAFVLRADPAHIETVAEKYAEMAQNMTHEWGILSAVNG
	670 680 690 700 710 720
a665-1.pep	730 740 750 760 770 780
m665-1	NESDTRNRLLAQFADKFSD DALVMDKYFALVGSSRRSDTLQQVQTALQHPKFSLENPNKA
	730 740 750 760 770 780
a665-1.pep	790 800 810 820 830 840
m665-1	RSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNLCNKLEPHRKNL
	790 800 810 820 830 840

1068

	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQRI	RAQEGLSKDVGEIVGKILD	X			
m665-1	VKQALQRI	RAQEGLSKDVGEIVGKILD	X			
	850	860				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1   ATGCTTTGTA TGAATTATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTAGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTGT GTATTGGGAC AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1   MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTHSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1   ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTTGGC
51  TAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCAGAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTGTGTGT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGTACGCCT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1   MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

	10	20	30	40	50	60
m666.pep	MPCMNHQSNS	GEGVLVAKTY	LLTALIMSMT	ISGCQVIHAN	QGKVNTHSAV	ITGADAHTPE
		:				
g666	MLCMNYQSNS	GEGVLVAKTY	LLTALIMSMT	ISGCQVIHAN	QGKVNTHSAV	IAGADAHTPE
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQ	VIASDFMVAS	ANPLATQAGY	DILKQGSAA	DAMVAVQTTL	SLVEPQSSGL

```
a666.seq
1  ATGCCTTGTA  TGAATCATCA  ATCAAACCTCA  GGCGAAGGAG  TGCTTGTTGGC
51  TAAAAACATAT  TTATTGACTG  CATTGATAAT  GTCTATGACA  ATCTCTGGAT
101  GTCAGTCAT  CCATGCCAAT  CAAGGTAAGG  TTAATACTCA  TTCTGCTGTC
151  ATCACAGGTG  CAGACGCTCA  CAGCCTGAA  CATGCAACGG  GACTGACCGA
201  ACAAAAGCAG  GTGATTGCAA  GTGATTTTAT  GGTAGCGTCA  GCCAATCCAT
251  TAGCAACACA  AGCTGGCTAT  GATATCTTAA  AGCAAGGCGG  TAGCGCTGCA
301  GATGCGATGG  TGGCGGTGCA  GACGACACTA  AGCTTGGTAG  AGCCACAGTC
351  GTCAGGCTTG  GGCAGTGGTG  CATTGTGTGT  GTATTGGGAT  AATACCGGCA
401  AAACATTGAC  CACATTGTAT  GGGCGTGAGA  CCGCACCGAT  GCGTGCCGACG
451  CCGGAATTAT  TTTTGGATAA  AGATGGTCAA  CCATTGAAAT  TGTGGAAGC
501  GGTGGTCGTG  GTCGCTCGGT  GGGTACGCCT  GCTATCCCTA  AACTGA
```

```
a666.pep
1  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSVA
51 ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGGSA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GRETAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLLSL N*
```

		10	20	30	40	50	60
m666.pep		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHSA	VITGADAHTPE
a666		MPCMNHQSN	SGEGLVAKTYLL	TALIMSMTIS	GCQVIHANQ	GKVNTHSA	VITGADAHTPE
		10	20	30	40	50	60
		70	80	90	100	110	120
m666.pep		HATGLTEQKQ	VIASDFMVASAN	PLATQAGYDIL	KQGGSAADAMV	AVQTTL	SLVEPQSSGL
a666		HATGLTEQKQ	VIASDFMVASAN	PLATQAGYDIL	KQGGSAADAMV	AVQTTL	SLVEPQSSGL
		70	80	90	100	110	120
		130	140	150	160	170	180
m666.pep		GGGAFVLYWD	NTAKTLTTFD	GRE	TAPMRATPEL	FLDKDGQPL	KFMEAVVVVARWVRLLSL
a666		GGGAFVLYWD	NTAKTLTTFD	GRE	TAPMRATPEL	FLDKDGQPL	KFMEAVVVVARWVRLLSL
		130	140	150	160	170	180
m666.pep		NX					
a666		NX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1   atgcgggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggtttcgc aatAAAttgcg
151 GAttcccttc agcgtgcccgc cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggtG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GCGGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCGA AACCGCCGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATACAG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCCT TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCAg tACCTTGCAT tcaAAAACAG ActTGCGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1   MRFVFCLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVYQGA V MQYQVETAA
151 VPADQLRRMF FNQFEKLG NH DFFAIVHLAD GADMNVLPP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHFVIRQGR RQVIQRTDTL HIGYGFNIES
251 QNRHGSTLH SKTDLRL LCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1   ATGCGGCTTT TCCCCGGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
51  TTTCCATTTT GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTGCGCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GCGGTTGATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TAGCAATGAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCCT TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1   MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFIIA
51  DFLQPARMEC LPNLAAVHTQ LARKTAQFRH IVQRHVCPR L VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHIPIAR GVDVYQGA V MQYQIETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHL
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

              10      20      30      40      50      60
m667.pep    MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFIIADFLQPARMEC
              ||:  | |::  | ||:||||:| |||||:| | :  : ||||| | | ||:|
```

```
a667.seq
1 ATGCGGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51 TTTCCATTTC GTATTCGTCT GCGTCGAATC TGCGCTCTGAC CAGACAGAAA
101 CCGAGATACA TACAGATAGT ATTACCGCA TCGGTTTCGC AATAATGCG
151 GATTTCCTTC AGCCTGCCCG CGTGGAACGC CTCCACACC TTGCTGCCGT
201 CCATACCAG CTTGCCCGGA AAACCGCAC GTTCGCCAT ATCGTCCAAC
251 GGCACATTGC CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAAATCGCA
301 ATGACGTGG TGGTAGCGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCCGCGAA ATCGCCGTCG CCATATCCC AATAGCGCGC GCGCTTGATG
401 CCGTGTA GCA GCGAACGGTA ATGCAGAAC GGCAGGTCGA AACCGCCGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCTCTG CCGTCATCCA TCTCGCCGAT TGTACCGGCA
551 TGGACTTTAT CTTGCCCCCA AGCATGCGAG CACGAAATCG CACAATCTG
601 ATGAAGATGA TGCTGCATAA AATCCCCACC CGTCTGAGCA CGGCGTTTTT
651 GCTGGGCAA CAGCACCAC TCATCGTCGG GCAGCGAGGA CGGCAAGTCA
701 TACACGCTAC GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTG GTCATGACAG CACCTTGAT TTAATAA.CAG ACTTGCGCCT
801 ATTGTGCAT TAA
```

a667.pep

1	MRFVFC LGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIHQIG	IYRIGFAIIA
51	DFLQPARVER	LPHLAAVHTQ	LARKTAQFRH	IVQRHIRPRL	VKREQIHQIA
101	MTLVVAADV	VPLEIAAAVE	IAVAHIPIAR	GVDAV*QRTV	MQNRQVETAA
151	VPTDQLRRMF	FNQLEKFGDN	HFLAVIHLAD	CTDMDFILPP	THAARNRHNH
201	MKMMHLHKIPT	RLSTAFLLGK	QHHFIVGQRG	RQVIQRHDTL	HIGYGFNIIES
251	QNRGHDSSTLY	LKXDLRLLC	*		

	10	20	30	40	50	60
m667.pep	MRLFPGLCGQVIPHFPDFHFVVFVRIQPAADQTETQVHQISVCRVGF	AIADFLQP	ARM	EC		
	:	::	:	:	:	:
a667	MRFVFC	LGGEIVSDPLDFHFVFCV	ESAADQTETQIHQIGIYRIGF	AIADFLQP	AR	VER
	10	20	30	40	50	60
	70	80	90	100	110	120
m667.pep	LPNLA	AVHTQLARKTAQFRHIVQRHVC	PRLVKREQIHQIAVALVITADVVVPLEIA	AAVAE		
	:		:	:	:	:
a667	LPHLA	AVHTQLARKTAQFRHIVQRHVC	PRLVKREQIHQIAVALVITADVVVPLEIA	AAVAE		

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	70	80	90	100	110	120
m667.pep	130	140	150	160	170	180
	IAVAHIPIARGVDAVYQGAVMQYQIETAAVPTDQLRRMFFNQFEKFSNDHFLAVIHLAD					
a667	IAVAHIPIARGVDAVXQRTVMQNRQVETAAVPTDQLRRMFFNQLEKFGDNHFLAVIHLAD					
	130	140	150	160	170	180
m667.pep	190	200	210	220		
	GADMYFILPPTHAAARNRHNLMKMMLHKIAARLSTAFVLGNQHHL					
a667	CTDMDFILPPTHAAARNRHNLMKMMLHKIPTRLSTAFLLGKQHHFIVGQRGRQVIQRTDTL					
	190	200	210	220	230	240
a667	HIGYGFNIESQNRGHDSTLYLKXDLRLLLCHX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2183>:

```

g669.seq
1   ATGCGCCGCA TCGTTAAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AGCGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2184; ORF 669.ng>:

```

g669.pep
1   MRRIVKKHQV VNAPHIVLEI RIMKLHRAV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2185>:

```

m669.seq
1   ATGCGCCGCA TCATTAAAAA ACACCAGCCC ATAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACAGCAGCC TTCGGCGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2186; ORF 669>:

```

m669.pep
1   MRRIIKKHQV INAPHIVLEI RIMKLHRAV FLGRKRPHHH DSSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m669/g669 96.2% identity in 106 aa overlap

	10	20	30	40	50	60
m669.pep	MRRIIKKHQVINAPHIVLEIRIMKLHRAVFLGRKRPHHH	DSSLRRQHGI	EGMGFDFKQI			
g669	MRRIVKKHQPVNAPHIVLEIRIMKLHRAVFLGRKRPHHH	DRSLRRQHGI	EGMGFDFKQI			
	10	20	30	40	50	60
	70	80	90	100		

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```

m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              |||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1  ATGCGCCGCA TCATTA AAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51 TTTGGA AATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pep
1  MRRIIKKHQP VNAPHIVLEI RIMKLHRA FV FLGRKRPHHH DRSLRRQHGI
51 EGMGFDFKQI FRHVQSSNRQ NGRQPVCTK PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

              10      20      30      40      50      60
m669.pep    MRRIIKKHQPINAPHIVLEIRIMKLHRA FV FLGRKRPHHH DSSLRRQHGI EGMGFDFKQI
              |||
a669        MRRIIKKHQPVNAPHIVLEIRIMKLHRA FV FLGRKRPHHH DRSLRRQHGI EGMGFDFKQI
              10      20      30      40      50      60

              70      80      90      100
m669.pep    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              |||
a669        FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1  ATGACTTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTTGGTGAA
51 AAACGCTTCC GCGGTTTCGT CTTCAAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCTGT GGTTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CGGCTCGTCA AACAGCATCA
251 CCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGA AA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pep
1  MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
51 IIVMPLSAKS FITENTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRC CW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1  ATGACCTGTT GCAGGAACTG CTTGGCGCGT TCGTGTTTCG GGTTGGTAAA
51 AAACGCTTCG GCGGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCTGT GGTTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCTGTC AACAAACATTA

```

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```

251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGTAATGT TTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
g670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep      FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCCWPPESWEGKASFLCASPTRSK
g670           FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCCWPPESWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep      SSIAFFSACS AFCPLTFIGARVMFSNTVRCGX
g670           SSIAFFSACS AFCPLTFIGARVMLSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAAGT CTTGGCGCGT TCGTGTTTCG GGTGGTAAA
 51 AAACGCTTCC GGCCTTTCGT CTTCGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCTGCA AACAAACATTA
251 CGCGCGGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
 51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep      MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
a670           MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

1075

	70	80	90	100	110	120
m670.pep	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.pep	SSIAFFSACSAFCPLTFIGARVMFSNTVRCGX					
a670	SSIAFFSACSAFXPLTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

```

g671.seq
1  ATGATCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACACC
51  GCCCAAATG CGGTTGGCAA AGCCCAGACC GACCGCCGAA ACTGCGCCGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAATG ACAGagccaa TGCAAACAgg cggggTTGGA ACGaggCAAA
201 GGCGAGGTcg gcgaaggGTG CGGCaaAGAG TTTggcaaAA AAGAaggAAA
251 ccaccCATGC cACCATCgaa ccTGCTTCCG CAATCACGCC GCGCATCGTG
301 GAAATGACGA TGCAGGCGGC GATGACGGcg gAGGCGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTCTGT ACCTGGCCGG CGATGCCGTG CACGCGCAGT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

```

g671.pep
1  MISRVTIKTP FNA PNT PPKM RLAKPRPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKGA AKSLAK KKETTHATIE PASAITPRIV
101 EMTMQAAMTA EARRSAMGRL FIRYLAGDAV HAQFVQIAFG IPCVFIVA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

```

m671.seq
1  ATGACCAGCA GGGTAACAAT CAAAACGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAATG CGGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCGCTGG
101 TCAGCAGCGA ACGGAGCATT TTCTGGATCA GACAGGCAAT GACGAACAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTGGA ACGAGGCAAA
201 GGCGAGGTCG GCGAAGGAGG CGGCAAAGAG TTTGGCGAAA AAGAAGGAAA
251 CCACCCATGC CGCCATTGAG CCTGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGACGGCG GAGACGAGGA GGTCGGCAAT
351 GGGGAGGCTA TTCATTCTGT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

```

m671.pep
1  MTSRVTIKTP FNA PNT PPKM RLAKPKPTAE TALVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNEAKARS AKEA AKSLAK KKETTHAAIE PASAITPRIA
101 DSTMQAAMTA ETRRSAMGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.pep	MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR					
g671	MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.pep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					

```

g671      |||||:|||||:|||||:|||||:
          RGWNEAKARSAGAAKSLAKKKETTHATIEPASAITPRIVETMQAAMTAEARRSAMGR
          70      80      90      100      110      120

          130      140      149
m671.pep  FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
          ||||:||||:|||||:|||||:
g671      FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
          130      140

```

```
a671.seq
1  ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CGGTGTGGCAA AGCCCCAAAC GACCCCGCA ACTGCCCCGG
101 TCAGCAGCGA CGGTGAGTATT TTCTGGATCA CAGAGGCAAT ACGGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA GCGATGCAAA
201 GGCATGTCTG GCGAAGGGTG CGGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCAGCCG GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGATGGCG GAGACAGGGA GGTCTGGCAAC
351 GGGGAGGTTA TTCATTCTGT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTTCGGC ATCCCTTGCG TTTTATAGT  TGCTTTGA
```

a671.pep

1	MTSRVVIKMP	FNAPNTPPKM	RLAKPKPTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNDAKAMS	AKGAAKSLAK	KKATTHAAIE	PASAITPRIA
101	DSTMQAAMMA	ETRRSATGRL	FIRYLTGDTV	YAQFVQIAFG	IPCVFIVA*

		10	20	30	40	50	60
m671.pep		MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDRANANR					
a671		MTSRVVIKMPFNAPNTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDRANANR					
		10	20	30	40	50	60
		70	80	90	100	110	120
m671.pep		RGWNEAKARSAKEAAKSLAKKKETHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					
		:					
a671		RGWNDAKAMSAGAAKSLAKKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL					
		70	80	90	100	110	120
		130	140	149			
m671.pep		FIRYLTGDTVYAQFVQIAFGIPCVFIVAX					
a671		FIRYLTGDTVYAQFVQIAFGIPCVFIVAX					
		130	140				

g672.seq

1	ATGAGGAAAA	TCCGCACCAA	AATCTGCGGC	ATCACCACAC	CGGAAGACGC
51	ACTGTATGCC	GCCCACGCCG	GCGCAGACGC	ATTGGGACTG	GTTTTTTACC
101	CCCAAAGCCC	CGCGCTATC	GACATCATT	AAGCAAAAA	AATCGCCGCG
151	GCACTGCCGC	CGTTTGTCAG	CGTTGTGCGC	CTTTTCGTCA	ACGAAAGCGC
201	GCAAAACATC	CGCCGCATCC	TTGCCGAAGT	GCCGATACAC	ATCATCCAAT
251	TCCACGGCGA	CGAAGACGAT	GCATTCTGCC	GGCAGTTCGA	CGCCCCCTAT
301	ATTAAAGCCA	TTCGTGTTCA	CACGGCATCA	GACATCCGAA	ACGCCGCCAC
351	GCGCTTCCCC	AACGCTCAGG	CGCTGCTGTT	GCGATGCTAT	CACCCCTTCG
401	AATACGGCGG	CACCGGACAC	CGCTTCGact	GGacgctgtt	ggcggAATAT
451	TCGGGCAAGC	CGTGGGTGCT	TGCCGGCGGG	CTGACCCCTG	AAAACGTCGG
501	CGAAGCCGTC	CGCATCACCG	GAGCGAAGC	GGTCGACGTA	TCCGGCGGCG
551	TGGAAGCGTC	TAAAGGCAAA	AAAGACCCCG	CCAAAGTCGC	CGCCTTTATC
601	GCAACCGCCA	ACCGCCATATC	CCGTTAA		

1077

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```
g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATRF NAQALLFDAY HPSEYGGTGH RFDWTLLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAEFI
201 ATANRLSR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```
m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCG GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTGTC CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAAGCCA TTCGTGTTCG GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATACCGG GAGCGGAATC GGTCGATGTA TCCGGCGGTG
551 TGAAGCGTC TAAAGCAAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```
m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQGSSRAV DIARAKKITA
 51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATRF DAQALLFDAY HPSEYGGTGN RFDWTLLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDKAAKVAEFI
201 ATANRLSR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

	10	20	30	40	50	60
m672.pep	MRKIRTKICG	ITTPEDAAAA	AAAGADAVGL	VFFQGSSRAV	DIARAKKITA	ALPPFVSVVA
g672	MRKIRTKICG	ITTPEDALYA	AHAGADALGL	VFYPQSPRAI	DIIKAQKIAA	ALPPFVSVVA
	10	20	30	40	50	60
	70	80	90	100	110	120
m672.pep	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFHRPY	IKAIRVQTAS	DIRNAATRF
g672	LFVNESAQNI	RRILAEVPIH	IIQFHGDEDD	AFCRQFDRPY	IKAIRVQTAS	DIRNAATRF
	70	80	90	100	110	120
	130	140	150	160	170	180
m672.pep	DAQALLFDAY	HPSEYGGTGN	RFDWTLLAEY	SGKPWVLAGG	LTPENVGEAV	RITGAESVDV
g672	NAQALLFDAY	HPSEYGGTGH	RFDWTLLAEY	SGKPWVLAGG	LTPENVGEAV	RITGAEAVDV
	130	140	150	160	170	180
	190	200	209			
m672.pep	SGGVEASKGK	KDKAAKVAFI	ATANRLSRX			
g672	SGGVEASKGK	KDKPAKVAFI	ATANRLSRX			
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

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```

1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGCTGTC GACATCATT AAGCACAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCAG CGTTGTCGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
301 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
351 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GGCGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGA
501 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTCGATGTA TCCGGCGGCG
551 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTTGC CGCCTTTATC
601 GCAACGCCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1  MRKIRTKICG ITTPEDALYA AHAGADALGL VFYPQSPRAV DIIKAQKITA
51  ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRF DAQALLFDAY HPSEYGGTGH RFDWTLLEAY
151 SGKPWVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAEFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

m672.pep	10	20	30	40	50	60
	MRKIRTKICGITTPEDAAGADAVGLVFFQGSSRAVDIARAKKITAALPPFVSVVA					
a672	MRKIRTKICGITTPEDALYAAHAGADALGLVFYPQSPRAVDIIKAQKITAALPPFVSVVA					
	10	20	30	40	50	60
m672.pep	70	80	90	100	110	120
	LFVNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF					
a672	LFVNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRF					
	70	80	90	100	110	120
m672.pep	130	140	150	160	170	180
	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVGEAVRITGAESVDV					
a672	DAQALLFDAYHPSEYGGTGNRFDWTLLEAYSGKPWVLAGGLTPENVDEAIRITGAEAVDV					
	130	140	150	160	170	180
m672.pep	190	200	209			
	SGGVEASKGKKDAAKVAEFIATANRLSRX					
a672	SGGVEASKGKKDPAKVAEFIATANRLSRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51  TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCAGCCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CCGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGATCAACA
401 AAATCGACAA GGACAAGCGC AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAAGTGC GCGCGGAATT TGAATTTGCG GCGGCGGAGG CGGTCAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAACTCT TCCGCTATTT

```

1079

```

651 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
751 AGCCAAAAGG CGATTTTGAT CGGTAAAGGC GGGGAGCGTT TGAAAAAAT
801 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGAT AACAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR LTDADRVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEVSAKHG LRIANLLELL KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CCGGCTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGCGTGGAT
301 GTGGTGTTT TCGTCGTGGA GGCGATGCGC TTTACCGATG CCGACCGCGT
351 CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGTTTGTG
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CGGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CAATTTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
801 TTCCACCGAA GCGCGTTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVFVVEAMR FTDADRVLK QLPKHTPVIL VVINKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEVSAKHG LRIANLLELI KPYLPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

          10      20      30      40      50      60
m673.pep MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          |||
g673      MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTRNRVTGI
          10      20      30      40      50      60

          70      80      90     100     110     120
m673.pep YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVLK
          |||

```


1080

```

g673      YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||
g673      KPYPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           |||||
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTTGAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CCGTCAGCGC
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACGCG ATCTATATCG CCGTTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YTDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFEEFA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFRYLGE E LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLF DTKVFLKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60

```

1081

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETYPY
101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCGGAC TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCCGACGA GCCCAAACGC CGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL

```

1082

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	:					
g674	YIQKIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAAACAG	CCCGCCGCGG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCAGAAC	GCCCTACCCC
301	GTCATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTCGC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLDRDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

```
g675.seq
  1  ATGAACACCA TCGCCCCcaa cctcgacgGC AAACACCTCC GCATCGGCAT
 51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
101  GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcacgctc
151  gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
201  CTCTTCCGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251  GCGAAACCTA CCATTTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
301  GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
351  CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
401  ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
451  GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

g675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
 101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq
 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
 201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
 301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
 351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCGGTC GAATGCGCCA ACCTCGTCAA CCTGCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
 101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCRTLQELGVADENITVATVPGALEIP					
g675						
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
g675						
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
g675						
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq
 1 ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
 51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
 101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
 151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACCTTGC
 201 CTCTTCTGAA AAATTTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
 251 GCGAAACCTA CCATTTCGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
 301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
 351 CACGGAAAAC GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
 401 ATGCCGCCAA AGTCGCGGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
 451 GAAGAACAGT TTGAAGACGA AGAATAA

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep
 1 MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCRTLQE LGVADENITV
 51 ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

1085

101 SRVALDYNIP IANAVLT TEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
 151 EEQFEDEE*

m675/a675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLT TEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLL EEQFEDEE X					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLL EEQFEDEE X					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTtg
 51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTC AATT TCCTCACGGC CTCCGGCGT
 151 GTTCAA AACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGG CAACGCGCCA
 201 ACGGCGAAAT CCAAGAAATT TTGTTT TCGC CGGTATCGAT TTCATCGACG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCGCGCA ACAGACCGAC
 301 GGTGCGCGCG AAAAATACTT GGTGCGT GCGC TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
 451 GTCGCCGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GGCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep
 1 MPQILVRIFL IRYFSIWETV RLCRFRRHSR SVDFDVDRK DFNFLTAFR
 51 VQNHVFAFAR FNQATRQRRN PRNFVLRGID FIDADDFDGL LAPVAAQQT
 101 GRAEKYLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq
 1 ATGCCGCAGA TTTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTTG
 51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT
 101 TTGATGTATT CGACAGAAAG GATTTC AATT TCCTCACGCC CTTCGGCGT
 151 GTTCAA AACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGA CAACGAGCCA
 201 GCGGCGAAAT CCAAGAAATT TTGTTT TCGC CGGTATCGAT TTCATCGATG
 251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC
 301 CGTCGCGCGG AAAAACACTT GGTGCGT GCGC TTCGCGCAAT TCGGGATCGA
 351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTGCG
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCCGT TTTCGCTGCG
 451 GTCGCCGTTG CCTGCCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT
 501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG
 551 GGCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep
 1 MPQILVRIFL IRYFSIWETA RLCRFRRHSR SVDFDVDRK DFNFLTPFR

1086

51 VQNHFAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD
 101 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA
 151 VAVACRPVDD LDDFGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAFAR				
g677	MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDRKDFNFLT	AFRRVQNHFAFAR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m677.pep	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGR	FAQFGIDDDG				
g677	FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQT	DGRAEKYLVGRFAQFGIDDDG				
	70	80	90	100	110	120
	130	140	150	160	170	180
m677.pep	SLQTFGQETDAAVDFAHTAF	FAVKIVAVFAAVAVACRPVDDLDDFGAFFVD	QLIKLVFQCL			
g677	SLQTFGQETDAAVDFAHTAF	FAVKIVAVFAAVAVACRPVDDLDDFGAFFID	QLIKLVFQCL			
	130	140	150	160	170	180
	190	199				
m677.pep	PSGGRNVVFGFGTHIVCGX					
g677	PSGGRNVVFGFGTHIVCGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq

1	ATGCCGCAGA	TTTTGGTGCG	GATTTTCCTC	ATTCGGTATT	CCTTTATTGT
51	GGAAACGGCG	CGTTTGTGCC	GTTTCAGACG	GCATTCCCGA	TCAGTCGATT
101	TTGATGTATT	CGACAGAAAG	GATTTCGAAT	TCCTCACGCC	CTTCCGGCGT
151	GTTTAAAC	ACTTCGTCGC	CTTCACGCGC	TTAATCAGA	CAACGAGCCA
201	GCGGCGAAAT	CCAAGAAATT	TTGTTTGGCG	CGGTATCGAT	TTCATCGATG
251	CCGACGATTT	TGACGGTTTG	CTCGCGCCCG	TCGCCGCGCA	ACAGACCGAC
301	GGTCGCGCCG	AAAAACACTT	GGTCGGTCGC	TTTCGCGCAAT	TCGGGATCAA
351	CGACGACGGC	GGCTTCCAAA	CGCTTGGTCA	GGAAACGGAT	GCGGCGGTGC
401	ATTTCGCGCA	TACGGCGTTT	GCCGTAAAGG	TAGTCGCCGT	TTTCGCTGCG
451	GTCGCCGTTG	CCTGCCGCCC	AGTTGACGAT	TTGGACGATT	TCGGGGCGTT
501	CTTTATTAAC	CAGTTGATAA	AGCTCGTCTT	TCAATGCCTG	CCATCCGGCG
551	GCGGTAATGT	AGTTTTTGGT	TTTCGGTACTC	ATATTGTGTG	CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep

1	MPQILVRIFL	IRYSFIWETA	RLCRFRHRSR	SVDFDVFDRK	DFNFLT	PFRR
51	V*NHFVAFTR	FNQTSQRRN	PRNFVLRGID	FIDADDFDGL	LAPVAAQQT	D
101	GRAEKHLVGR	FAQFGINDDG	GFQTLGQETD	AAVDFAHTAF	AVKIVAVFAA	
151	VAVACRPVDD	LDDFGAFFIN	QLIKLVFQCL	PSGGRNVVFG	FGTHIVCG*	

m677/a677 93.4% identity in 198 aa overlap

	10	20	30	40	50	60
m677.pep	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAFAR				
a677	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDRKDFNFLT	PFRRVXNHFAFTR				
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m677.pep  FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG
a677       FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGGRAEKHLVGRFAQFGINDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.pep  SLQTFGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDFGAFFVDQLIKLVFQCL
a677       GFQTLGQETDAAVDFAHTAFVAVFAAVAVACRPVDDLDDFGAFFINQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.pep  PSGGRNVVFGFGTHIVCGX
a677       PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51 CTGCATCGTC ATTTCCACGA TCGCGGCGGT GATTGCGGAA GCAGgttcGA
101 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
151 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
201 tCTGTCATTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCGGC GCAGTTTCGG CGGTCGGTCT GGGCTTTGCC
301 AACCGCATTT TGGGCGGTGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCAACA GTCCTATACC GTACCGTTTT TCGTATCGCT TTCCGAAGCG
451 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1  MNSLPIADLL ASAVIAACIV ISTMRGVIAE AGSMVAWVVS FFFAKLFAAP
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
101 NRILGGVFGE LKGVLIIVTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
151 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1  ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TCGCGGCGGT GATTGCGGAG GCAGGCTCAA
101 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTCT TGCCGCCTCC
151 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
201 TCTGTGCTTC ATTTCCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
251 TCCGTTCGCT GCTGACCAGC GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCG TTTTGATTGT
351 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1  MNSLPIADLL VSAVIAACIV LSAMRGVIAE AGSMAAWVVS FFFAKLFAAS
51 FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTS AVSAVGLGFA
101 NRILGGVFGE LKGVLIIVTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap

1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFI SLFVIACLIQKMLRSLLTSAVSAVGLGFANRILGGVFGALKGV LIVTLL					
g678	PRLFALALSFI SLFVIACLIQKMLRSLLTGAVSAVGLGFANRILGGVFGALKGV LIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
g678	IMLASKTDLPDTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCCTCG CCAAACCTCTT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTCG ATCGTTCCAA CCCCCTGTGT TTGCATTGGC
201 TCTGTCGTTT ATTTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCTGTTT GGGCTTTGCC
301 AACC GCATTT TGGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51  FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLLTG AVSAVGLGFA
101 NRILGGVFGA LKGILITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFI SLFVIACLIQKMLRSLLTSAVSAVGLGFANRILGGVFGALKGV LIVTLL					
a678	PRLFALALSFI SLFVIACLIQKILRSLLTGAVSAVGLGFANRILGGVFGALKGILITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
a678	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG

```

```

151  CGGCGCACCA GTTCGCGCGT TACGCGGTCTG ACGCTTTGTT TGGTtttgCA
201  AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251  GGTTCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301  GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451  TCGATAAAAC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501  TTCGGCTTTG TTTAACTGA TGTTTTTCTG TTTACATGG TCGAGCAGCC
551  GTCCGACGGT GGCACGACT ATTTTCGAGC CGGCACGCAG GTCGGCGGTT
601  TGTGTGTTCA TGTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651  GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
  1  MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
 51  RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101  ALVVFWAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151  SINPISNMRS ASSRTTISAL FKLMMFCFTW SSSRPTVATT ISQPARRSAV
201  CLSMLTTPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
  1  ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
 51  GGCGACGAGG ACGCGCAGGT TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101  GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151  CGGCGCACCA GTTCGCGCGT TACGCGGTCTG ACGCTTTGTT TGGTTTTGCA
201  GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251  GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301  GCGTTGGTGG TGTTCGCGC GGCAGCTTCG ACGGTTTCGG GCGCGTTCAT
351  GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401  GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451  TCGATAAAAC CCATATCCAG CATAACGGTCG GCTTCGTCCA AAACGACGAT
501  TTCGACTTTG TTCAAATGGA TGTTTTTCTG TTTACAGTGG TCGAGCAGCC
551  GTCCGACGGT GGCACGACG ATTTTCGAGC CGGCACGCAG GTCGGCGGTC
601  TGTGTGTTCA TATCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651  GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
  1  MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
 51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101  ALVVFCAATS TVSGAFMKSC ASLRIGAEKV AEKSRVWRWR GSICMILRMS
151  SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201  CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

	10	20	30	40	50	60
m680.pep	MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS					
g680	MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m680.pep	TLCLVLQNTMTWFICKSTISRSSRLRFKXVMVSTAMMCCSTLALVVFWAATSTVSGAFMKSC					
g680	TLCLVLQKTITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFWAATSTVSGAFMKSC					
	70	80	90	100	110	120
	130	140	150	160	170	180
m680.pep	ASLRIGAEKVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMFFCFTW					

q680

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

a680.seq

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

a680.pep

m680/a680 98.6% identity in 220 aa overlap

m680.pcp

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

g681.seq

```

101  tgatgtTTTC  GTCTGCTACG  CCCAATTCTT  GGAGGGTGCG  GCAGCAGACT
151  TTGAGCATTT  GGCTGCCGAT  TTCGTTGGTG  AAGCGTGCC  GTACGATGCC
201  GATGCCGAGG  TGTTCGCGT  cgaggttgGG  GGCGATGGTG  TTCATTGGGT
251  GTCCTTTGGT  ATTCGGGGTT  TCGGAATGCC  GTCTGAAGGT  TTCAGTCTTG
301  CGGCTGCCAG  TCGGCAACGG  TTTGGAATGT  GCCGTCTTCG  GCAAGCTCCC
351  ACGCGCTGCC  TTCGGGTTGG  GAAAGCAGTG  CGGCGGTTTC  AGGGTTGGTT
401  TTGGTCGATG  CGGCGAGGCT  GACGATGCTG  AAGTTGTCGG  GGTCTCGGT
451  GTATTCGTCG  GTTTCGTCGC  CGCTGAAGAA  ACGCCAGCCG  CTGTCGTTTT
501  CAAAAACGGG  GGCTTCGCGG  TAAAGGAAGC  CGACGGGCCG  GTTTTGTTTG
551  GCGACGGTGT  TGGTGGCGAT  GCAGCGGTCG  AGTGCCGAGG  AAAGTGCTTG
601  TGCAAATGCG  TTCATTGCGG  GAATACGTTG  GGGGGGGGGA  AACTTGCGGA
651  TTTTACCACG  ATTCCCGCGT  TGTCGCGAGA  CGGCGGCGGT  TTGGTGGTAC
701  AATGTGCGCC  GTTTCGAGCC  TTAAGGTGTT  TCTGTATTTT  TGGAGTATGG
751  AAACGCATTC  GGGCTGTTTT  TTGCGGAAGA  CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

g681.pep

```

1  MTPMAISAS  NFSEEAKFIS  AMGISSAPGT  VATVMFSSAT  PNSWRVRQQT
51  LSIWLPISLV  KRACTMPMRR  CLPSRLGAMV  FIGCPLVFGV  SECRLKVSVL
101 RLPVNGLEEC  AVFGKLPRAA  FGLGKQCGGF  RVGFGDVGEA  DDAEVVGVVG
151 VFVGFVAAEE  TPAAVVFKNG  GFAVKEADGP  VLFGDGVGGD  AAVECRGKCL
201 CKCVHCGNTL  GGGKLADFTT  IPALSADGGG  LVVQCAPFAA  LRCFCIFGVW
251 KRIRAVFCGR  R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

m681.seq

```

1  ATGACGACGC  CGATGGCAAT  CAGTGCGTCA  AACTTTTCGG  AAGAGGCAAA
51  GTTCATCAGC  GCGATGGGGA  TTTCAAGCGC  GCCGGGTACG  GTGGCGACGG
101 TAATGTTTTT  GTCTGCCACG  CCCAATTCTT  GGAGGGTGCG  GCAGCAGACT
151 TTGAGCATTT  CGCTGCCGAT  TTCGTTGGTG  AAGCGTGCC  GTACGATGCC
201 GATGCCGAGG  TGTTTGCCGT  CGAGGTTGGG  GGCGATGGTG  TTCATTGGGT
251 GTCCTTTGGT  ATTCGGAGTT  TCGGAATGCC  GTCTGAAGGT  TTCAGTCTTG
301 CGGCTGCCAG  TCGGCGACGG  TTTGGAATGT  GCCGTCTTCG  GCAAGCTCCC
351 ATGCGCTGCC  TTCGGGTTGG  GAGAGCAGTG  CGGCGGTTTC  AGGGTTGGTT
401 TTGGCGATGT  CGGCGAGGCT  GACGATGCTG  AAGTTGTCCG  GATCGTCGGT
451 GTATTGCTCG  GTCTCGTCGC  CGCTGAAGAA  ACGCCAGCCG  CTGTCGTTTT
501 CAAAAACGGG  GGCTTCGCGG  TAGAGGAAGC  CGACGGGCCG  GTTTTGTTTG
551 GCGACGGTGT  TGGTGGCGAT  ACAGCGGTCG  AGTGCCGAGG  AAAGTGCTTG
601 TGCAAATGCG  TTCATTACGG  GAATACGTTG  GGGG.AAAAC  TTACGGATTT
651 TACCACGATT  CGTGCCTTGT  CGGCAGACGG  CGGCGGTTTG  GTGGTACAAT
701 GTGCGCCGTT  TGCAGCCTTA  AGGTGTTTCT  GTATTTTGG  AGTATGAAA
751 CGCATTCGGG  CTGTTTTTTG  CGGAAGACGG  TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

m681.pep

```

1  MTPMAISAS  NFSEEAKFIS  AMGISSAPGT  VATVMFSSAT  PNSWRVRQQT
51  LSIWLPISLV  KRACTMPMRR  CLPSRLGAMV  FIGCPLVFGV  SECRLKVSVL
101 RLPVNGLEEC  AVFGKLPRAA  FGLGKQCGGF  RVGFGDVGEA  DDAEVVRIVG
151 VFVGLVAAEE  TPAAVVFKNG  GFAVEADGP  VLFGDGVGGD  TAVECRGKCL
201 CKCVHYGNTL  GXKLDTFTT  RALSADGGGL  VVQCAPFAAL  RCFCIFGVWK
251 RIRAVFCGRR  *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

m681/g681

```

m681.pep      10      20      30      40      50      60
               MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV
               |||
g681          10      20      30      40      50      60
               MTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV

```

1092

	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVG DGLECAVFGKLPCAA					
g681	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVGNGLECAVFGKLPRAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m681.pep	FGLGEQC GGF RVGFGDVG EADDAEVVRIVGVFVGLVAAEET PAAVVFKN GGF AVEEADGP					
g681	FGLGKQC GGF RVGFGDVG EADDAEVVG VGVFVGFVAAEET PAAVVFKN GGF AVKEADGP					
	130	140	150	160	170	180
	190	200	210	220	230	239
m681.pep	VLFGDGVGGDTAVECRGKCLCKCVHYGNTLGX-KLTDFTTIRALSADGGGLVVQCAPFAA					
g681	VLFGDGVGGDAAVECRGKCLCKCVHCGNTLGGGKLADFTTIPALSADGGGLVVQCAPFAA					
	190	200	210	220	230	240
	240	250	260			
m681.pep	LRCFCIFGVWKRIRAVFCGRRX					
g681	LRCFCIFGVWKRIRAVFCGRRX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2247>:

```

a681.seq
1  ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTC GTCTGCCACG CCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTGGG GCGATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGTCTGAAGG GTCAGTCCTT
301 AGGTTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCT GCCAATTCCC
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGGCGGTTT AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCTG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT GCAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAAATGCG TTCATTGCGG GAATACGTT. GGGGAAAAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAG
751 CGCATTCGGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2248; ORF 681.a>:

```

a681.pep
1  ITPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51  LSISLPISLV KRACTMPMRR CLPSRLGAMV FIECPLVFGG FGMPSEGSVL
101 RLPVGDGLEC AVFCQFPRAA FRLGEQC GGF RVGFGDIGEA DDAEVVRVVG
151 VFVGLVAAEE TPAAVVFKN GGF AVEEADGL VLFGDGVGGD AAVECRGKCL
201 CKCVHCGNTX GGKLADFTTI LALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGRR *

```

m681/a681 90.8% identity in 260 aa overlap

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGT VATVMFSSATPNSWRVRQQTLSISLPISLV					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGT VATVMFSSATPNSWRVRQQTLSISLPISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRRCLPSRLGAMVFIGCPLVFGVSECRLKVSVLRLPVG DGLECAVFGKLPCAA					
a681	KRACTMPMRRCLPSRLGAMVFIECPLVFGGFGMPSEGSVLRLPVG DGLECAVFCQFPRAA					
	70	80	90	100	110	120

	130	140	150	160	170	180
m681.pep	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKN	GGFAVEEADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVRV	GVFVGLVAAEET	PAAVVFKN	GGFAVEEADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pep	VLFGDGVGGDTAVE	CRGKCLCKCVHYG	NLTGXLTDFTTIR	ALSADGGGLVVQ	CAPFAAL	
a681	VLFGDGVGGDAAVE	CRGKCLCKCVHCG	NLTGXLTDFTTIR	ALSADGGGLVVQ	CAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pep	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

g682.seq

```

1   ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAAAT GCCGCTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGCTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

g682.pep

```

1   MRDFAVWPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIRFPTDR
101 PILTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

m682.seq

```

1   ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCC ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTG
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCCATTCGGA CAAGGCAGTC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

m682.pep

```

1   MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY.. EMAMPSEP DWIQTAFDMA YGFIRFPTDR
101 PIRTRQSGVV RISPRTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

1094

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          ||||:|||| |: ||||||||| |||:| ||||||||| ||||||||| |||||||||
g682      MRDFAVWVPYGERRKNWDIRYCLPHLIRLSPTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110
m682.pep  PILILIDY-----EMAMPSEPDWQIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFR
          |||||:| : ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
g682      PILILIDYICVNDEIKMPSEPDWQIQTAFMA-GFIRFPTDRPILTRQSGVVRISPRTGFR
          70      80      90      100     110

      120     130
m682.pep  YPTRSLPKSKKAYGX
          |||||||||
g682      YPTRSLPKSKKAYGX
      120     130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2253>:

```

a682.seq
  1  ATGCGCGATT TTACCGTATG GGTGTCTTAC GGGAAATGGC GGAAAAATTG
 51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101  TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151  ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201  ATAT.....
251  .....TATA TTCGGTTTCC AACTGACCGA
301  CCCATTCTGA CAAGGCCGAC AGGCGTTGTT CGGATTTTCG CACGAACGGG
351  TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401  GA

```

This corresponds to the amino acid sequence <SEQ ID 2254; ORF 682.a>:

```

a682.pep
  1  MRDFTVWVSY GKWRKNWDIR YCLLHLIHL SSTRLRKCGRI LSGICEPFCL
 51  ITPDLTMHYC PILILIEY.. ..YIRFPTDR
101  PILTRPTGVV RISPTGFRY PTRSLPKSKK AYG*

```

m682/a682 80.6% identity in 129 aa overlap

```

      10      20      30      40      50      60
m682.pep  MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
a682      MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFCLITPDLTMHYC
          10      20      30      40      50      60

      70      80      90      100     110     120
m682.pep  PILILIDYEMAMPSEPDWQIQTAFCMAYGFIRFPTDRPIRTRQSGVVRISPRTGFRYPTRS
          |||||:| : ||||||||| || || ||||||||| |||||||||
a682      PILILIEY-----YIRFPTDRPILTRPTGVVRISPRTGFRYPTRS
                      70      80      90      100

      130
m682.pep  LPKSKKAYGX
          |||||||
a682      LPKSKKAYGX
      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2255>

```

g683.seq
  1  ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTACT
 51  CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101  AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151  GACAGTGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
201  TGTTACCAAT CTGAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
251  CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
301  AGTTCGCTAC AGTTATTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
351  CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA

```

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683 >:

g683.pep
 1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
 101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq.
 1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
 151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT
 201 TGTTACCAAT CTAAAACAAG AACGTTTTCG CAACACCCCC GCATACAAGA
 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
 301 AGTTCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
 351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep.
 1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL
 101 SSLQLFDTKN TEISTQNYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPI	FLSFVLPIL	ITACSTPDKS	ARWENIGTIS	NGNIHTYINK	DSVRKNGNLM
g683	MIKETLMRPI	FLSFVLPIL	ITACSTPDKS	ARWENIGTIS	NGNIHTYINK	DSVRKNGNLM
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVVN	LNKQERFANT	PAYKTAIAEWE	IHCNNKTYRL	SSLQLFDTKN	TEISTQNYTA
g683	IFQDKKVVVN	LNKQERFANT	PAYKTAIAEWE	IHCNNKTYRL	SSLQLFDTKN	TEISTQNYTA
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLS	GTLTEKQYET	VCGKKLX			
g683	SSLRPMISLS	GTLTEKQYET	VCGKKLX			
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq
 1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTTATT
 51 CCCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
 101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA
 151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT
 201 TGTTACCAAT CTAAAACAAG AACGTTTTCG CNACACCCCC GCATACAAGA
 251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA
 301 AGTTCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA
 351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA
 401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAA ACTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep
 1 MIKETLMRPI FLSFVLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK
 51 DSVRKNGNLM IFXDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL

101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPILFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPILFLSFVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFXDKKVVTNLKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
a683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACCGCCGTGC	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAC	CTTTGTTTCT
301	GCCTCACGCA	GCGGCAGTAC	CGACAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLFPIAAL	TLAACGTQVS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGVLVQT	DPYRINTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAAL	QGLKQAAQQM	VE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTGC	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTTCT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLFPIAAL	SLAACGTQVS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGVLVQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD

Computer analysis of this amino acid sequence gave the following results:

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m684 . pep	MRLFP	IAAALS	LAACG	TVQST	QYFV	LPDSRY
g684	MRLFP	IAAALT	LAACG	TVQST	QYFV	LPDSRY
	10	20	30	40	50	60
m684 . pep	DPYRL	NTAQN	HVWAD	TLDDM	LEAALS	NAFNRL
g684	DPYRL	NTAQN	HVWAD	TLDDM	LEAALS	NAFNRL
	70	80	90	100	110	120
m684 . pep	STDFV	PASR	SGS	TEK	WTVY	IDAF
g684	STDFV	PASR	SGS	TEK	WTVY	IDAF
	70	80	90	100	110	120
m684 . pep	YTGKT	LISGY	AVLPD	GTNR	PFHIE	TEQQ
g684	YTGKT	LISGY	AVLPD	GTNR	PFHIE	TEQQ
	130	140	150	160	170	
m684 . pep	GDGYA	AMTAA	LEQGL	KQAA	QOMV	EX
g684	GDGYA	AMTAA	LEQGL	KQAA	QOMV	EX
	130	140	150	160	170	

```
a684.seq
1  ATGCGCCTCT TCCCGATTGC CGCCGCCCTG ACGCTTGCCG CCTGCGGTAC
51  TGTGCAAAAG ACACAATATT TCGTGTGTGC CGACACGCCG TACATCCGTC
101 CTGCAACGCA AGCGGCGGAA ACGTCCGTCG AAGTCCGTCT CTGCGAAGCCG
151 CTCAAACGCG GCGGACTGGT CTATCAAACC GACCCTTACC GCCTCAACAC
201 CGCACAAAAC CACGTCCTGG GACAGACCTT GGACGATATG CTCGAAGCGG
251 CGTTGAGCAA TGCATTCAAC CGTTTGGACA GCACACGCAT CTTTGTTCCT
301 GCCTCAGCGA CGCGGAGTAC CGAAAAATGG ACGGTCTATA TGCAGCGATT
351 CCAAGGCAGC TACACGGGCA AAACCTTCAT CAGCGGCTAC GCCGTCCTAC
401 CCGACGGTAC GAACAGACCC TTCCATATCG AAACCGAACA GCAGGGTGAC
451 GGCTACGCCG CCATGACCGC CGCATCGAA CAGGGACTGA AACAGGCGGC
501 GCAACAGATG GTCGAGTAA
```

a684.pep

1	<u>MRLFPIAAAL</u>	<u>TLAACGTVQS</u>	TQYFVLPDSR	YIRPATQGGE	TAVEVRLAEP
51	LKRGGLVYQT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQQM	VE*		

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

	10	20	30	40	50	60
m684.pep	MRLFP	IAAALS	LAACGTVQSTQYFVLPDSRYIRPATQGGETA	VEVRLAEPLKRGGLV	YQT	
a684	MRLFP	IAAALT	LAACGTVQSTQYFVLPDSRYIRPATQGGETA	VEVRLAEPLKRGGLV	YQT	
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQN	HVWADTLD	DDMLEAALSNAFNRLDSTRIFV	PASRSGST	EKWT	VYIDAFQGS
a684	DPYRLNTAQN	HVWADTLD	DDMLEAALSNAFNRLDSTRIFV	PASRSGST	EKWT	VYIDAFQGS
	70	80	90	100	110	120
	130	140	150	160	170	

```

m684 . pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
                |||
a684            YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
                130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685 . seq
1   TTGTTTGGCC GTATCGGGAA TTTTGCGTTT TGC GCGGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGcct GCGCCGTCTT GCCGGCCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATccgCCG CATCCCAAGC
201 CGCATCCACA CCTGTCGCCA CGCTGACCGT GCCGACCGCG CGGGGCGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgctg ccgtgtAcga CtggGCGGCG
301 TtggATACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTCG AGCCTGCATT TGACAAGGCG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TGCGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCATTA CCGGCGGGCC GGGTGC GGATATGAAC AGTTGGCGAA
501 AAACGCGACC ACCATAGATT TGACGGTGGG CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTTCGG TAAGGAAGCG
601 CCGCTGGCGG AATTGAATGC GCAGATTGAC GCGCTGTTTCG CCCAAAAGCG
651 CGAAGCCGCC AAAGGCAAAAG GACGCGGGCT GGTGCTGTCTG GTTACAGGCA
701 ACAAGGTGTC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGCGA
801 CCGGCAGCCC GTTCTCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAGG GCCGGCTGCC
901 GTGGAAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTGGAAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCGCGAA CTACATTGTC GCGGGCGGCG
1001 CCGGGCAGTT GATACAGGCG GCGGAACAGT TGAAGGCGGC GTTTGAAAAA
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685 >:

```

g685 . pep
1   LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAAEKT VSAASQAAST PVATLTVPTA RGDVAVPKNP ERVAVYDWAA
101 LDTLTPGVN VGATTAPVRV DYLPAPFDKA ATVTGLFEPD CESLHRHNPO
151 FVITGGPGAE AYEQLAKNAT TIDLTVDNNGN IRTSGEKQME TLSRIFGKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAGF TQSRLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFEYIKEKN PGWIFIIDRT AATGQEGPAA
301 VEVLNDAVLC GTNAWKRKQI IVMPAANYIV AGGARQLIQA AEQLKAFAFEK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

m685 . seq
1   TTGTTTGGCC GTATCGGGAA TTTTGCGTTT TGC GCGGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCCGTCTT GCTGACCGCC
151 TGTTCCGCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGGTGGA
351 TTATTTGCAG CCTGCATTTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTATTACC
451 GCGGGGCGCG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAG GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGCG
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGACG GGCAGCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGCGGCGT TTA AAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

m685 . pep

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51 CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKGKG RGLVLSVTGN KVSAGFTQSR LASWIHGDIG
251 LPPVDESLRN EHGQPVVSFE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQL KAAFKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

              10      20      30      40      50      60
m685.pep      LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT
              10      20      30      40      50      60
g685           LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPPEAAEKT

              70      80      90      100     110
m685.pep      VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
              70      80      90      100     110
g685           VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV

              120     130     140     150     160     170
m685.pep      DYLPAPFDKAATVGTLEFDPYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGN
              120     130     140     150     160     170
g685           DYLPAPFDKAATVGTLEFDPCESLHRHNPQFVITGGPGAEAYEQLAKNATTIDLTVDNGN

              180     190     200     210     220     230
m685.pep      IRTSGEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKGKGRGLVLSVTGNKVSAGF
              180     190     200     210     220     230
g685           IRTSGEKQMETLSRIFGKEARVAELNAQIDALFAQKREAAKGKGRGLVLSVTGNKVSAGF

              240     250     260     270     280     290
m685.pep      TQSRLASWIHGDIGLPPVDESLRNEGHGQPVVSFEYIKEKNPDWIFIIDRTAAIGQEGPAA
              240     250     260     270     280     290
g685           TQSRLASWIHGDIGLPPVDESLRNEGHGQPVVSFEYIKEKNPDWIFIIDRTAAIGQEGPAA

              300     310     320     330     340     350
m685.pep      VEVLDNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKAEPVAAAGKKX
              300     310     320     330     340     350
g685           VEVLDNALVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFEKAEPVAAQX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTTGCCTTT TGCGGCGTGG TTTCTGCAGG
51 TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTATAT TGGGCAGCCT GCGCCGTCTT GCTGACCGCC
151 TGTTCCGCCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTGTCAG CCTGCATTG ACAAGCGCGC AACGGTGGGG ACGCTGTTCTG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCTCAGCT TGTCATTACC
451 GCGCGGCCCG GCGCGGAAGC GTATGAACAG TTGGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGGAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAACT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

a685.pep

```

1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPAGAEAYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAAKKGK RGLVLSVTGN KVSFAGTQSR LASWIHGDIG
251 LPPVDESRLN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQL KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

m685/a685 98.9% identity in 355 aa overlap

	10	20	30	40	50	60
m685.pep	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
a685	LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m685.pep	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
a685	VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m685.pep	PAFDKAATVGTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
a685	PAFDKAATVGTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGNIRTS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m685.pep	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSTGNKVSFAGTQSR					
a685	GEKQMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSTGNKVSFAGTQSR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m685.pep	LASWIHGDIGLPPVDESRLNEGHPVSFEYIYEKNPDWIFIIDRTAAIGQEGPAAVEVL					
a685	LASWIHGDIGLPPVDESRLNEGHPVSFEYIYEKNPDWIFIIDRTAAIGQEGPAAVEVL					
	250	260	270	280	290	300
	310	320	330	340	350	
m685.pep	DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQLKAAFKKAEPVAAGKKX					
a685	DNALVRGTNAWKRKQIIVMPAANYIVAGGSRLIQAAEQLKEAFEKAEPVAAGKEX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

g686.seq (partial)

```

1  ..AATTTCTCCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgcGATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCGGCAA GCCGTTGTCC GGTGCTCGCG TTGTCGGTCA
201 GGTGAGGCGC GATATTTTGG GCAACGCCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)

```

1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..

```

1  ATGATGTTGA AAAAATTCGT ACTCGGCGGT ATTGCCGCAT TGGTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCTCCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTGCGCT ACTCCTTGGC TCAGCATACT ACCGGCATTG
251 TGGAACCGGT CGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTCTGA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTCAACG GGAATACCG CTTCATCAGA ATCGGAATGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep

```

1  MMLKKFVLGG IAALVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
51  GFGGIARSVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGGMVFV SVPMDAVKAK
151 SVNGTTGFIR IGM*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

				10	20	30
g686.pep				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACGGSEGGSGAXX	XXNFSCSADDVFNDICSAVEGFGGIARSVQLG				
	10	20	30	40	50	60
	40	50	60	70	80	90
g686.pep	AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS					
m686	AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS					
	70	80	90	100	110	120
	100	110	120	130		
g686.pep	GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFVRIGMX					
m686	GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)

```

1  ..AATTCTCCT GCCGCGCGGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAAGCTTC GCGGCGCATG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCGTCAGCA TACTACCGGT
151 ATTTGGGAAA CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGTAGGCG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAAGGC
351 TGATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG
51  IVETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVS PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N meningitidis*:

```

m686/a686 96.2% identity in 131 aa overlap

      10      20      30      40      50      60
m686.pep LKKFVLGGIAALVLAACGGSEGGSGAXXXNFSCSADDVFNDCISAVEGFGGIARSVQLG
a686                                     NFSCRADDVFDDICSAVESFGGIARSVQLG
                                     10      20      30

      70      80      90      100     110     120
m686.pep AVSGGAFESVAYSRLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
a686      AVSGGAFESVAYSRLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
      40      50      60      70      80      90

      130     140     150     160
m686.pep GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
a686      GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
      100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GCGGTTGCCG CCCTGTTCGC
51  CCTTGCCGCG TCGCAGACGA AAGTCCAAAC CAGCGTCCCC GCCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGCG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCCGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTTCG GCTATTTTTC TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAACAC GCCAAGTCTT TTAAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCGC TGGCAGCct
351 cGCCGCCGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACAA ACcgctTTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCAGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
601 GTCGGCGGCA AATATAAAGT CGAATTGCGC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687 >:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGQ
51  NYTVLANPIP QQAGKVEVL EFGYFCPhC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWQKE MLPLARLAAA VDMAAASKD VANSHFDAM VNQIKLQEP
151 EVLKKWLGEQ TAFDGKKVLA AYESPESQAR AGKMQLTET FQIDGTPTVI
201 VGGKYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCgGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCC GCCGAC AGCGCGCCTG
101 CGCGTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAAACTAT
151 ACGGTCTTTC CCAACCGGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCCGTGCGT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT

```

m687 . per

Computer analysis of this amino acid sequence gave the following results:

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

		10	20	30	40	50
m687.pep		MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIP				
g687		MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIP				
		10	20	30	40	50
		60	70	80	90	100
m687.pep		QQQAGKVEVLEFFGYFCPHCAHLEPVLSSHAKSFKDDMYLRTHEVWVWQKEMLTLARLAAA				
g687		QQQAGKVEVLEFFGYFCPHCARLEPVLSSHAKSFKDDMYLRTHEVWVWQKEMPLARLAAA				
		70	80	90	100	110
		120	130	140	150	160
m687.pep		VDMAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQAR				
g687		VDMAAAESKDVANSHIFDAMVNQIKLQPEVLKKWLGEQTAFDGKKVLAAYESPESQAR				
		130	140	150	160	170
		180	190	200	210	220
m687.pep		ADKMQLTETETQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAQX				
g687		AGKMQLTETETQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAQX				
		190	200	210	220	230

a687.seq

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

a687.pgp

```

1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51 TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWVQKEML TLARLAAAVD MAAADSKDVA NSHIFDAMVN QKIKLQPEEV
151 LKKWLGEQTA FDGKKVLAAV ESPESARQAD KMQELTETFQ IDGTPTVIVG
201 GYKVFEDAW ESGMNTIDLL ADKVREEOKA AH*

```


Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSRLHALGVAALFALAACDSKVQTSVPADSAPAASAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m687.pep	QAGKVEVLEFFGYFCPHCAHLEPVLKSKHAKSFKDDMYLRTEHVWQKEMLTARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLKSKHAKSFKDDMYLRTEHVWQKEMLTARLAAAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m687.pep	MAAADSKDVANSHIFDAMVNQIKIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m687.pep	KMQELTETFTQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAQX					
a687	KMQELTETFTQIDGTPVIVGGKYKVEFADWESGMNTIDLLADKVVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

```

1 GTGCTACACT AGACATCCCG ATTTGCACAG AAAGGTTCTC CCGTGAACAA
51 AACCCCTCATC CTCGCCCTTT CCGCCCTGTT CAGCCTGACC GCGTGCAGCG
101 TCGAACGCGT CTCGCTGTTT CCTCCTACA AACTCAAAAT CATCCAAGGC
151 AACGAACTCG AACCGCGCGC CGTTGCCGCC CTGCGCCCCG GCATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCTTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCGCAA CGGCATCATC
301 AAAGAACGCA GCAACCTGAC CGTCTATTTT GAAAACGGCG TACTCGTCCG
351 CACCGAAGGC GACGCCCTCC AAAATGCCGC CGAAGCCCTC CGCGCGAAAC
401 AAAACGCAGA CAAACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >:

g688.pep

```

1 VLH*TSRFAQ KGSPVNKTLI LALSALFSLT ACSVERVSLF PSYKLKIIQG
51 NELEPRAVAA LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTRNGII
101 KERSNLTVYF ENGLVLRTEG DALQNAEAL RAKQNADKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

```

1 GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGTG
101 CCGAACGCGT TTAAGTCTTC CCTCGTACA AACTCAAAAT CATAAGGGC
151 AACGAACTCG AACCGCGCGC CGTTGCCGCC CTCCGCCCCG GCATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCTTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCGCAA CGGCATCATC
301 AAAGAACGCA GCAATCTGAC CGTCTATTTT GAAAACGGCG TACTCGTCCG
351 CACCGAAGGC GACGCTCTGC AAAACGCTGC CGAAGCCCTC AAAGACCGCC
401 AAAACACAGA CAAACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

```

1 VLHYPSTRFAQ KGISVNKTLI LALSALLGLA ACSAERVSLF PSYKLKIIQG
51 NELEPRAVAA LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTRNGII
101 KERSNLTVYF ENGLVLRTEG DVLQNAEAL KDRQNTDKP*

```

1105

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

```
m688/g688      90.6% identity in 138 aa overlap

                10      20      30      40      50      60
m688.pep      VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPSYKLKIIQGNELEPRVAA
                ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688           VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVVERVSLFSPSYKLKIIQGNELEPRVAA
                10      20      30      40      50      60

                70      80      90      100     110     120
m688.pep      LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688           LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
                70      80      90      100     110     120

                130     140
m688.pep      DVLQNAAEALKDRQNTDKPX
                |:||||| |:|:|
g688           DALQNAAEALRAKQNAKQX
                130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
1  GTGTACTACT ACCATCCCG ATTTGCACAG AAAGGCATTT CCGTGAACAA
51 AACCCCTCATC CTCGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTTACTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTTT GAAACGCGC TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
1  VLHYPSRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLKIIQG
51 NELEPRAVAS LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLT VYF ENGVLVRTEG NALQNAAEAL RVKQNAKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688      93.5% identity in 138 aa overlap

                10      20      30      40      50      60
m688.pep      VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPSYKLKIIQGNELEPRVAA
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688           VLHYPSRFAQKGISVNKTLILALSALLGLAACSVERVSLFSPSYKLKIIQGNELEPRAVAS
                10      20      30      40      50      60

                70      80      90      100     110     120
m688.pep      LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
                ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688           LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKDRSNLT VYFENGVLVRTEG
                70      80      90      100     110     120

                130     140
m688.pep      DVLQNAAEALKDRQNTDKPX
                ::||| ||||| |:|:|
a688           NALQNAAEALRVKQNAKQX
                130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ..TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCCAT CGATGCCTAC CTGCCCGCGA
101 TTCCCGAAAT GGCGCAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGTATTATGTT CGGCACGGCG TTCGGGCAAG TGGCCGGCGG
201 CGCGGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTC ACCGGTTTGA
251 TTGTATATTG CCTTGCCGTT GCCGCCATCG TATTTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTC ggtgcatggt tgcgcgatTA TTATCCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTC TGATGGTTGT GCCGCTGGCC
451 GCACCATAGG TCGGCGCATT GTTGCAAGGA TTGGGCGGAT GCGGGCGCAT
501 TTTTCGTTTT ttggcGgcgt ATTCCCGGT GCTGCCCGGT TTGGTACAGT
551 ATTTCTTGCC CAATCCGCGC GTCGGCGGCA AAATCGGCAG GGATGTGTTC
601 GGGCTGGTGG CCGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCCGCAT
651 GGGTtatCTG TTTTTTCAGG CATTACAGCT CGGTTTCGATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CCGTACGCAT GGGTGTTCG ACTCAACATC ATCAGCATGA TGTTTTTCAG
801 CCGCGTTACC GCGTGGCGGC TAAAACCGG CGCGCATCCG CAAAGCATCC
851 TGCTGCGGGG GATTGTCGTC CAATTGCGC CCAACCCGTC CCAACTCGCC
901 GCCGTGCTGT TTTTCGGGTT GCCCCCGTTT TGGCTGCCGG TCGCGTGCCT
951 GATGTTTTTC GTCGGTACGC AGGGCCTGGT CCGTGCGGAC ACGCAGGCAT
1001 GCTTTATGTC TTATTTCAAA GAAGAGGGCG GCAGCGCGAA CGCCGTGTTCG
1051 GGTGTATTCC GGTCTTAAT CGGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGAAGGAAA ACGAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

g689.pep (partial)

```

1  ..SPPLPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFETA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYYSG RKAQMFAFI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPG LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAAMGYL FFQAFSFGSM FAFLTESSFV YRQLYHVTPH
251 RYAWWFALNI ITMMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSOLA
301 AVLFFGLPPF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTGTGCGG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CTTCTGCCCC ATTATCTGA AATGAGCGAA AAATGATGG CGGTTTTGAT
201 GCGGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCC
251 CGATTCCCGA AATGGCGCAA TCCTGAACG CGGATGTTC CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCGG
351 CCGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTGTG TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGTG CCGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCGCGA TTATTATTCC GGACGCAAAG
551 CCGCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTCTGGCGG CGTATTGCTG GGTGCTGCTC GGTTTGTGAC
701 AGTATTTTCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTCGGTTTC ATGTTTCGCT
851 TTCTGACCGA ATCTTCTTTC GTGTACGAG AGCTCTACCG TGTTACGCCT
901 CATCAATACG CTTGGGCGTT TGCACTCAAC ATCATCAGTA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAC CCGCGTGCAT CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTCGGTGCA AACACGAGG
1151 CGTGTTTTTT TCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGACG GACGGTTCGG CAACCGTGAT GCGCGCAACG ATGACCGCGT
1301 CCACCTCTTG CCGCATTCGG CTCTGTGGC TCTGCTCGCA TCGTGCGTGG

```

1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA

This corresponds to the amino acid sequence <SEQ ID 2294; ORF 689>:

```

m689.pep
1  LLIHIVPVR  PVLPGLLP  VCAGVLKFSV  SAYCVFRRRA  VCLRIGREFM
51  PSAHYPEMSE  KLMAVLMAML  VTLMPFSIDA  YLPAIPEMAQ  SLNADVHRIE
101 QSLSLFMFGT  AFGQVVGGSV  SDIKGRKPVA  LTGLIVYCLA  VAAIVFVSSA
151 EQLNLNRVVO  AFGAGMTVVI  VGAMVRDYYS  GRKAAQMFAL  IGIILMVVPL
201 VAPMVGALLQ  GLGGWQAI  FLAAYSLVLL  GLVQYFLPKP  AVGGKIGRDV
251 FGLVAGRFKR  VLKTRAAMGY  LFFQAFSFGS  MFAFLTESSF  VYQQLYRVTP
301 HQYAWAFALN  IITMMFFNRV  TAWRLKTGVH  PQSILLWGIV  VQFAANLSQL
351 AAVLFFGLPP  FWLLVACVMF  SVGTQGLVGA  NTQACFMSYF  KEEGGSANAV
401 LGVFQSLIGA  GVGMAATFLH  DGSATVMAAT  MTASTSCGIA  LLWLCSHRAW
451 KENGQSEYL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

```

          30      40      50      60      70      80
m689.pep  CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSIDAY
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
g689      SPPLPPMSGKLMAVLMAMLVVALMPFSIDAY
          10      20      30

          90      100     110     120     130     140
m689.pep  LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLAV
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
g689      LPAIPEMAQPLNADIHRIEXSLSLFMFGTAFGQVAGGAVSDIKGRKPVALTGLIVYCLAV
          40      50      60      70      80      90

          150     160     170     180     190     200
m689.pep  AAIVFVSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYSGRKAAQMFALIGIILMVVPLV
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
g689      AAIVFASSTEQLLNLRVQAFGAGMAVVIVGAMVRDYSGRKAAQMFALIGIILMVVPLA
          100     110     120     130     140     150

          210     220     230     240     250     260
m689.pep  APMVGALLQGLGGWQAI  FLAAYSLVLLGLVQYFLPKPAVGGKIGRDV  FGLVAGRFKRV
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
g689      APMVGALLQGLGGWRAIFVFLAAYS  PVLPGLVQYFLPNPAVGGKIGRDV  FGLVAGRFKRV
          160     170     180     190     200     210

          270     280     290     300     310     320
m689.pep  LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
g689      LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYRQLYHVT  PHRYAWVFALNIITMMFFSRVT
          220     230     240     250     260     270

          330     340     350     360     370     380
m689.pep  AWRLKTGVHPQSILLWGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMF  SVGTQGLVGAN
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
g689      AWRLKTGAHPQSILLRGIVVQFAANPSQLAAVLFFGLPPFWLPVACVMF  SVGTQGLVGAD
          280     290     300     310     320     330

          390     400     410     420     430     440
m689.pep  TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDG  SATVMAATMTASTSCGIAL
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
g689      TQACFMSYFKEEGGSANAVSGVFRSLIGAGVMAAT-----VMAATMTASASCGIAL
          340     350     360     370     380

          450     460
m689.pep  LWLCSHRAWKENGQSEYLYX
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
g689      LWLCSHKAWKENEKKRIL
          390     400

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTGC CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTTCCGTT TCCGCGTATT
101 GTGTTTTCCG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAACGTATGG CGGTTTTGAT
201 GGCATGCTG GTTACGCTGA TCCGTTTTTC CATCGATGCC TACCTGCCCC
251 CGATTCCCCA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCACG GCGTTCGGAC AGGTGGTCGG
351 CGGTTCCGGT TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCGGAC
401 TGCCCGTCTA CTGCCTTGCC GTTGCCGCCA TCGTATTTGC TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGGT CCGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGC CGA TTATTATTCC GGACGCAAAG
551 CCGCCCAGAT GTTTGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGGCG ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATTTTTGTT TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTTCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAAA CCGGTGCCGC
801 GATGGGTTAT CTGTTTTTTC AGGCATTGAG CTTCCGGTTCG ATGTTCCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CACCAGTACG CTTGGGCGTT TGCACCAAC ATCATCACGA TGATGTTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CCGCGTGCA TCCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTC GTCCCAACTC
1051 GC CGCCGTCG GTTTTTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTCCGGTGA AACACGCAGG
1151 CGTGTTTTAT GTCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGGAC
1251 CTTCTTGCAC GACGGTTCGG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CCGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTGCCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1  LLIHYIVPVR PVLPGLLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPFSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLNLNRVQ AFGAGMTVVI VGAMVRDYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAQSFSG MFAFLTESSV VYQQLYHVT
301 HQYAWAFALN IITMMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

```
m689/a689 99.1% identity in 459 aa overlap

m689.pep      10      20      30      40      50      60
               LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE
a689          10      20      30      40      50      60
               LLIHYIVPVRPVLPGLLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE

m689.pep      70      80      90      100     110     120
               KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV
a689          70      80      90      100     110     120
               KLMAVLMAMLVTLMPFSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV

m689.pep     130     140     150     160     170     180
               SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYS
a689         130     140     150     160     170     180
               SDIKGRKPVALTGLAVYCLAVAAIVFSSAEQLNLNRVVQAFGAGMTVVIVGAMVRDYS

m689.pep     190     200     210     220     230     240
               GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP
```

```

|||||
a689      GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAI FVFLAAYSLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFRKRLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFGVLVAGRFRKRLKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYHVT
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          |||||
a689      HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFFGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLVGFQSLIGAGVGMAATFLH
          |||||
a689      FWLLVACVMFSVGTQGLVGANTQACFMSYFKEEGGSANAVLVGFQSLIGAGVGMAATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEYLX
          |||||
a689      DGSATVMAATMTASTSCGIALLLWLC SHRAWKENGQSEYLX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

g690.seq (partial)

```

1   ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGCCGCGCGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCTTC GTCTTCCGCG TCATCGGCTT CTTCCTCAAC CGATTGCAA
151 CCGGCCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATGCG ACCGGCCTGC ACCCGCCGCG CGGCATTGGC GATCTCATAC
251 AGCAAATCGC CGAACACATC GACTCGGACT GTCTGTTTGC CCTTCCCAT
301 AACGAACTGG AAACCCGTTT CGGCTTACCC GCGCGCGGCT ATGACAACAT
351 ACAGCGGctG CTgtttCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGccgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACCCGC GGaCAAGGCG
551 AGGAACCGAA ACGCGCACGT TATTTTGAAG TTTCGGCAAC ATctgcCtaT
601 TTgaaccgGc ACAaacaacGG ACTTggcgGc AATTTCCAAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTtagAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTGc TTTACGAAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

g690.pep (partial)

```

1   MKNKTSSLPL WLAAIMLAAR SPSKEDKtKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVQ QAESAPL*NC TGLHPAAGIG DLIQQIAEHI DSDCLFALSH
101 NELETRFGLP GGGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSQKTR GQGEePKRAR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPFLD
251 IHFDENGKIT RIVVYEKNiY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

m690.seq..

```

1   ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACCGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGCAT
101 CCGCTGCTTC GTCTTCCGCG TCATCAGCTC CTTCCTCAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATGCG ACCAGCCTGC ACCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAATCGC CGAACACATT GACTCGGACT GTCTGTTTGC CCTTCCCAT
301 CACGAACTGG AAACCCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCACGATC
451 AGCCGGCAGG CAAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

```

1110

```

551 AGGAGCCGAA ACGCAGCGGT TATTTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTTCGAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTGTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
  1 MKNKTSSLLL WLTAIMLTAC SPSKDDKTKE VGASAASSA SSAPSQTDLQ
 51 PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQKIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEEPKRTR YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKIHGEMLE NQSLFRLSNR ERNPDKPFLD
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690      89.3% identity in 408 aa overlap

      10      20      30      40      50      60
m690.pep  MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSASSAPSQTDLQPTASAPDNVK
          |||||  |||||  |||||  |||||  |||||  |||||
g690      MKNKTSSLPWLAAIMLAARSPSKEDKTKENGASAASSASSASSQTDLQPAASAPDNVK
          10      20      30      40      50      60

      70      80      90      100     110     120
m690.pep  QAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNIQRL
          |||||  |||||  |||||  |||||  |||||  |||||
g690      QAESAPLXNCTGLHPAAGIGDLIQIAEHIDSDCLFALSHNELETRFGLPGGGYDNIQRL
          70      80      90      100     110     120

      130     140     150     160     170     180
m690.pep  LFPDIRPEDPDYHQKIILAIEDLRYGKRTISRQAQNALMEQERRLREATL LLIQGSQETR
          |||||  |||||  |||||  |||||  |||||  |||||
g690      LFPDIRPEDPDYHQKIMLAIEDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
          130     140     150     160     170     180

      190     200     210     220     230     240
m690.pep  GQGEEPKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRLSNR
          |||||  |||||  |||||  |||||  |||||  |||||
g690      GQGEEPKRARYFEVSATSAYLNRHNNGLGGNFQYIGQLPGYLMKHGEMLENQSLFRLSNR
          190     200     210     220     230     240

      250     260     270     279
m690.pep  ERNPDKPFLDIHFDENGKITRIVVYEKNIYFNPNTGRIX
          |||||  |||||  |||||  |||||
g690      ERNPDKPFLDIHFDENGKITRIVVYEKNIY
          250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
  1 ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
 51 GACCGCGTGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCGCTC GTCCACGGCA TCCGCGCGCTT CGTCTTCCGC GCCCAAACC
151 GATTTGCAAC CGGCCGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCCGCG TCAAATTGCA CCGACCTGCA CCCCGCCACC GGCAATTGACG
251 ATCTCATGCA GCAAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG CGGCGGGCTA
351 TGACAAACATA CAGCGGCTGC TGTTCCCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGCG TTACGGAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGCAGTCAA GAAACCCGCG
551 GACAAGCGCA GGAGCCGAAA CGCACGCGTT ATTTTGAAGT TTCGGCAACC
601 CCTGCCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG
 751 TTTTTAGACA TCCATTTTGA CGAAAATGGC AAAATCACGC GTATTGTCGT
 801 TTACGAAAAA AACATCTACT TCAATCCAAA CTTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep
 1 MKNKTSSLLL WLAAMMLTAC SPSKEDKKE NGASAASSTA SAASSSAPQT
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPPK RTRYFEVSAT
 201 PAYSSRHNNG LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP
 251 FLDIHFDENG KITRIVVYEK NIYFNPNLGR R*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

	10	20	30	40	50
m690.pep	MKNKTSSLLLWLTAIMLTACSPSKDDKTKEVGASAASSSASSAPS---QTDLQPTASAPD				
a690	MKNKTSSLLLWLAAMMLTACSPSKEDKTKEVGASAASSTASAASSSAPQTDLQPAASAPD				
	10	20	30	40	50
	60	70	80	90	100
m690.pep	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
	70	80	90	100	110
	120	130	140	150	160
m690.pep	QRLFPDIRPEDPDYHQKIILAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ				
a690	QRLFPDIRPEDPDYHQKIILAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ				
	130	140	150	160	170
	180	190	200	210	220
m690.pep	ETRGQGEPPKRTTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLENQSLFRL				
a690	ETRGQGEPPKRTTRYFEVSATPAYSSRHNNGLGGNFQYIGQLPGYLKIHGEMLENQSLFRL				
	190	200	210	220	230
	240	250	260	270	279
m690.pep	SNRERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNTGRIX				
a690	SNRERNPDKPFLLDIHFDENGKITRIVVYEKNIYFNPNLGRRX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq
 1 GTGCCGCTGC CTGCTCCCTG CCGTTTTGCC AAACCTGCCG CCTCTTTTTT
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCGGCC ACGGCTTATA
 101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGGCTG
 151 ACACAGGGTC AGCACAATGA GCTGCGTAA ATCCGCGGCC CCTTCAAAAT
 201 GCGGGGCGAC AGGGCGCGTT TGAAGGTAT GCATTCCGAA CACAGCCGCC
 251 GCCGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG
 301 GCGCGCGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTTGCGGT
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC
 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep
 1 VLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
 51 TQGHNELRK IRAAFKMAGD RARLKVHSE HSRRSVVEI ISSDVFNRE
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*

1112

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCGGAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GCTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCTT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGAD RARLKMVHSE HSRRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQHRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691    97.2% identity in 144 aa overlap

          10      20      30      40      50      60
m691.pep    VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
          |||
g691         VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
          10      20      30      40      50      60

          70      80      90     100     110     120
m691.pep    IRTAFKMGADRARLKMVHSEHSRRRSVVEI ISSDVFNENE ARDYVESRYLSGMDFAVDEL
          |||
g691         IRTAFKMGADRARLKMVHSEHSRRRSVVEI ISSDVFNENE ARDYVESRYLSGMDFAVDEL
          70      80      90     100     110     120

          130     140
m691.pep    EIQHRFFHILTPQQQMWLS SCLKX
          |||
g691         EIQHRFFHILTPQQQMWLS SCLKX
          130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCCCCCTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTCCTCGG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACCGCAAC
401 AGCAGCAAAT GTGGCTTCTT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGAD RARLKMVHSE HSRRRSVVEI ISSDVFNENE
101 ARDYVESRYL SGMDFAVDEL EIQHRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

m691/a691 97.2% identity in 144 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2309>

This corresponds to the amino acid sequence <SEQ ID 2310; ORF 692 >:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2311>:

```
m692.aae
1  GTGTTGCACA  CGCTTTGTCTG  CTGTTTCGGAA  TCGATACGCC  GGATTTCGGCG
51  GAATGGCAGG  GAATGGCGGA  TTAAGGACA  AAAATGCCGT  CTGAACACGG
101 ATACAGTTCA  GACGGCATCA  TTTTATACGA  CTGCCTTATT  TGGCTGCGCC
151 TTCATTCCAT  CGCGCAGGGG  ATTTGTAGCC  CTCGAAGCGT  TTGTGCGCGT
201 AGGCTTTGAA  CGCCTCGGAG  TTATAGCCCT  CGGTTACGTC  TTTAAGCACT
251 TGGCTGTCTT  TGTCTGGCGGT  TTTGACGGCA  GACCAGTTGA  CATAGGCAAA
301 GCTCGGTTCT  TGTAAACAGG  CTCCTGGTCA  CTTACATGCC  CTGCTTTATG
351 CGTAGTTGCC  GTTGACGACG  CGAAAATCCA  CGTCGGCGCG  GCTACGCGGG
```

m692.pgp

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m692 . pep	VLHTLCRCSESIRRI	RNRNGREWRIK	GQKCR	LNTDTVQTASFY	TALFGCAFIP	PCGRGFVA
g692	VSHTRCRCSESIRRI	WRNGREWRIK	GQKCR	LNTDAVQTASFY	TALFGCAFIP	PCGRVFVA
	10	20	30	40	50	60
m692 . pep	70	80	90	100	110	120
	LEAFVRVGF	ERVIGLVYFK	PLAVFVG	GDFGRPVDIG	KARFLEQG	FGQLHAAAYGVVA
g692	LEAFVRVGF	ERVIGLVYFK	PLAVFVG	GDFGRPVDIG	KARLLEQG	FGQLHAAAYGVVA
	70	80	90	100	110	120
m692 . pep	130	140	150	160	170	180
	VDDGKI	HVGAA	TRLRGL	KLDDFDV	FQVLGDV	RFVGGCQRIDAVFE
g692	VDDGKI	HVGAA	ARQLCG	FKLDDFDV	FQVFRDV	GFVGGCQRIDAVFE
	130	140	150	160	170	180
m692 . pep	190	200	210	220	230	240
	VGRVVGR	GYGAAV	DFDFQRF	QQLARVQS	QRRGRH	LEDFGDVQIVFFFEVVKIGFVLEDVDV
g692	VGRVVGR	GYGAAV	DFDFQRF	QFARIQS	QRRGRH	LEGFGDVQVFFFEIVKIGFVLEDVDV
	190	200	210	220	230	240
m692 . pep	250	260	270	280	290	
	QLALSQC	QIRAYI	VGKLDQ	FDGVAFFL	QLGLDL	FFDHIAEVADGRAEDDDFFERRAVVG--
g692	QLALRQC	QIRAHV	VGKFDQ	FDGVAFFL	QLGLDL	FFDHIAEVAHGRAEDDDFFERRAVIGRR
	250	260	270	280	290	300
m692 . pep	300	310	320	330		
	GGRSGCG	GRAVFL	TAAAGDE	RECGGKG	FEEGFH	IFSX
g692	GGRSGCG	-RAVFL	TAAAGDE	RECGGKG	FEEGFH	IFSX
	310	320	330			

a692.seq

1 GTGTTGCACA CGCTTTGTCG CTGTTCGGAA TCGATACGCC GGATTCGGCG

1115

```

51 GAATGGCAGG GAATGGCGGA TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCATTCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGGCTGTCTT TGTCGGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTTCT TGGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTG ATGTTTTTCA GGTTTTCGGC
451 AATGTCCGCT TTGGATGCGG TCAGCGGATT GATGCCGTCT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGCGCAA GTTGACGCGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGGTACAGTC CCAAAGGCGC GGTGCGCACT TGGGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTTCG
751 GCGCACATAG TCGGTAAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCGGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCGGTTGT CGGCGGCGGC
901 AGAAGCGGAT GCGGCGGGCG CGCTATCTT TTGACGCGC CAGGCGGCGA
951 GGATGAGCGC GAGTGCGGCG GCGGAAAGG TTTGAAGAA GGTTTTCATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

a692.pep

```

1 VLHTLCRCSE SIRRIIRNGR EWRIGQKCR LNTDTVQTAS FYTTALFGCA
51 FIPCGRGFVA LEAFVRVGF E RVGVIGLYV FKPLAVFVGG FDGRFPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVVFQVFG
151 NVRFQCGQRI DAVEFDPTQ FVEHHQDAGE VGRVVGGRYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251 AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVGGG
301 RSGCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

m692/a692 98.8% identity in 336 aa overlap

	10	20	30	40	50	60
m692.pep	VLHTLCRCSE	SIRRIIRNGR	EWRIGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
a692	VLHTLCRCSE	SIRRIIRNGR	EWRIGQKCR	LNTDTVQTAS	FYTTALFGCA	FIPCGRGFVA
	70	80	90	100	110	120
m692.pep	LEAFVRVGF	ERVGVIGLYV	FKPLAVFVGG	FDGRFPVDIG	KARFLEQGF	QLHAAAYGVVA
a692	LEAFVRVGF	ERVGVIGLYV	FKPLAVFVGG	FDGRFPVDIG	KARFLEQGF	QLHAAAYGVVA
	130	140	150	160	170	180
m692.pep	VDDGKIHVGA	ATRQLRGFKL	DDFDVVFQV	LGDFRFGCG	QRI DAVFE	FDPTQFVEHHQDAGE
a692	VDDGKIHVGA	ATRQLRGFKL	DDFDVVFQV	LGDFRFGCG	QRI DAVFE	FDPTQFVEHHQDAGE
	190	200	210	220	230	240
m692.pep	VGRVVGGRYG	AAVDFDFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
a692	VGRVVGGRYG	AAVDFDFQRF	QLARVQSQR	GRHLEDFGDV	QIVFFFEVVK	IGFVLEDVDV
	250	260	270	280	290	300
m692.pep	QLALSQCQIR	AYIVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRRAVVGGG
a692	QLALSQCQIR	AYIVGKLDQF	DGVAFFLQLG	LDLFFDHIAE	VADGRAEDDF	FFRRAVVGGG
	310	320	330			
m692.pep	RSGCGGRAIF	LTAAGGEDER	ECGGKGFEF	GFHIFS		
a692	RSGCGGRAIF	LTAAGGEDER	ECGGKGFEF	GFHIFS		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```
g694.seq
1   TCGGCATTTG TGTGCCCCAA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGCA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGGCCTGCC GTTACGCCGA CTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GcaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
401 GTTTGCCGGT TGGTCGTCGC ATAGCAGATG TCTTCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
501 CGACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTG GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCTTCGAC CTCGGCGTGC CCCTTATGCC
651 CGATCATGAT GATTTTCAGT TCTTGGGCAT CCACTCGGGC GACTTCCTTA
701 TGCACTTTCC TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAACCGCG
751 CTCCGCCGCT TCTTGCTGCA CCGCCTTCGA TACGCCGTGT GCCGAATAAA
801 CAGTGTGCGC GCCCGGCGGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATTCTTC CAAAGCACGT TCGACAATAC
951 TGATTGCCCG ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTTC CGTTCATAAG TTTTGCATTC CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694 >:

```
g694.pep (partial)
1   SAFVLPKHPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPPFAHG
51  FMPPSAYGCO YFPHQHFGRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVQRG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHFRHQR ASRIKYPETA
251 LRRFLLHRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQVV HDEFVVDDEV
301 AHNRRRAEFF QSTFDNTDCP IHTGAEEAARI GKDDGFSVHK FCIPCSDGIH
351 VFLLXLCDGR YCQAPPTPHR RR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```
m694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCCGAC TTTGTTTTTG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTC TGCCAACCTT TTGACGGCGG TTTGCCGGTT
451 GGTGCTCGCA TAGCAGATAT CTTCTTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GCGCAAGCT
651 GCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG
701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGGA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTCTCC AAAGCACGTT CGACAATACT GATT GCCCGA
1001 TCCACACCCG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTT GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTTCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA
```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```
m694.pep
1   LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGGLPV
```

1117

```

151 GRRDIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VENKHRTFFT
301 QVVHDEFVFN DVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

m694/g694 86.8% identity in 372 aa overlap

```

m694.pep      10      20      30      40      50
LVSASGTRQKRLKPVTAFVLPKHS---TPASTFAQIGFGFALAAQLFGQDEHNAFFR
g694          10      20      30      40
SAFVLPKHMPALTPASTFAQIGFGFALAAQLFGQDEHDAFFR

m694.pep      60      70      80      90     100     110
TLAFAYGFVPPSAYGCQYFPHQHFGGRGRACRYADVFALKPCALQVACIIHHIRIDSARC
g694          50      60      70      80      90     100
APPPAHGFMPPSAYGCQYFPHQHFGGRGRACRYADFAFAFKPRALQVGRVHHIRIDSARC

m694.pep     120     130     140     150     160     170
RHFAQAVAVGRIGRTDHNHDFALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
g694         110     120     130     140     150     160
RHFAQAVAVGRIGRTDHNHDFALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV

m694.pep     180     190     200     210     220     230
FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARRKLPHRSFDLVPLMPDHDDFT
g694         170     180     190     200     210     220
FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKHFAARCKLPHRAFDLGVPLMPDHDDFT

m694.pep     240     250     260     270     280     290
VLGIQSGDFLMHFRHQASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
g694         230     240     250     260     270     280
VLGIQSGDFLMHFRHQASRIKYPETALRRFLHRLRYAVCRINQCRARRHFRQVFDKHR

m694.pep     300     310     320     330     340     350
TFFTQVVHDEFVVDVFAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
g694         290     300     310     320     330     340
AFFAQVVHDEFVVDVFAHINRRAEFFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI

m694.pep     360     370     380
SFSDDGINIFLLGFYGGRCCTPPTPHRRRX
g694         350     360     370
PCSDGIHVFLXXLCDGRYCAFPPTPHRRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGGCG AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTTCGCACT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCGGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTC TGCCAACCTT TTAGCGGCGG TTTGCCGGTT
451 GGTCGTCGCA TAGCAGATAT CTTCTTGTG CCGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTCT GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTGCCC GGCACAAGCT
651 GCCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG

```

1118

```

701 ATTTACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACCAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAAT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGCCAAC ACCGCCAACA CCGCACCGAC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

a694.pep

```

1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDVALF CQLFDGGLPV
151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRVAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DFVAHINRRA ELFQSTFDNT DCPIHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

m694.pep	10	20	30	40	50	60
a694	10	20	30	40	50	60
m694.pep	70	80	90	100	110	120
a694	70	80	90	100	110	120
m694.pep	130	140	150	160	170	180
a694	130	140	150	160	170	180
m694.pep	190	200	210	220	230	240
a694	190	200	210	220	230	240
m694.pep	250	260	270	280	290	300
a694	250	260	270	280	290	300
m694.pep	310	320	330	340	350	360
a694	310	320	330	340	350	360
m694.pep	370	380				
a694	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```

g695.seq
1   TTGCCTCAAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGTTGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTATGC GCCGCCCAGT
101 GTCAAAATTC TCAAAGATTT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGTCCCCATC ACCCTGCCCG TCGGCGACGG TTGACCCTG CTTCTGAAAA
201 AATAATGAAG ACCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCTG
251 CCTCCTGTGC TTCCGTTTCA CCGTTCGGG AGGCGAGCCG AACCGAAATG
301 CCGACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAT GTTAAACGGG AAAGTCAAAG CATTTGGAGCA TACGAAAATA
451 CACCCTTCCG GCAGGACATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAAACGGC
601 AGGTTTTCTG CCGCAGCCGC CTGTGTGAAG GGGCGGACG GCGGAGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGTGCAA AGCAGGGCGC
701 GTATGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCGAA GTCATATTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTACGCA AACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```

g695.pep
1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCQNSQRF QSKPAERYAD
51  CPHPPARRRR FDPASEKIMK TKLPLFIIWL SVSASCASVL PVEGSRTEM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLV NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAACKRAAA
301 AVRKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```

m695.seq
1   TTGCCTCAAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATTT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGTCCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTTGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCGTTCGGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTCGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTGC
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAAGCGGC
601 AAGTTTTCTG CCGCTGCCTC CTGTGTGAAA GGCAGGACG GAGGCGACGG
651 CGGCAGCATC GCGCAACGCA GTATGTACCT GTTGTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCGAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATGCCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG CGCCGCCGCA
901 GCCGTGCGCA AACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```

m695.pep
1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHAKT
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQNLV NQALKHYKSG
201 KFSAAASLLK GADGGDGGSI AQRSMYLLQ SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQQKDIARA TWRSLIQTYP GSPAACKRAAA
301 AVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:

1120

m695/g695 90.8% identity in 305 aa overlap

m695.pep	10	20	30	40	50	60
	LPQTRPSRRHRRHQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR					
g695	10	20	30	40	50	60
	LPQTRPARRRHRRHQYFVERKGDARSGFXCAAQCQNSQRFQSKPAERYADCPHHHPARRRR					
m695.pep	70	80	90	100	110	120
	LDPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
g695	70	80	90	100	110	120
	FDPASEKIMKTKLPLFIIWLSVSASCASVLPVPEGSRTTEMPTQENASDGIPYPVPTLQDR					
m695.pep	130	140	150	160	170	180
	LDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTEGGSASA					
g695	130	140	150	160	170	180
	LDYLEGKIVRLSNEVEMLNGKVKALEHTKIHPSGRITYVQKLDLDRKLKEHYLNTEGGSASA					
m695.pep	190	200	210	220	230	240
	HTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGIAQRSMYLLQLQSRARMGNCS					
g695	190	200	210	220	230	240
	HTVETAQNLYNQALKHYQNGRFSAAALLKGADGGDGGGIAQRSMYLLQLQSRARMGNCS					
m695.pep	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
g695	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAAKRAAA					
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

1	TTGCCTCAAG	CTTGTCGGCG	AAGGCGGCAT	CATTGCCATC	GACAATATT
51	TGTTGAACGG	AAGGGTGATG	CGCGAAGCGG	CTTCCGATGC	GCCGCCAGC
101	GTCGGCATCC	TCAAAGATT	TAATCAAAC	CTGCCGAACG	ATACGCGGAT
151	TGTCCCATC	ACCCTGCCCG	TCGGCGACGG	TTTGACCCTG	CTTCTGAAAA
201	AATAATGAAG	ACCAAATTAC	CGCTTTTAT	CATTGGCTG	TCCGTATCCG
251	CCGCCTGTC	TTCCCTGTT	TCCCGCAATA	TTCAGGATAT	GCGGCTCGAA
301	CCGCAGGCAG	AGGCAGGTAG	TTCGGACGCT	ATTCCCTATC	CCGTTCAC
351	TCTGCAAGAC	CGTTTGATT	ATCTGGAAGG	CACACTCGTC	CGCTGTGCGA
401	ACGAAGTGA	AACCTTAAAC	GGCAAAGTCA	AAGCACTGGA	GCATGCGAAA
451	ACACACCCTT	CCAGCAGGCG	ATACGTCCAA	AAACTCGACG	ACCGCAAGTT
501	GAAAGAGCAT	TACCTCAATA	CCGAAGGCGG	CAGCGCATCC	GCACATACCG
551	TGGAAACCGC	ACAAAACCTC	TACAATCAGG	CACTCAAACA	CTATAAAGC
601	GGCAGGTTT	CTGCCGCTGC	CTCCCTGTTG	AAAGGCGCGG	ACGGAGGCGA
651	CGCGGCGCAG	ATCGCGCAAC	GCAGTATGTA	CCTGTTGCTG	CAAAGCAGGG
701	CGCGTATGGG	CAACTGCGAA	TCCGTCATCG	AAATCGGAGG	GCCTTACGCC
751	AACCGTTTCA	AAGACAGCCC	AACCGCGCCT	GAAGCCATGT	TCAAATCGG
801	CGAATGCCAA	TACAGGCTTC	AGCAAAAAGA	CATTGCAAGG	GCGACTTGCC
851	GCAGCCTGAT	ACAGACCTAT	CCGCGCAGCC	CGCGGCAAA	ACGCGCCGCC
901	GCAGCCGTGC	GCAAACGATA	G		

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

1	LPQACPARRH	HCHRYFVER	KGDARSGFRC	AAQRRHPQRF	*SKPAERYAD
51	CPHHPARRRR	FDPASEKIMK	TKLPLFIIWL	SVSAACSSPV	SRNIQDMRLE
101	PQAEAGSSDA	IPYPVPTLQD	RLDYLEGLTV	RLSNEVETLN	GKVKALEHAK
151	THPSSRAYVQ	KLDDRKLKEH	YLNTEGGSAS	AHTVETAQNL	YNQALKHYKS
201	GRFSAAASLL	KGADGGDGGG	IAQRSMYLLL	QSRARMGNCE	SVIEIGGRYA
251	NRFKDSPTAP	EAMFKIGECQ	YRLQKQDIAR	ATWRSLIQTY	PGSPAAKRAA
301	AAVRKR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 695 shows 88.3% identity over a 308 aa overlap with a predicted ORF (ORF 695) from *N. meningitidis*:

m695/a695 88.3% identity in 308 aa overlap

```

      10      20      30      40      50      60
m695.pep  LPQTRPSRRHHRQYFAERKGDARSGFRCAAQRRHPQRFQSKPAERPAHRPHHPARRRR
      |||: ||:|||| |||||:||||| ||||| ||||| ||||| ||||| |||||
a695      LPQACPARRHCHHRQYFVERKGDARSGFRCAAQRRHPQRFQSKPAERYADCPHHPARRRR
      10      20      30      40      50      60

      70      80      90      100     110
m695.pep  LDPASEKIMKIKLPLFIWLSVSASCASVSPVPAGSQT--EMSTRENASDGIYPVPTL
      :||||| ||||| |||||:|:| ||:| |::: ||:|||||
a695      FDPASEKIMKTKLPLFIWLSVSAACSS--PVSRNIQDMRLEPQAEAGSSDAIYPVPTL
      70      80      90      100     110

      120     130     140     150     160     170
m695.pep  QDRLDYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLLDRKLKEHYLNTEGGS
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a695      QDRLDYLEGLTVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLLDRKLKEHYLNTEGGS
      120     130     140     150     160     170

      180     190     200     210     220     230
m695.pep  ASAHTVETAQNLYNQALKHYKSGKFSAAASLLKGADGGDGGGIAQRSMYLLQLSRARMGN
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a695      ASAHTVETAQNLYNQALKHYKSGRFSAAASLLKGADGGDGGGIAQRSMYLLQLSRARMGN
      180     190     200     210     220     230

      240     250     260     270     280     290
m695.pep  CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAR
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a695      CESVIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAR
      240     250     260     270     280     290

      300
m695.pep  AAAAVRKRX
      |||||
a695      AAAAVRKRX
      300

```

The following partial DNA sequence was identified in *N. gonorrhoeae*

g696.seq: not found

This corresponds to the amino acid sequence < ORF 696.ng>:

g696.pep: not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2327>:

```

m696.seq
1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTCCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAAGCAACG GCTTGAACCG CTCCTTAAC
301 CTCCTGTTTG GCTTCTTTCG AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2328; ORF 696>:

```

m696.pep
1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRVFN IGLNGLNRFN
101 LLFGFLRTSC QGSRHHCNQ *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:

a696.seq

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```

1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATTTGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCTTTGTTCA AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGTTACAGCT TCCTCGGCAC TTGCCTTTGC ATCAGCCGCA GCATCTTTGA
201 CTTGGTCTTT CGCTTCTTCG ACGGCAGAAG CGGCAGACTC GGCGGCAGAA
251 GCCGCAGTGT CTTTAACATC GGAACAACG GCTTGAACCG CTTCTTAAC
301 CTCCTGTTTG GCTTCTTGGC AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

a696.pep

```

1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCGNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

m696/a696 100.0% identity in 120 aa overlap

```

m696.pep      10      20      30      40      50      60
               LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
               |||||
a696          10      20      30      40      50      60
               LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFSYSFLGTCLC
               |||||

m696.pep      70      80      90      100     110     120
               ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFLNLLFGFLRTSCQGSRHHCGNQ
               |||||
a696          70      80      90      100     110     120
               ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFLNLLFGFLRTSCQGSRHHCGNQ
               |||||

```

```

m696.pep      X
               |
a696          X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

g700.seq

```

1  ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTTCCCA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTGCGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCTG
151 CGCGTGGAGG ATTTGGGTTT GCGGTTGGGC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 TGGGAAAGTT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGCG AAATTGATGT GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTG CTTAACCGGC GGGGCATCCG
501 GCTGTGCGTT TGGTTTATAT TGTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GCGGATATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCC GGATGCGGCG
751 GTGGGGGTCT GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTT CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

g700.pep

```

1  MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSLS
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSPW RIGGKGKGV
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMP ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

m700.seq

m700.pgp

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLFPWRIKGGKGGVSVGVSQGLGCVLLGFAGF					
g700	DMALTVLWLFVCTVGANLLALAVLGKLSPPWRIGGKGGVSVGVSQGLGCVLLGFVSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFMLSSLSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYSLSGLVMTAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYSLSGLVMTAYGAVWGSIMLLNDLARELFALAFIP					

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSTLG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```

a700.seq
1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTGTGTC
151 CGCGTGGAGG ATTTGGGTTC GCGGTTGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAACGTATGC GCGATATTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTTCG
501 GTTGTCCGTC TGGTTTATGC TTTCATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTGATGACCG AGGCTTACGG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTGGCA CGAGAGCTGT
701 TCGCGCTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCG CGATGCGGCA
751 GTGGGGGTGC GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTTCG
801 GGGTGCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTTTC CGCTTTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```

a700.pep
1  MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPW RIKGKGKVS
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYLSLGL VMTEAYGAVW GSIALNLNLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF TLPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *

```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKGKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m700.pep	KLMRDIWMPSEAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
a700	LLFAASADGVSWVKGLAMASGFGWYLSGLVMTEAYGAVWGSIALLLNDLARELFALAFIP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFTLPIVQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
a700	LLMKRFPDAAVGVGGATSMDFTLPIRGAGGLEAVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
a700	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2337>:

g701.seq

```

1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACCG CTTCGATGGC
51  ACAATCTACG CCGTCTTCGC CGACGATGGC GAAACTTGT TTGGAGACGT
101 CGCCGGAAGC GGGGCTGATG GTATGGGTCG CGCCCACTC TTTCGCCGGT
151 TTCAAACGGT TTTCGTCCAT ATCGCACACG ATAATGGCGG CAGGGCTATA
201 CAGTTGGGCG GTCAACAAGG CGGACATACC GACAGGGCCG GCACCTGCGA
251 TGAATACGGT ATCGCCGGGT TTCACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCT GTAAAGCGTC GCTCAACAGC AGGGCGATT CTTCGTTGAC
351 GTTGTCTGTC GCGGCACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2338; ORF 701>:

g701.pep

```

1  MSWHIFQVAG IPTASMAQST PSSPTMAKTC LETSPEAGLM VWVAPNSFAG
51  FKRFSSISHT IMAAGLYSWA VNKADIPTGP APAMNTVSPG FTSPYCTPIS
101 WAVGKASLNS RAISLTLSC GSTRLLSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2339>:

m701.seq

```

1  ATGTCTTGGC ACATATTCCA TGTAGCAGGG ATACCGACGG CTTCGATGGC
51  GCAATCCACG CCGTCTTCGC CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTCG CACCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGGGCGGTCT GCAAAGCGTC GCTCAACAAC AGGGCGATT CTTCGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2340; ORF 701>:

m701.pep

```

1  MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPPEAGLM VWVAPNSFAS
51  FKRFSSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS
101 WAVGKASLNN RAISLTLSC GSTRLLSA*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 701 shows 92.2% identity over a 128 aa overlap with a predicted ORF (ORF701.ng) from *N. gonorrhoeae*:

m701/g701

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCCLDTSPEAGLMVWVAPNSFASFKRFSSISQT					
g701	MSWHIFQVAGIPTASMAQSTPSSPTMAKTCLETSPEAGLMVWVAPNSFAGFKRFSSISHT					

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : : :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISSLTLSG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
	:
g701	GGTRLLSAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGTCTTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCAACTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGGGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VWVAPNSFAS
51  FKRFSSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTLSG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSSISQT					
	: : : : :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPEAGLMVWVAPNSFASFKRFSSISQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	: : : : :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTLSG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
a701	SGTRLLSAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGTt ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCGTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTCGAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAA t cgCCATCACA GGCACAACTG CGCCGGCGGT
351 CAGGATTTCG cgggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

1 MPCSKASWTS PGVATPGIRG MPLLRLPALAR DSCKPGLMAK TAPASSTALS
51 C~~SG~~LVTPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGVS*

m702.seq

1	ATGCCGTGTT	CCAAAGCCAG	TTGGATTTCG	CCCGGGGTGG	CAACACCGGG
51	AATCAGGGGG	ATGCCGCTGT	TGTGGCCGGC	TTTGCCGAGG	GATTTCATGCA
101	GCCCCGGGCT	GATGGCGAAA	ACCCGCGCTG	CGTCTTCGAC	GGCTTTGAGC
151	TGTTCCGGAT	TGTTTACCGT	ACCTGCGCCG	ACGATGGCGT	TGGGCACTTC
201	TTTGGCAATC	AGGCCGATGG	CATCGAGGCC	GACAGGGGTG	CGCAGGGTGA
251	TTTCGAGGGT	AGGGATGCCG	CCTTCGACAA	GGGCGTGGGA	CAATTCGATG
301	GCGGTGCTTA	AGTCGTCAAT	CGCCATTACC	GGCAACAATG	CGCCGGCGGT
351	CAAAATTTTC	CGGGGGGTCA	GTTTGACATC	TTTCGGTTCTC	CGGGTGGAAAT
401	GGGGTATTTT	ATTAAGATGG	GACAGGTTGT	AG	

m702.ppt

1 MPCSKASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51 C~~SG~~LVTPAP TMALGTSLAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

m702/q702

		10	20	30	40	50	60
m702.pep		MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTV	PAP				
g702		MPCSKASWTS	PGVATPGIRGMPLLR	PALARDSC	KPGLMAKTAPASSTALSCSGLVTV	PAP	
		10	20	30	40	50	60
		70	80	90	100	110	120
m702.pep		TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTR	AWDKSM	AVLKSSIAITGTTAPAVKIS			
g702		MMALGISLAIRRMAS	SPTGVRKVISRVGMPPSTR	ARDKSTAVLKSSIAITGTTAPAVRIS			
		70	80	90	100	110	120
		130	140				
m702.pep		RGVSLDISVLRV	EWGILLRW	DRLX			
g702		RGVSX					

a702.seq

1	ATGCCGTGTT	CCAAAGCCAG	TTGGATTTTCG	CCCGGGGTGG	CAACACCGGG
51	AATCAGGGGG	ATGCCGTGT	TGTGGCCGGC	TTTGGCGAGG	GATTCAATGCA
101	GCCCCGGGCT	GATGGCGAAA	ACCGGCGCTG	CGCTTTCGAC	GGCTTTTGAGC
151	TGCTCGGGAT	TGTTTACCGT	ACCTGCGCCG	ACGATGCGCT	TGGGCACTTC
201	TTTGCAATC	AGGCGGATGG	CATCGAGGCC	GACAGGGGTG	CGCAGGGTGA
251	TTTCGAGGGT	AGGGATGCCG	CCTTCGACAA	GGGCGTGGGA	CAAATCGATG
301	GCGGTGCTTA	AGTCGTCAAT	CGCCATTACC	GGCAACAAGT	CGCCGGCGGT
351	CAAAATTTTCG	CGGGGGGTCA	GTTTGGACAT	TTTCGGTTCTC	CGGGTGGAAAT
401	GGGGTATTTT	ATTAAGATGG	GACAGGTTGT	AG	

a702.pcp

```

1      1  MPCSKASWIS  PGVATPGIRG  MPLLWPALAR  DSCSPGLMAK  TAPASSTALS
51     51  CSQLVTV PAP  TMLGTS LAI  RRMASRPTGV  RRVISRVGMP  PSTRAWDKSM
101    101  AVLKSSIAIT  GTTAPAVKIS  RGVSLDISVL  RVEWGILLRW  DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10 20 30 40 50 60

1128

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m702.pep      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTV PAP
a702          MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTV PAP
              10      20      30      40      50      60

              70      80      90      100     110     120
m702.pep      TMLAGTSLAIRRMASRPTGVRRVISRVGMFPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
a702          TMLAGTSLAIRRMASRPTGVRRVISRVGMFPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
              70      80      90      100     110     120

              130     140
m702.pep      RGVSLDISVLRVEWGILLRWDR LX
a702          RGVSLDISVLRVEWGILLRWDR LX
              130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

g703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAGAAAAA GCGGTGCGCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGAAG CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTGTACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GGCGGAACGG ATTGACCGTG CCGTctgTGc gcTGTtggt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

g703.pep

```

1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51  EDTPQLRQSL LENEVNTTV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKDL E QGVPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVND SREV
251 KVPSFDEMKG QIAGNLQAE R IDRVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

m703.seq

```

1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51  CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTGCGCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGAAG CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

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1129

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
 751 AAAGTGCCCT TTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
 801 GCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
 201 VGYVPLKDLE QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703						
	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
m703.pep	70	80	90	100	110	120
	LENEVNTVVVAQEVKRLKLDLSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703						
	70	80	90	100	110	120
	LENEVNTVVVAQEVKRLKLDLSAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703						
	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
g703						
	190	200	210	220	230	240
	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG					
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
g703						
	250	260	270	280		
	VYYVNSREVKVPSFDEMKGQIAGNLQAERIDRAVCALLGKANIKPAKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT
 101 CCGTCATTGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAAACG AAGTGGTCAA
 201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CCGTCGGCAG
 251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
 301 GACGACAAGA AACCGTCCCT CAAAACCGTT TGGCAGGCGG TAAAATATGG
 351 CTGTAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA
 451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
 551 TCTTGAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CCGTGCGCCG
 601 GTCGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTC CGCCGCTTTA
 651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

1130

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701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA
751 AAAGTGCCCT CTTTTGATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA
801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA
851 TCAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

```

a703.pep
  1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
 51 EDTPQLRQSL LENEVVNTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP
201 VGYVPLKDL E QGVPPYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV
251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK*

m703/a703 100.0% identity in 288 aa overlap

      10      20      30      40      50      60
m703.pep MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL
a703      |||
      10      20      30      40      50      60
a703      MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL

      70      80      90      100     110     120
m703.pep LENEVVNTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG
a703      |||
      70      80      90      100     110     120
a703      LENEVVNTVVAQEVKRLKLDRSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG

      130     140     150     160     170     180
m703.pep EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG
a703      |||
      130     140     150     160     170     180
a703      EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG

      190     200     210     220     230     240
m703.pep FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG
a703      |||
      190     200     210     220     230     240
a703      FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPYQAIKDLKKGEFTATPLKNGDFYG

      250     260     270     280     289
m703.pep VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX
a703      |||
      250     260     270     280
a703      VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

```

a704.seq
  1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT
101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC
151 AAACAACGCA CCGCGACGCG GCAAAAAACC GAGCTGCCGC CCCAAGAAAT
201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG
251 TGGAACCCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC
301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA
351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG
401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAAATCAGG
451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC
501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC
551 TGGGGATGAT GCAGACGATG ATGTTTCGCG TGCCGACCTA CCTTTACGGC
601 GGCGACATCG AACCCGATTT CCTGCAAATC CTCCATTGGG GCGGCTTTTT
651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGCG
701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC
751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

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1131

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801 TGC GGGG CAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACGCTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCTT GCGTTTTGCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCGGGCA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGCGAC TGTCGCACAT CGTCCGCCCTG CTCGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCCTG TCTTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCCGTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCCTG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCGCGCGAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCTCG CCCAAACAC CGACATCATC TTCGACAAAA CCGGCACGCT
1551 GACCAAGGC AAACCGCGC TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTTCTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCTTG CCCGCGCCAT CCTCAACTGC CGCATTTTCA ACGGCAGCGT
1701 CCCGACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GGCGAAACAC AGGTTTGGGC ATTTGGGCGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGGCGG
1851 CGGACGCGCG GTTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCGG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGCGATC AACGACGCGC CCGTTTTTGG
2151 GCAGGCAGAC GTATCCGCGG CCGCAGCGGG CGGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATTGTGTTA TTGAACGAAG ATTTGCGTAC CGTCGCCCAC
2251 CTGCTCGATC AGGCGCGGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCACAAA CGGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1  MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAQS IIDAGLGSYY
51  KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVLMLGGI
101 TCAACVWLIE QQLRDTGIV RIDLNYSTHR CRVWDDGKI RLS DILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMMQTM MFALPTYLYG
201 GDIEPDLQI LHWGGFLMVL PVVFCYAVPF YQGAALRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPGETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAELAEQYAS SFIFGELLIA VPVFIWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTLARE GILIGGKQAI
501 ETLAQTTDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPQTEGGGSA VYLGSQSGFQ AVFYLQDPLK DSAAEAVRQL
651 AGKNLTLHL SGRETAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAGGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQNLIWAG AYNIIAVPLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

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m704/a704 99.8% identity in 823 aa overlap

```

          10      20      30      40      50      60
m704.pep  MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVAQSIIDAGLGSYYKQRTADAQKT
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a704       MKKTCFHCGLDVPEHLHLTVRYENEDRETCCAGCQAVAQSIIDAGLGSYYKQRTADAQKT
          10      20      30      40      50      60

          70      80      90     100     110     120
m704.pep  ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLRDTGIV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a704       ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVLMLGGITCAACVWLIEQQLRDTGIV

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1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNSTHRCRVVWDDGKIRLS DILLKIRQIGYTAAPYDAQKIEAANQKERKQYIVRLA					
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMMQTMFALPTYLYGGDIEPDLQILHWGGFLMVLPPVVFYCAVPFYQGALRDLKN					
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGVYSLATNAGQGMFESIAMLLFFLLGGRFMEHIARRKAGD					
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLI PAFCHHMPDYPDTQETCEAAVVKLKAGDIVLVKPGETIPVDGTVLEGSSAV					
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEKVTAGTLNTQSPLIIRTDRTGGGTRL SHIVRLLDRLAQAQKPR					
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAELEQYASSFIFGELLAVPVFIGWTLYADAHTALWITVALLVITCPCALSLATPTAL					
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGKQAIETLAQTDDIIFDKTGTLTQGKPAVRRISLLRGTDEAFVLA					
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAILNCRISDGSVPDIAIKQRLNRIGEGVGAQLTVNGETQVWALGR					
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVAEISGKEPQTEGGGSAVYLGSSQSGFQAVFYLTDPKDSAAEAVRQLAGKNLTLHIL					
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAETARALGVAHYRAQAMPEDKLEYVKALQKEGKKVLMIGDGINDAPVLAQAD					
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDGADIVLLNEDLRTVAHLLDQARRTRHIIRQNLIWAGAYNIIAVPLA					
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMSFSSSLAVLGNALRLHKGKMQSEKMPSEQX					
	790	800	810	820		

1	GTGTTCAATA	ATTTCCttgc	CTCTCTGCCG	TTTATGACGG	AAACACGCGC
51	TGATATGTCT	ATTGCGCGGT	GTTTGGCCAT	GGTTAAAGCC	GGCTTTACAG
101	TGTGTTtgc	TTTGGCGATG	CTCTCTTTCC	TTATCGGCAT	GATTATTGCC
151	GTAGCCGTTG	CTTTGGTAAG	AATCATGCCT	TCCGGCGGTA	TTTTCCAAAA
201	ATGCTTGTGT	AAGCTGTGGG	AATTTTATAT	TTCCGTCGTT	CGCGGTCACG
251	CGCTTGTGGT	TCAGCTTGTG	ATTGTGTTTT	ACGGGCTGCC	TCCTCGCGCG
301	ATCTATATCA	ATCCGATTCC	CGCCGCCATC	ATCGGCTTTT	CGCTCAATGT
351	CGGCGCATG	GCTTCCGAAA	CCATACGCGC	GGCGATTTTG	TCCGTGCGCA
401	AAGGCGAGTG	GGAAGCAGGT	TTTCTCATCG	GTATGACCTA	TATGACAGAC
451	TTCCGCCGCA	TCGTGCGACC	GCAGGCATTC	CGCGTCGCCG	TTCCGCCCGT
501	GAGCAACGAG	TTTATGTGCT	TGTTTCAAAA	CACCTCGCTT	CGCCGCGGTG
551	TAAACGTAGC	GGAGCTTTTC	CGTGTCCGAC	AGGAAACACG	AAACCGCACT
601	TATGACTTTT	TGCCTGTCTA	TATCGAAGCT	GCATTGGTTT	ATTGGTGTTT
651	CTGTAAAGTG	CGTTTTTTGA	TTCAGGCGCG	TTTGAAAAAA	CGTTTCGACC
701	GTTATGTTCG	CAATAAA			

```

1  VENNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51  VAVALVRIMP SGGIFQKCLL KLVEFYISVV RGTPLLVLQV IVFYGLPSVG
101 IYINPIPAAI IGFSLNVGVA ASETIRAAIL SAKQGWQEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLEKNTSL AAVTVTTELF RVAQETANRT
201 YDFLVPYIEA ALVYWCFCCKV LFLIOARLEK RFDRYVAK*

```

51	GTGTTCAATA	ATTTCTTTCG	TTCGCTGCCG	TTTATGACGG	AAACACGCGC
101	CGATATGATT	GTCAGCGCGT	TTTTGCGCAT	GGTCAAAGCC	GGCTTCGCGG
151	TCTCTCTGCC	TTTGGCGCGA	GCTTCTTTCG	TTATTCGGAT	GATGATTGCG
201	GTAGCCGTGG	CTTTGGTGCG	GATTATGCCC	GCCGGCGGCA	TCGTGCGGAA
251	AATCCCTGCT	AAATCTGTGG	AATTTTATAT	TTCCGTCATT	CCGCGGTACG
301	CGCTGTFTGT	TCAGCTTGTG	ATTGTGTATT	ACCGGCTGCC	TTCCGTCGCG
351	ATCTATATCG	ACCCGATTCC	TGCCGCCATC	ATCGGCTTTT	CGCTCAATGT
401	CGGCGCATAG	GCTTCCGAA	CCATACGCGC	GGCAATTTTG	TCGCTACCTA
451	AAGGCCAATC	GGAAGCAGGT	TTCTCATCAT	GCATGACCTA	TATGACGACG
501	TTCCGCCGCA	TTGTCGCGCC	GCAGGCATT	CGCGTTGCCG	TGCCGCCCTT
551	GAGCAACGAG	TTTATCGGTT	CGCTTTAAAA	CACCTCGCTC	CGGGCAGTCG
601	TATGACTTTT	GGAAATTATTC	TGCTTCTCGC	AGGAACACGC	AAACCGCATC
651	TATGACTTTT	TGCCCGTCTA	TATCGAAGCC	GCTTTGGTTT	ACTGGTGT
701	TTGTAAGTCT	CTGTTCCCTG	TTCAGCGCGC	TTTGAAAAA	CGTTTCGACC
751	GCTACGTCGC	CAAAATAA			

1	VFNNFLASLP	FMTETRADMI	VSAFLPMVKA	GFAVSLPLAA	ASFVIGMMIA
51	VAVALVRIMP	AGGIVRKILL	KLVEFYISVI	RGTPLLVLQV	IVFYGLPSVG
101	IYIDPIPAAI	IGFSLNVGAS	ASETIRAAIL	SVPKQWQEG	FSIGMTYMQT
151	FRRIAPQAF	RVAPVPLSNE	FIGLFKNTLS	AAVVTGVTELF	RVAQETANRT
201	YDFLPVYIEA	ALVYWCFCVK	LFLIOARLEK	RFDRYVAK*	

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m705.pep	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP					
g705	VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m705.pep	AGGIIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIIYIDPIAAIIGFSLNVGAY					

1134

```

g705      SGGIFQKCLLKLVEFYISVVRGTPLLVQLVIVFYGLPSVGIYINPIPAAIIGFSLNVGAY
           70      80      90      100      110      120

           130      140      150      160      170      180
m705.pep  ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           |||
g705      ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
           130      140      150      160      170      180

           190      200      210      220      230      239
m705.pep  AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
           |||
g705      AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
           190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2361>:

```

a705.seq
1  GTGTCAATA ATTCCTTGC TTCGCTGCCG TTTATGACGG AAACACGCGC
51 CGATATGATT GTCAGCGCGT TTTTGCCTAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTGCGGAA
201 AATCCTGCTG AAATTGGTGG AATTTTATAT TTCCGTCATT CGCGGTACGC
251 CGCTGTGGT TCAGCTTGTG ATTGTGTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAT GCTTCGAAA CCATACGCGC GGCAATTTT TCCGTACCGA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCCGCA TCGTCGCGCC GCAGGCATT CGCGTGCCG TGCCGCCTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCAGTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTTT
651 TTGTAAAGTG CTGTTCTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2362; ORF 705.a>:

```

a705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGMMIA
51 VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDFIPAAI IGFSNLVGAY ASETIRAAIL SVPKGQWEAG FSIQMTYMQT
151 FRRIVAPQAF RAVVPPLSNE FIGLFKNTSL AAVVTVTLEF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVKV LFLFIQARLEK RFDYVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:

a705/m705 100.0% identity in 238 aa overlap

```

a705.pep      10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP
|||||
m705          10      20      30      40      50      60
VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP

a705.pep      70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY
|||||
m705          70      80      90      100     110     120
AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIYIDPIPAAIIGFSLNVGAY

a705.pep      130     140     150     160     170     180
ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL
|||||
m705          130     140     150     160     170     180
ASETIRAAILSVPKGQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL

a705.pep      190     200     210     220     230     239
AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX
|||||
m705          190     200     210     220     230
AAVVTVTLEFRVAQETANRTYDFLPVYIEAALVYWCFCVKVFLFIQARLEKRFDRYVAKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq

```

1 ATGAACTCCT CGCAACGCAA ACGCCTTTCC GgccGCTGGC TCAACTCCTA
51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCGgaa
101 ccgtCCTGTT CGCCACCGCA CTCGCCGgC tACTCCACCT CCAacacggc
151 gAATGGATAG GGAatgaCCGT CTTcGTCGTC CTCGGCATGC TCCAGTTCCA
201 AGGcgcgatt tActccaacg cggtgGAacg taTgcctcgt acggtcatcg
251 ggctgGGCGC GGGTTTGGGc gTTTATAGGc TGAACCAGCA TTAtttccac
301 ggcaacCTcc tcttctacct gaccatcggc acggcaagcg cactggccgg
351 ctGGGCGGGC GTCGGCAAAA acggctacgt ccctatgctg GCGGGGctgA
401 CGATGTGCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC
451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATTGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGC CGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGTATGA CGCGGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC
751 CGCAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 CGAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCGCGCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep

```

1 MNSSQRKRLS GRWLSYERY RHRLIHAVR LGGTVLFATA LARLLHLQHG
51 EWIGMTVFVV LGMLQFQGA IYNAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWLDSG
151 LMRAMNVLI GAAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMVKMRQINA RMVKSRSILA ATSGESRISP SMMEAMQHAH
251 RKIVNTTELL LTAAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTALING
301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
351 TRRWLDAHE RQHLRQSLLE TREHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq

```

1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA
51 CGAACGCTAC CGCTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG
101 CCGTCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC
151 GAGTGGATAG GGATGACCGT CTTcGTCGTC CTCGGCATGC TCCAGTTTCA
201 AGGGGCGATT TACTCCAAGG CGGTGGAACG TATGCTCGGC ACGGTCATCG
251 GGTGCGGCGC GGGTTTGGGc gTTTATAGGc TGAACCAGCA TTATTTCCAC
301 GGCAACCTCC TCTTCTACCT CACCGTCGGC ACGCCAAGCG CACTGGCCGG
351 CTGGGCGGGC GTCGGCAAAA ACGGCTACGT CCTATGCTG GCAGGGCTGA
401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA
451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATCGCCGC
501 CGCCAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG
551 CCGACAACCT GGCCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC
601 AGGCGCATGA CCGCGGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA
651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCATCTCGCC GCCACATCGG
701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC
751 CGTAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT
801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT
851 TCACACTGCT CCAAACCGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC
901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCGCGCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep

```

1 MNTSQRNRLV SRWLSYERY RYRLIHAVR LGGAVLFATA SARLLHLQHG
51 EWIGMTVFVV LGMLQFQGA IYKAVERMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTIG TASALAGWAA VGKNGYVPM LAGLTMCMLIG DNGSEWLDSG
151 LMRAMNVLI GAAIAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSILA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING

```


1136

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMRQE ISALVILLQR
 351 TRRKWLDAHE RQHLRQSLLE TREHG*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQRNRLVSRWLSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHGEWIGMTVFVV					
g706	: : : : : : : : :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAISKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIVGTASALAGWAA					
g706	: : : : : : : :					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCMMLIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR					
g706	: : : : : : : :					
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMAIEISNGRRMTRERLEENMAKMRQINARMVKSRSRLAATSGESRISP					
g706	: : : : : : : :					
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTTELLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING					
g706	: : : : : : : :					
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF LWLSTNMRQEISALVILLQRTTRRKWLDAHE					
g706	: : : : : : : :					
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHGX					
g706	: : : : : : : :					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCCTGTT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GT TTTATGGC	TGAACCAGCA	TTATTTCCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CAGTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCACCG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACGGC

1137

```

901 AGACACGCCC GCCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA
951 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA
1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC
1051 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG
1101 CCTGCTTGA ACACGGGAAC ACAGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

```

a706.pep
  1 MNTSQNRNLV SRWLNSYERY RYRRLIHAVR LGGAVLFATA SARLLHLQHG
 51 EWIGMTVFVV LGMLQFQGA IYKAVRMLG TVIGLGAGLG VLWLNQHYFH
101 GNLLFYLTVG TASALAGWAA VGKNGYVPM LAGLTMCLIG DNGSEWFDSG
151 LMRAMNVLI GAAIAIAAAKL LPLKSTLMWR FMLADNLTDC SKMIAEISNG
201 RRMTRERLEE NMAKMRQINA RMVKSRSHA ATSGESRISP AMMEAMQHAH
251 RKIVNTTELL LTAAKLQSP KLNSEIRLL DRHFTLLQTD LQQTVALING
301 RHARRIRIDT AINPELEALA EHLHYQWGF LWLSTNMRQE ISALVILLQR
351 TRRKWLDAHE RQHLRQSLLE TREHS*

```

a706/m706 99.5% identity in 374 aa overlap

a706.pep	10	20	30	40	50	60
m706	10	20	30	40	50	60
a706.pep	70	80	90	100	110	120
m706	70	80	90	100	110	120
a706.pep	130	140	150	160	170	180
m706	130	140	150	160	170	180
a706.pep	190	200	210	220	230	240
m706	190	200	210	220	230	240
a706.pep	250	260	270	280	290	300
m706	250	260	270	280	290	300
a706.pep	310	320	330	340	350	360
m706	310	320	330	340	350	360
a706.pep	370					
m706	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

1138

m707.seq

```

1 ATGGAAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51 GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CATTGGAGAA GAACAATTAT GTCCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCGTGCGTG GCTACCTCAC TTCCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGGCGAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTCC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTAAAA
551 CAGATATTCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAAATGGC AGCAGAATAA ACCCATACGG TTCAGTATCG GTATAGATGA
651 TCGGGGCGGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTTC ATATGGACGC
751 GGTTTGCGGC ACAAACGCGA CTGACTGAT GCCACCGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAT
851 GGCTGTTTTC TTTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCTATTCCG TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GGCCGCCGAG CGCATGCTTT GGCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAATGAAATT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCCG CTCTGCAGGC TGGGAAGCCG AATTGCGCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGC CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGGCGGC
1201 GATATTTCTT CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGG
1251 CGCAGCCGCC CCATTTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCCGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1 MEIINDAELI RSMQROQHID AELLTDANVR FEQPLEKNNY VLSEDETPCT
51 RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 TVRGYLTSA IIQPNMDSG ILKLRVSAGE IGDIREYEEK DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE QGLENLRRLP SVKTDIQIIP SEEEGKSDLQ
201 IKWQQNKPIR FSGIDDAGG KTTGKYQGNV ALSFDNPLGL SDFYVVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYNG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAE LRHRAY LNRWQLDGKL SYKRGTGMRQ SMPAPEENG
401 DILPGTSRMK IITASLDAEA PFILGKQFF YATAIQAWN KPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGK LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1 NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51 GAGCAGGCTA CAAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTC GGGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAGAAC TGCGTCGTTT GCCGAGTGT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTT ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCAAT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NTTAAGCGAT TNGTTTTATG TTTTATATGG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TGNTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGTT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

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1139

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751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCCGCACCTG AAGAAAACGG CGGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATT CAGCTCAATG
1101 GAACAAAACG CCTTTGGTTG CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGCGAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
  1 XKETAFKTM CLGSNNLSRL QKAAQQILIV RGYLTSQAI QPQNMDSGIL
  51 KLRVSAGEIG DIRYEKRDY KSAEGSISAF NNKXPLYRNK ILNLRDVEQG
 101 LENLRLPSV KTDIQUIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
 151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
 201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDYNKQ YQSSLAERM
 251 LWXXFXXTS VXMKLWTRQT KYIDDAEIE VQRRRSAGWE AELRHRAYLX
 301 RWQLDGKLSY KRGTMGRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
 351 MLGKQQFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
 401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
 451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

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a707/m707 95.3% identity in 486 aa overlap

```

a707.pep                                10      20      30
                                XKETAFKTMCLGSNNLSRLQKAAQQILIVR
                                |||
m707      EDETPCTRVNYISLDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQQILIVR
              50      60      70      80      90     100

a707.pep      40      50      60      70      80      90
GYLTSQAI IQPQNMDSGILKLRVSAGEIGDIRYEKRDYKSAEGSISAFNNKXPLYRNKI
|||
m707      GYLTSQAI IQPQNMDSGILKLRVSAGEIGDIRYEKRDGKSAEGSISAFNNKXPLYRNKI
              110     120     130     140     150     160

a707.pep      100     110     120     130     140     150
LNLRDVEQGLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
|||
m707      LNLRDVEQGLENLRLPSVKTDIQUIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
              170     180     190     200     210     220

a707.pep      160     170     180     190     200     210
GKYQGNVALSXDNPLGLSDXFXFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
|||
m707      GK YQGNVALSFDNPLGLSDLFYVSYGRGLAHKTDLTDATGTETESGSRYSVHYSVPVKK
              230     240     250     260     270     280

a707.pep      220     230     240     250     260     270
WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWXXFXXTSVXMKLWTRQTY
|||
m707      WLFNFHNGHRYHEATEGYSVNYDYNKQYQSSLAERMLWRNRLHKT SVGMKLWTRQTY
              290     300     310     320     330     340

a707.pep      280     290     300     310     320     330
KYIDDAEIEVQRRRSAGWEAELRHRAYLXRWQLDGKLSYKRGTMGRQSM PAPEENGGGTI
|||
m707      KYIDDAEIEVQRRRSAGWEAELRHRAYLNRWQLDGKLSYKRGTMGRQSM PAPEENGGDIL
              350     360     370     380     390     400

```

```
g708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCCT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCTC CGGGCAGAA AAGGCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151 GACTACCGTG AGGCAACGGC AAGATTAGAA GATGCCTTGA AATCGAACCC
201 TAAAAACGAA CTTGCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAGGCCCT CTTCCATCAA
301 CCCGACAGTG CCGAAATCAA CAACAAC TAC GGCTGGTTCC TGTGGGCGC
351 GCTCAACCGC CTGCGGCAAT CTATGGCATA TTCTGCAGAA GCCCTGGCCG
401 ACCCCACCTA CCGGACCCCT TATATTGCCA ACTCGAATAA AGGTATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501 CCTCGCGCGC CAGCCGCGAT TCCACC CGC ATTTAAAGAA CTGGCGGCCA
551 CCAAATGCT GGCCGGGCG TTTGGCGATG CCGATTACTA CTTTAAAAAT
601 TACCAAGACA GGTGAGCAAG CTTTCAGGCC GATGATTTGC TGTAGGCTT
651 GAAAATTGCC AAAGCCCTCG GCAACGTGCA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCTC
751 ACCGGTCAAT AA
```

```
g708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51  DYRQATASIE DALKSNPKNE LAWLVRAEIY QYLKVNDAKQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRLAA QPQFPFAFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLLGWKIA KALGNVQAAY EYEAQLQANF PYSEELQTVL
251 TGS*
```

```
m708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51  GGGCGCGTGC AGCATCTTCT ACCGCCCTC GCGGGCAGAA AAGCGCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGGCGCTAG
151 GACTACCGTC AGGCGACGGC AAGTATTGAA GACGCCCTGA AATCGGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC GGAATCTGAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GCGAAGCCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACAC GGTGGTTTCC TATGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAAA GCTCTGGCCG
401 ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCATTAT TGAACGTTG
501 CCTCGCCGCC CAGCCCGAGT TCCCACCCGC ATTTTAAAGAA CTGGCGCGCA
551 CCAAATTGCT GGCCGGGCAG TTTGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTC
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCCTCCTC
751 ACCGGTCAAT AA
```

m708.pap

1141

```

1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQALSIK
101 PDSAEINNNY GWFLCGRLLR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLGLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

              10      20      30      40      50      60
m708.pep      MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              |||
g708           MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
              10      20      30      40      50      60

              70      80      90      100     110     120
m708.pep      DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSDAEINNNYGWFLCGRLLR
              |||
g708           DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSDAEINNNYGWFLCGRLLR
              70      80      90      100     110     120

              130     140     150     160     170     180
m708.pep      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPAPFKE
              |||
g708           PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPAPFKE
              130     140     150     160     170     180

              190     200     210     220     230     240
m708.pep      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF
              |||
g708           LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNVQAAYEYEAQLQANF
              190     200     210     220     230     240

              250
m708.pep      PYSEELQTVLTGQX
              |||
g708           PYSEELQTVLTGQX
              250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCCTT
51 GGGCGCGTGC AGCACTTCCT ACCGCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACACTAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GGCGAATTTC CCCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAQ ESFRQXLSIK
101 PDSAEINNNY XWFLCGRLLR PAESMAYFDK ALADPTYXPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLGLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIYQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRNLNR					
m708	DALKSDPKNELAWLVRAEIYQYLKVNDKAQESFRQALSIPKPSAEINNXYWFLCGRNLNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYPIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE					
m708	PAESMAYFDKALADPTYPTPYPIANLNKGICSAKQGQFGLAEAYLKRSALAAQPQFPFAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

1	ATGTTTGCTT	TCAAATCCTT	ACTCGATATG	CCGCGCGGTG	AGGCACTTGC
51	CGTCGTCGTC	GCTCTGATTG	CCGCAATGGG	CTATACCATC	ATTTCATTGG
101	AGTGGCTGCC	GCATATGTCC	ATTATTGCCG	CCATCGTCGT	GCTGATTTTG
151	TACGGCTTGG	CGCGCGGTTT	GAAATACAAC	GATATGCAGC	CAGGGATGAT
201	AGGCGCGTTG	AATCAGGGTA	TGGGCGCGGT	TTACCTGTTT	TTCTTCATCG
251	GGCTGATGGT	CAGCGCGCTG	ATGATGAGCG	GCGCGATTCC	GACGCTGATG
301	TATTACGGTT	TCGGGCTGAT	TTCCCCGACT	TATTTTATT	TTTCCGCCTT
351	CGCGCTGTGT	TCCGTCATCG	GCGTGTCAT	CGGCAGCAGC	CTGACCGCCT
401	GCGCCACTGT	CGCGCTTGCC	TTTATGGGGA	TGGCGGCGGC	GTTTCAGGCC
451	GATATGGCGA	TGACGgcggg	cgcgattgTT	tccggtGTGT	TTTTCGGCGA
501	TAAAATGTCC	CCGCTTTCCG	ACACCACGGG	CATTCCGCG	TCCATCGTCG
551	GTATCGACCT	GTTGAACAC	ATCAAAAACA	TGATGTACAC	CACCATCCCT
601	CGCTGGCTTA	TCAGCGCGGC	ACTGATGCTT	TGGCTTCTTC	CCAGCGTCGC
651	CGCGCAGGAT	TTGAACAGCG	TCGAATCCTT	CCGCAGCCAG	CTTGAAGCCA
701	CGGGATTGGT	GCACGGCTAT	TCGCTGATTC	CGTTTGCAT	GTTGGTCGTT
751	TTGGCATTGA	TGCGCGTCAA	TGCCGTGGTC	GCCATGCTCT	TTACCGTCAT
801	TGCCGCCGTT	GCCGTAACGT	ATCTGCACAG	CACGCCCGAT	CTGCGTCAGC
851	TCGGCGCGTG	GTTTATGGC	GGCTACAAAC	TCGAAGGCCA	AGCGTTTAAA
901	GACATTGCCA	AACTGATTTT	GCGCGGCGGC	TTGGAGAGTA	TGTCTTTTAC
951	GCAGACCATC	GTTATCCTCG	GTATGAGTTT	GGGCGGGGTG	CTGTTTGCGC
1001	TCGGTGTGAT	TCCTTCCTTG	CTGGAGGCCG	TCCGTACCTT	CTTGACGAAT
1051	GCCGGACGCG	CGACGTTTCA	CGTTGCCATG	ACTTCGGTCG	GGGTCAATTT
1101	CCTGATTGGA	GAGCAATATT	TGAGCATCCT	GCTTCGGGGA	GAAACGTTCA
1151	AACCCGTTTA	CGACAACTC	GGCCTGCATT	CGTGCAACCT	GTCGCGGACT
1201	CTGGAAGATG	CGGGGACGGT	GATTAACCCG	CTCGTGCCGT	GGAGCGTGTG
1251	CGGCGTATTT	ATCAGCCACG	CCCTTGGCGT	ACCCGTTTGG	GAATATCTGC
1301	CTTATGCCTT	TTTCTGCTAT	TTGAGTTTGG	CTTTAACCCCT	GTTATTGCGC
1351	TGGACGGGGC	TGACTTTTGA	CAAAAAATAA		

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

1	MFAFKSLDDM	PRGEALAVVV	ALIAAMGYTI	ISLEWLPHMS	IIAAIVVLIL
51	YGLARGLKYN	DMQAGMIGAL	NQGMGAVYLF	FFIGLMVSAL	MMSGAIPTLM
101	YYGFLISPT	YFYFSAFALC	SVIGVSIGSS	LTACATVGVA	FMGMAAAFQA
151	DMAMTAGAIV	SGVFFGDKMS	PLSDTTGISA	SIVGIDLFEH	IKNMMYTTIP
201	AWLISAALML	WLLPSVAAQD	LNSVESFRSQ	LEATGLVHGY	SLIPFALLVV
251	LALMRVNAV	AMLFTVIAAV	AVTYLHSTPD	LRQLGAWFYG	GYKLEGEAFK
301	DIARKLISRG	LESMTFTQTI	VILGMSLGGL	LFALGVIPSL	LEAVRTFLTN

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq
 1 ATGTTTCGCTT TCAAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
 51 CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTCAATTGG
 101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
 151 TACGGCTTGG CCGCGCGGTT GAAATACAAC GATATGCAGC AGGGCATGAT
 201 AGGCGCGGTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG
 251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
 301 TATTACGGTT CCGGACTGAT TTCCCGGACT TATTTTATT TTTCTCCTT
 351 CCGCGCTGTG TCCGTCATCG GCGTGTCCAT CCGCAGCAGC CTGACCACCT
 401 GCGCCACTGT CCGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
 451 GATATGGCGA TGACGGCGGG CCGGATTGTT TCGGGCGCAT TTTTGGCGA
 501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCCGCG TCCATCGTCG
 551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC
 601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTGCG
 651 CCGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
 701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCCT GTTGGTCATT
 751 TTGGCATTGA TCGCATCAA CGCCGTCGTC GCCATGCTCT TTACCGTCAT
 801 GGTGTCGGT GCTGTAACGT ATCTGCACAG CACGCCGAT CTGCGTCAGC
 851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAA
 901 GATGTTGTCA AACTGATTTC GCGCGGCGGT TTGGAAAGTA TGTTTTTCA
 951 GCAAACCATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTTGGC
 1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT
 1051 GCCGGACGCG CGACGTTTCA GCTTGCCATG ACTTCGGTCG GGGTTAATTT
 1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCGGGT GAAACGTTC
 1151 AACCCGTTTA CGATAAGCTC GGCTGCAATT CCGCAATCT CTCGCGGACG
 1201 CTGGAAGATG CGGGGACGGT GATTAACCG CTCGTACCGT GGAGCGTATG
 1251 CCGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
 1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
 1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep
 1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL
 51 YGLARGLKYN DMQQGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM
 101 YYGFLISPT YFYFSSFALC SVIGVSIGSS LTTCATVGVA FMGMAAFQA
 151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFH IKNMMYTTP
 201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI
 251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
 301 DVVKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAIRTFTLN
 351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLSRT
 401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQAGMIGALNQMGAVYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	DMQQGMIGALNQMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSSFALC					
g709	DMQAGMIGALNQMGAVYLFFFIGLMVSALMMSGAIPTLMYYGFLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFHEIKNMMYTTPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFHEIKNMMYTTPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
m709.pep	SIVGIDLFHEIKNMMYTTPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFHEIKNMMYTTPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240

1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFTVMVAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	: : : : : : : : : :					
g709	SLIPFALLVVLALMRVNAVVMVAMLFTVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLESMFFTQTIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM					
	: : : : : : : : : :					
g709	DIAKLISRGGLESMFFTQTIVILGMSLGGLLFALGVIPSLLEAVRTLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSRNLSTRTLEDAGTVINPLVPWSVCGVF					
	: : : : : : : : :					
g709	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSCNLSRTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
	: : : : : : : : :					
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKXX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGCTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNNTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCCGACT TATTTTTATT TTTCCGCCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CCGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGGNCGCAT TNTTNGGCGN
501 CAAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCTG
551 GTATCGACCT GTTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGGCGT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCCA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGGAAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGCGGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTCAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCTNGG GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCANCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQQGMIGAL NQGMGAIYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFSAFALC SVIGVSIGSS LTTTCATVGA XMGXXXAFXA
151 XMXXXXXXIV XXAXXGXKMS PLSDTXGXA SIVGIDLFH IKNNMYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLV
251 LALMRVNAV VAMLFTVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAXX
301 DIAKLISRGG LESMFFTQTI VILGMSLGG L FALGAIPSL L DAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG
 451 WTGLTLSKK*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709.pep	MFAFXSLDMPRGEALAVVVALIAAMGYTII	XLEWLPHMSIIAAIVVLILYGLARGLKYN				
m709	MFAFKSLDMPRGEALAVVVALIAAMGYTII	SLEWLPHMSIIAAIVVLILYGLARGLKYN				
	10	20	30	40	50	60
	70	80	90	100	110	120
a709.pep	DMQQGMIGALNQGMGAIY	LEFFIGLMVSALMMSGAIPTLMYYGFLISPT	YFYFSAFALC			
m709	DMQQGMIGALNQGMGAIY	LEFFIGLMVSALMMSGAIPTLMYYGFLISPT	YFYFSSFALC			
	70	80	90	100	110	120
	130	140	150	160	170	180
a709.pep	SVIGVSIGSSLTTCATVG	VAXMGXXXAFXAXMXXXXXIVXXAXXG	KMSPLSDTXG	SA		
m709	SVIGVSIGSSLTTCATVG	VAFMGMAAFQADMAMTAGAIVSGAFFG	DKMSPLSDTTG	ISA		
	130	140	150	160	170	180
	190	200	210	220	230	240
a709.pep	SIVGIDLFEHIKNM	MYTTIPAWLISXXLMLXLLPSVAAQDLNS	VESFRSQLEATGLV	HVCY		
m709	SIVGIDLFEHIKNM	MYTTIPAWLISAAALMLWLLPNVAAQDLNS	VESFRSQLEATGLV	HGHY		
	190	200	210	220	230	240
	250	260	270	280	290	300
a709.pep	SLIPFALLVVLALMR	VNAVAMLFTVIAAVAVTYLHSTPDLRQL	GAWFYGGYKLEGE	AAXX		
m709	SLIPFALLVILALMR	INAVAMLFTVMVAVAVTYLHSTPDLRQL	GAWFYGGYKLEGE	AFK		
	250	260	270	280	290	300
	310	320	330	340	350	360
a709.pep	DIAKLISRGGLESM	FFTQTIVILGMSLGGLLFALGAIPSL	LDVRSFLT	NAGRXTFS	VAM	
m709	DVVKLISRGGLESM	FFTQTIVILGMSLGGLLFALGVIPSL	LEAIRFTLT	NAGRATFS	VAM	
	310	320	330	340	350	360
	370	380	390	400	410	420
a709.pep	TSVGVNFLIGEQYLS	ILLSGETFKPVYDKLGLHSRNL	SRTLEDAGTVINPL	VPSVCGVF		
m709	TSVGVNFLIGEQYLS	ILLSGETFKPVYDKLGLHSRNL	SRTLEDAGTVINPL	VPSVCGVF		
	370	380	390	400	410	420
	430	440	450	460		
a709.pep	IXHALGVPVWEYLPYA	FFCYLSLALTLLFGWTGLT	LSKKX			
m709	ISHALGVPVWEYLPYA	FFCYLSLALTLLFGWTGLT	LSKKX			
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq
 1 ATGGAACCC ACGAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC
 51 CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA
 101 AAATCGAACG GGGCGAAACG CAGTTAAATA TCCCGCGTTT GGAGCAGTTG
 151 GCTCAGATTT TCAAAATCGA TATGTGGGAC TTGCTCAAAT CGGGCGGTGG
 201 TGGGATGGTG TTTCAGATTA ATGAAGGTGA TAGTGGTGGC GATATTGCGT
 251 TGTATGCGTC GGGTGATGTT TCGATGAAAA TAGAATTTTT AAAAATGGAG

301 TTGAAACACT GCAAAGAAAT GTTGGAAACAA AAAGACAAAG AAATCGAGCT
351 GCTCCGCAAG CTGACCGAAA CCGTTTAA

m710.pep
1 METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
51 AQIFKIDMWD LLKSGGGGMV FQINEGDSGG DIALYASGDV SMKIEFLKME
101 LKHCKEMLEO KDKEIELLRK LTETV*

```
a710.seq
1  ATGGAAACCC  ACGAAAAAAT  CCGCCTGATG  CGCGAATTGA  ATAAATGGTC
51  CCAGGAGGAT  ATGGCGGAAA  AGCTGGCGAT  GTCGCGAGGC  GGGTATGCCA
101 AAATCGAACG  AGCGCAAAAC  CAGTTGGAAT  TCCCGCGCTT  GGAGCATGTT
151 GCGCAGATTT  TCAAAATTGA  TATGTGGGAC  TTGCTCAAAT  CGGCGGCGCG
201 CGGGATGGTG  TTGCAGATTA  ACGATGTGGA  TACCAACAGC  GGGGAATTTG
251 CAATCTATAC  CGCTCAGGAT  GCATCNGGTA  AAGCTGGATT  TGTTAAATAT
301 GAATTA AAC  ACTGTAAGTA  ATAGTTGGAA  CACAAAGACA  AAGAAATCGA
351 GCTGCTCCGC  AAGCTGACCG  AAACCGTTTA  A
```

```
a710.pep
  1  METHEKIRLM RELNKSQED MAEKLAMSAG GYAKIERGET QLNIPRLEQL
 51  AQIFKIDMWD LLKSGGGGMV LQINDVDTNS GEFAIYTAQD ASGKAGFVKM
101  ELKHCKEMLE HKDKIEILLR KLTETV*
```

		10	20	30	40	50	60
a710.pep		METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
m710		METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
		10	20	30	40	50	60
		70	80	90	100	110	120
a710.pep		LLKSGGGGMVLQINDVDTNSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKIEILLR					
		: : : : : : :					
m710		LLKSGGGGMVFQINEGDSG-GDIALYASGDVSMKIEFLKMELEHKCKEMLEQKDKIEILLR					
		70	80	90	100	110	
a710.pep		KLTETVX					
m710		KLTETVX					
	120						

1147

g711.seq not found

g711.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

```
m711.seq
1  ATGCCCCGCGC CTGATTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAT ATGCAAAC TGCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAAC TGCC
551 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTTGGGC AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAACCAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AGGGGCAGAA TTTCGATGAC TCCTACTATG CTTTTTTGCC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG
```

This corresponds to the amino acid sequence <SEQ ID 2390; ORF 711>:

```
m711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSlyTTD RGFdynAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRQLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYYAFLPDM LQNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

```
a711.seq
1  ATGCCCCGCGC CTGATTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAAGGC
51  AATCGAGTGG CTGGAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
101 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
151 TTGGATATGC TCAACGACAT CAAACTTCG ATGGTTGAAT CGGCAAAAAG
201 TGGACAGTCG TTTGACGATT GGCGAAAAGG TATCTTGAAT CTGCTCAGCA
251 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
301 CCAGCCACCG GCGAGGTATT CGGTCGCCG CGGAGGTTGG AGACGATTTA
351 CCGTACCAAC ATGCAAAC TGCTACAACGC CGGTCAATAT CAAGGATATA
401 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
451 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
501 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAAC TGCC
551 GTTGTGCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
601 ATTGTCGGGC AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
651 CAACAAAAAA GGCGATACTT ATCTGACCCT TGCCTATAAA GCACCGGATG
701 GCAGTCTGTA CACGACCGAT CGAGGATTG ATTACAACGC CGGACGAATG
751 AACTACCGCC CCGATTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
801 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAACCAGC TTAAACAGC
851 TTGAAAAAGA GTTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
```

1148

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901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTTG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTTCGATGAC TCCTACTATG CTTTTTTTGGC
1101 GGATATGCTG CAAAACCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

```

a711.pep
1  MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAASEIA KVYTIARMTD
51  LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWMYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSlyTTD RGFdynAGRM
251 NYRPDLDKYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

	10	20	30	40	50	60
a711.pep	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAASEIAKVYTIARMTDLDMLNDIKTS					
m711	MPAPDLGFALSLPPKKAIEWLESKKVTAESYRNLTAASEIAKVYTIARMTDLDMLNDIKTS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a711.pep	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
m711	MVESAKSGQSFDDWRKGILNLLSNKGWLHPNGHNGKDIIDPATGEVFGSPRRLETIYRTN					
	70	80	90	100	110	120
	130	140	150	160	170	180
a711.pep	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
m711	MQTAYNAGQYQGYMANIDARPYWMYDAVGDSRTRPAHSAIDGLVYRYDDPFWATFYPPNG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a711.pep	YNCRCSVIALSERDVERQGRIVGQSTSDNLVETHKIYNKKGDTYLTLAYKAPDGSlyTTD					
m711	YNCRCSVIALSERDVERQGRIVGQSTADNLVETHKIYNKKGDTYLTLAYKAPDGSlyTTD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a711.pep	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEYVKQRLDIDGK					
m711	RGFDYNAGRMNYRPDLDKYDRALAHQFAKAEMGGADFKTSFKQLEKEFYEYVKQRLDIDGK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a711.pep	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
m711	PDKEQKIKIRNALSRLKFAAGVLSKETQELAGMTRATVWLSDDTLVKQVDSREGQNFDD					
	310	320	330	340	350	360
	370	380	390	400	410	420
a711.pep	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
m711	SYAFLPDMLQNPEHVIRDNRELIFTARYKGSALWAVLKYIKEVDEIYLQSYRISNDKEI					
	370	380	390	400	410	420

1149

a711.pep	AKFMAKKKVLKX
m711	AKFMAKKKVLKX
	430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```

m712.seq
1   ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CGGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTTGTTCGGA CAAGGCTCGC TGGCGCATTT GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GGCGGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTTCA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGCG GCCTTGAGCA CGGCCACCAC
801 CGCTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTGCGGTAGA GCCAAACGGC ATCATCGCCG CAGGTTATGC GGCGGTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA CTACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTTAAGAGC GAGATTTTGG ACGTGCTGAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GGCGCGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCCGCGG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GGCGCATTGA
1401 TTTGATTTTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2394; ORF 712>:

```

m712.pep
1   MMPHIDFDTI PGSIRVPQOY IEFNTRNAVQ GLPQNPKVL MVAPMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHLMVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNDDPA LLDITTIRTL DYVRRSVKER IALRFPRDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVARA QNDPNRVNAI
451 IPADVNVNGLH VFAGRIDLIL *

```

a712.seq not found yet

a712.pep not found yet

1151

g713.seq not found yet

g713.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGTTGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCGCTTTG GGCAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2396; ORF 713>:

```

m713.pep
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MVLDAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLVVGGAD YSSPPVATLC WSRTDSRCNI
201 ERMIDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLLKWVYKD PTMTLHRPKT
251 VVVSADANLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGKR KGVSHKGKKG GKKQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGTTGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGCAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCGCTTTG GACAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGCTGCACCG CCCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGCC GCATTGCAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACACTC ACGATAACCG
851 TGGGCGGCCA TAAAACCCGC GACGGCGTAT TGTGGCAACC TGGCCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCAGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```


1152

1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GCGGGTGTTC GAATGA

This corresponds to the amino acid sequence <SEQ ID 2398; ORF 713.a>:

a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSDFD VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTVLDAAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVGGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDWKVYKD PTMTLHRPKT
251 VVVSDADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FMLSMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGGK GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSDFDVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSDFDVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGSRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLLVGGVD					
m713	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLLVGGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKVYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTDNRFSEVTFLAQSHGRSGDSAKHDLKVYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGQR					
m713	PTMTLHRPKTVVVSADNLAALQKQAKKQLADWRLEGFTLTITVGGHKTRDGVWQPGLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
m713	VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVSHKGGKGGKKQAETAVFEX					
m713	KGVSHKGGKGGKKQAETAVFEX					
	370	380				

1153

g714.seq not found yet

g714.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```
m714.seq
1   ATGAGCTATC AAGACATCTT GCGGGGCTGT TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGG
201 CGGTACGGGC AAAAACC GCCGCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAAACCGC GCCGGCGACC GTCTTGC GCCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGC GCGGC GGCAACAACC GCATTACCCG ATCCGCGGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A
```

This corresponds to the amino acid sequence <SEQ ID 2400; ORF 714>:

```
m714.pep
1   MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  RSAGQMLADW ERLGLDGTG KNRQHRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```
a714.seq
1   ATGAGCTATC AAGACATCTT GCGGGGCTGT TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GGCGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGG
201 CGGTACGGGC AAAAACC GCCGCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAAACCGC GCCGGCGACC GTCTTGC GCCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGC GCGGC GGCAACAACC GCATTACCCG ATCCGCGGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A
```

This corresponds to the amino acid sequence <SEQ ID 2402; ORF 714.a>:

```
a714.pep
1   MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVAADAVDP
51  SSAGQMLADW ERLGLDGTG KNRQRRVLAV MAKLNETGGL SIPYFVRLAE
101 AAGYQIQIDE PQPFRAGVNR AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*
```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pep	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVAADAVDPSSAGQMLADW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a714.pep	ERVLGLDGTGKNRQRRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLNETGGLSIPYFVRLAEAAAGYQIQIDE PQPFRAGVNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a714.pep	AGDRLAPQEI MWVWHVNVVRG GNNRITRFRA GISAAGDRLT DYSDAVIESL FNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWVHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA
 130 140 150 160 170 180

a714.pep IRFTYRX
 |||||
 m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTCT
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCTT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWVGLKYRD GKPLSDSRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLD DD KQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTCT
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCTT CGGCGGTATG
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR
 51 PKWLGLKYRD GKPLSDSRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM
 101 AGRNRKVRIP QREFLTLD DD KQALMDDVQ DYFSGSLIP*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
 51 GGCCGCCGCG GCCGTGCGG CCCACAAACC GGCAAGCAAC GCAACAGGCG
 101 TTCAAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
 201 TAAAGCAGGC GAAGGCAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
 251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
 301 GAAGGCAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA

1155

101 EGKCGEGKCG SK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

```
m716.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

```
m716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

m716/g716 86.6% identity in 112 aa overlap

```

      10      20      30      40      50
m716.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g716      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG
          10      20      30      40      50      60

      60      70      80      90      100
m716.pep  ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g716      SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
          70      80      90      100      110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

```
a716.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51  GGCCGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

```
a716.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

a716/m716 100.0% identity in 102 aa overlap

```

      10      20      30      40      50      60
a716.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m716      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          10      20      30      40      50      60

      70      80      90      100
a716.pep  EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m716      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          70      80      90      100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

```
g717.seq
1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
```

1156

```

51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTCT  CGCGCGCTGC
251  TGTTTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCGCT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATCC  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  GCGGAACACC  TCCGTCCTGA  CCGCGGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CGCCCGCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CGCGCGCCTT  TTTCCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGGCCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCATTAT  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CGCCCGCCTT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCTCC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCTCCC  TCCTGCTGCC
951  GGAAAACACT  GCCGCCGTCC  GGTTTACCGT  CGTATCGTGT  ATGCTGCCGC
1001  cgtGTTTTTA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCGATCGCG  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGGTTGCCCT  TGCCGCCTCA  TTCTGGTTGT  TTTTGTGTTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATATGCA
1251  CACATTGTTT  TGCTTgCCCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCctgttt  gccggcgat  GGGCGGCATA  TCTGGCAGGC
1351  TGATCCTGCT  GCCACCGGAA  AAATTGACAC  AAATGTTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCCATTTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCLGLDQA  YVREYYAAAD  KDTLFKTLFL  PPLLFSAAlA  ALLLSRPSLP
101  SEILFSLDDA  AAGIGLVLE  LSFLPIRFL  LVLRMGRAL  AFSSAQLVPL
151  LAIIIIIIPLT  VGLLHFPANT  SVLTAVYALA  NLAAAFLLF  QNRCRLKAVR
201  RAFPSPAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKKY  AGLEQLGVYS
251  MGISFGGAAL  LLOSIFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGIFSP  LASLLLPENY  AAVRFTVVS  MLPLFYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFVFKTE
401  SSCRLWQPLK  RPLMYMTLF  CLASSAAYTC  FGTANYPLF  AGVWAAYLAG
451  CILRHRKNLH  KLFHYLKKQ  FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGTTTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCGGCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAAC  CCTGTTCTCT  CGCGCGCTGC
251  TGTCTGCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGTTTTCACT  CGACGATGCC  GCCGCCGGCA  TCGGGCTGGT
351  CTTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGTTTTCG
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCACTTTCC
501  AGCGAACACC  GCCGTCCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CGCCCGCCTT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CACGCACCGT  TTTCCGCCGC  CGTCCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTTCT  GAAAAAATAT  GCGGCGCTGG  AACAGCTCGG  CGTTTATTTC
751  ATGGGTATTT  CGTTCGGCGG  GCGGCATTAT  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCGGC
851  CGCCCGCCTT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCTCC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCTCCC  TCCTGCTGCC
951  GGAAAACACT  GCCGCCGTCC  GGTTTATCGT  CGTATCGTGT  ATGCTGCCGC
1001  CGCTGTTTTG  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCGATCGCG  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTGCCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCCCT  TGCCGCCTCA  TTCTGGCTGT  TTTTGTGCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTTT  TGCTTgACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  TGGCAAACTA  TCCCTGTTT  GCCGCGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGATCCTGCT  GCCACCGGAA  AGATTGACAC  AAATGTTTC  ATTATTTGAA
1401  AAAACAAGGT  TTCCCATTTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep

```

1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51  SVLCLGLDQA YVREYYATAD KDTLFKTLFL PPLLSAAAIA ALLSRPSLP
101 SEILFSLDDA AAGIGLVLEF LSFLPIRFLF LVLRMGRAL AFSSAQLVPK
151 LAILLLLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 HAPFSPAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSIFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS
301 ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLA EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE
401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTANYPLF AGVWAAAYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

```

m717/g717 96.4% identity in 473 aa overlap

m717.pep	10	20	30	40	50	60
	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
g717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
m717.pep	70	80	90	100	110	120
	YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF					
g717	YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLEF					
	70	80	90	100	110	120
m717.pep	130	140	150	160	170	180
	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVPKLAILLPLTVGLLHFPANTSVLTAAYALA					
	130	140	150	160	170	180
m717.pep	190	200	210	220	230	240
	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
	190	200	210	220	230	240
m717.pep	250	260	270	280	290	300
	AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENATPARLSATAESAAALLAS					
	250	260	270	280	290	300
m717.pep	310	320	330	340	350	360
	ALCLTGIFSPASLLLPENYAAVRFIVVSCMLPPLFCTLAISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPASLLLPENYAAVRFIVVSCMLPPLFYTLTEISGIGLNVVRKTRPIALAT					
	310	320	330	340	350	360
m717.pep	370	380	390	400	410	420
	LGALANLLLGLAVPSGGARGAACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLLGLAVPSGGTRGAACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF					
	370	380	390	400	410	420
m717.pep	430	440	450	460	470	
	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKLHYLKKQGFPLX					
g717	CLASSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKNLHKLHYLKKQGFPLX					
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq

```

1  ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC
51  GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG
101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGGG GCTGACGGTG
151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC
201 CGCCGCCGAC AAAGACACTT TGTTCAAAC CCTGTTCTCT CCGCCGCTGC

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1158

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTCGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTGC
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGTCCAAG
451 CTCGCCATCC TGCTGCTGCT GCCGCTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCCGTTTA CGCGCTGGCA AACCTTGCCG
551 CCGCCGCCTT TTTGCTGTTT CAAAACCGAT GCCGTCTGAA GGCCGTCGGG
601 CGCGCACCGT TTTCATCCGC CGTCCTGCAT CGCGGCCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGGCCTAG AACAGCTCGG CGTTTATTTC
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTTCCGCGC AATCGAAGCA AACGCCCCCG
851 CCGCCCGCCT CTCGGCAACG GCAGAAATCCG CCGCCGCCCT GCTTGCCCTCC
901 GCCCTCTGCC TGACCGGCAT TTTCTGCCCC CTCGCCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGTCC GGTTTATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCTGCTGCTG CTGGGGCTTG CCGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGGTTGCCTG TGCCGCCTCA TTTTGGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCCTGCC GCCTGTGGCA GCCGCTCAAA CGCCTGCCGC TTTATATGCA
1251 CACATTGTTT TGCTGGCCTT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCTGTTT GCCGCGGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGTCAC AAAGTGTTC ATTATTTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

```

a717.pep
  1  MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
 51  SVLCLGLDQA YVREYYAAAD KDTLFKTLFL PPLLSAAAIA ALLSRPSLP
101  SEILFSLDDA AAGIGLVLFE LSFLPIRFL LVLMEGRAL AFSSAQLVSK
151  LAILLLLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201  RAPFSSAVLH RGLRYGIPIA LSSIAYWGLA SADRLFLKKY AGLEQLGVYS
251  MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301  ALCLTGIFSP LASLLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351  RKTRPIALAT LGALAAANLLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401  SSCRLWQPLK RPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451  CILRHRKDLH KLFHYLKKQG FPL*

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a717/m717 97.9% identity in 473 aa overlap

```

              10      20      30      40      50      60
a717.pep      MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
              |||
m717           MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA
              10      20      30      40      50      60

              70      80      90      100     110     120
a717.pep      YVREYYAAADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLFE
              |||
m717           YVREYYATADKDTLFKTLFLPPLLSAAAIAALLSRPSLPSEILFSLDDAAAGIGLVLFE
              70      80      90      100     110     120

              130     140     150     160     170     180
a717.pep      LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
              |||
m717           LSFLPIRFLLLVLRMEGRALAFSSAQLVSKLAILLPLTVGLLHFPANTAVLTAVYALA
              130     140     150     160     170     180

              190     200     210     220     230     240
a717.pep      NLAAAFLLFQNRCRLKAVRRAPFSSAVLHRLRYGIPIALSSIAYWGLASADRLFLKKY
              |||
m717           NLAAAFLLFQNRCRLKAVRHAPFSPAVLHRLRYGIPIALSSIAYWGLASADRLFLKKY
              190     200     210     220     230     240

              250     260     270     280     290     300
a717.pep      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS

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1159

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|||||
m717      AGLEQLGVYSMGISFGGAALLFQSIFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250      260      270      280      290      300

           310      320      330      340      350      360
a717.pep  ALCLTGIFSPASLLLPENYA AVR FIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
           |||||||
m717      ALCLTGIFSPASLLLPENYA AVR FIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310      320      330      340      350      360

           370      380      390      400      410      420
a717.pep  LGALAANLLLLGLAVPSGGARGA AVACAASFVWLFVFKTESSCRLWQPLKRLPLYMHTLF
           |||||||
m717      LGALAANLLLLGLAVPSGGARGA AVACAASFVWLFVFAFKTESSCRLWQPLKRLPLYLHTLF
           370      380      390      400      410      420

           430      440      450      460      470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFPLX
           ||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLHKL FHYLKKQGFPLX
           430      440      450      460      470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCGA AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTTTGG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGCAGAT GGCCGACTGG
451 TGCGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCCGCA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCCTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTTGA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCCGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRTLRWLYM FKHYAVHDFE EFLELYGMPF RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLOMADW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRRDLLV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRE PKDIAVFADA IPKLVDVGVQ
251 IPESWVRDKL VIPDVQEGEA VLVVRQVPDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:

1160

a718.seq

```

1   ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CCGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCCTACCCG CGAAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTCATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GGCGGAAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

a718.pep

```

1   MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSL QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFS DGL
151 YLPRNFIHRP QSWFKWDKDN GLLRLTREN EGEALWPLGW VVHTQKSR SV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMP IRIK YGAGATKEEK
251 NTLRLAVAEI GHNAAGIMPE GMEIELHNA NGMTSAGNPF LQMADWCEKS
301 AARLILQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTPKDI AVFADAI PKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVFS					
m718	SDGLYVPRNFIHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKSRVQQARNGLFRTL					
m718	RENPEGEALWPLGWVVHTQKSRVQQARNGLFRTL					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMAW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNPFLQMAW					

1161

	100	110	120	130	140	150
a718.pep	300	310	320	330	340	350
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKVAQTITSQIIGPFLQ					
m718	160	170	180	190	200	210
	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKVAQTITSQIIGPFLQ					
a718.pep	360	370	380	390	400	410
	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEA					
m718	220	230	240	250	260	270
	INYPHADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEA					
a718.pep	420	430	440	450	460	470
	VLVRQVPDPNPNVRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	280	290	300	310	320	330
	VLVRQVPDPNPNVRTALAALSHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
a718.pep	480	490	500	510	520	
	VAAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					
m718	340	350	360	370	380	
	VAAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDCHARAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTCATA CCCAAAATCC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGAAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCCG CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAACCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQKEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFADI EERDS DIAAN MGTRKRALLT LNWRVAPPRN
101  ATPEEEKLSQ QAYEMMDSLP TLEDLIMDLM DAVGHGFSAL EVEWVFSDDL
151  YLPRNFIHRP QSWFKWDKDN GLLLRTRNRP EGEALWPLGW VVHTOKSRSV
201  QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251  NTLRLAVAEI GHNAAGIMPE GMEIELHNAA NGTTATSNPF LQADWCEKS
301  AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

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1162

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351 IGPFLQINYP HADPNRVPKF EFDTPREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

```

a718.seq
1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TGCGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCG GCTGGGCTGG GTCGTTCTAT CCCAAAAATC GCGCAGCGTC
601 AACACCGGCG GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTTGC TTTCGAGCGGT GGCGGAAATC GGTCACAACG CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGCG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGGTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 CCGGAAATTT GAATTTGACA CGCGCGAGCG GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCCG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

```

a718.pep
1  MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHELFDI EERDSIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEELSD QAYEMMDSLP TLEDLIMDL DAVGHGFSAL EVEWVFSGL
151 YLPRNFIHRP QSWFKWDKDN GLLLRTRN EGEALWPLGW VVHTQKRSV
201 QQRNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVPKF EFDTPREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718-1 99.0% identity in 526 aa overlap

```

          10      20      30      40      50      60
a718.pep  MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI
          |||
m718-1    MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRALFEDAESGDI
          10      20      30      40      50      60

          70      80      90     100     110     120
a718.pep  RAQHELFDIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP
          |||
m718-1    RAQHELFDIEERDSIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP
          70      80      90     100     110     120

          130     140     150     160     170     180
a718.pep  TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKDNGLLLRTRN
          |||
m718-1    TLEDLIMDLMDAVGHGFSALEVEWVFSGLYLPRNFIHRPQSWFKWDKDNGLLLRTRN
          130     140     150     160     170     180

```

1163

	190	200	210	220	230	240
a718.pep	EGEALWPLGWVVHTQKSRSVQQARNGLFRTL	SWLYMFKHYAVHDFAEFLELYGMP	IRIGK			
m718-1	EGEALWPLGWVVHTQKSRSVQQARNGLFRTL	SWLYMFKHYAVHDFAEFLELYGMP	IRIGK			
	190	200	210	220	230	240
	250	260	270	280	290	300
a718.pep	YGAGATKEEKNTLLRAVAEIGHNAA	GIMPEGMEIELHNAANGMTSAGNPFLQ	MADWCEKS			
m718-1	YGAGATKEEKNTLLRAVAEIGHNAA	GIMPEGMEIELHNAANGTTATSNPFLQ	MADWCEKS			
	250	260	270	280	290	300
	310	320	330	340	350	360
a718.pep	AARLILGQTLTSGADGKSSTNALGNIHNE	IRRDLLVSDAKOVAQTITSQIIGPFLQ	INYP			
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNE	VRDRLVSDAKOVAQTITSQIIGPFLQ	INYP			
	310	320	330	340	350	360
	370	380	390	400	410	420
a718.pep	HADPNRVPKFEFDTREPKDIAVFADA	IPKLVDVGVIPE	SWVRDKLVIPDVQEGEAVLVR			
m718-1	HADPNRVPKFEFDTREPKDIAVFADA	IPKLVDVGVIPE	SWVRDKLVIPDVQEGEAVLVR			
	370	380	390	400	410	420
	430	440	450	460	470	480
a718.pep	QVPDNPVNRTALAALSAHTVPSKATGRHQE	ILDGALDDALVEPDFNSQLNPMVRQ	AAVAAL			
m718-1	QVPDNPVNRTALAALSAHTVPSKATGRHQE	ILDGALDDALVEPDFNSQLNPMVRQ	AAVAAL			
	430	440	450	460	470	480
	490	500	510	520		
a718.pep	NACNSYEEADAALNALYPNLDNAKLRTY	MQQALFISDILGQDHARAX				
m718-1	NACNSYEEADAALNALYPNLDNAKLRTY	MQQALFISDILGQDHARAX				
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1   ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAAATCGCG GCGCCAACTT GAACGGCAAA GCCATACTTA TGCGTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TGCGTTTAAC CGTTTGGCGC GCAGCGGCAA GGCATCACAA AATGATTTGG
251 CACGGCGGCG GGTGCTACG CGTAACCGAA TTCGCGAGCT GAACGCGGAA
301 CTGAAACAGG GCACGGGATT TGCGGACAAG ATGGGAAAAA TCGGAAGATT
351 CGGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTGGC ACTTGAACCT GTCGAGAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGCTCTGA ATTTTGCCCA AACCAAGAAT GAAGCGCAGG CGGCATATGC
651 TTTTGCACCT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAACCTGATTA
701 AAACCTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTCGAGG TGCGGGATAT
801 GGTTCTGGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGGTGTGCG CGGTTTGGAC TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCCTGC CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAAACT CTGTCGCTG ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTGCAA
1051 GGCAAGCAAA ACGGCGAAAA CGCAGTGCAG GTGTTGTCCC GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTGACGGCGA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGGCGCG
1201 CTTTGGCGC AACTGCTGCC TGATTGTCAG GCAAAACAA GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTTGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTTGGCT GCTCCGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAGTG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CGGTATCAAG TGGCCATGTT
2151 CGGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

m719.pep

```

1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51 GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAAVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAAFAL ASEGSGEDTA KLIKTLKDDG MSGKDLQLGL
251 EHVLSQGLDG TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSAA
301 NKSQSPAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNGK IAKNNEARML
451 SAAAQQEQQE SLAMLRESLT GTLVDMETSF KKLAAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNNPALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGGVPPQYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQQT AAYQAALAQD TAAVTTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVs RYQVAMFGRG AGQ*

```

a719.seq not found yet

a719.pep not found yet

g720.seq not found yet

g720.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

m720.seq

```

1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCGG
51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTTGTGCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGGCGGTGC
251 TGGTGCACCC TGTTTGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTTT GAAAACGCCT
401 TTTTGGTCTG GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TGCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGCGGCA TCGGGTACGT
551 TTGGCGCGGT GCGCCGTTTG TTTGATTTGG ACAAATTCG CTTTCCCGAT
601 CCGGCGCGAT ACAGTGCAGC GGCGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TGCGGATATA TCGGTCATGG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTTT GGTGCGCCGC ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGCGCC GCCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCGGTTAA

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1165

```

851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CCGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGGGTGGC AACGGCATTG ATCGAGGCGC ATGGCGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCCG CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTTAC GGCGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
  1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
 51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAEIIFVF ENAFLVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPRQRF
251 DGAAAVADRA AAIPDNLLTG RFSDGLQNRL NRLTAKQVQP VAQAVRLLST
301 SSLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGGLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
  1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAACAGG TGCAGCCGGT
 51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GGCGAAGAGA TGACCGCGCC CGATTGATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGCGGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGGCA
301 GGCCGTCTGA ATGCGTTGGT TGCGGCGGTC ATCAACCAA AGCCGCCGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCCGCGTT TATCAAGCGC GGCACTTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
  1 GLQNRLNRLT AKQVQVQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
 51 EVNRAMRRRM QAEIAALRAV QTAAAESGGL TANAVYTEAY QTAESLRAAA
101 GRNLALVA AV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

      250      260      270      280      290      300
m720.pep  SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNRLNRLTAKQVQVQAQAVRLLSTSSLL
a720      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      10      20      30
      310      320      330      340      350      360
m720.pep  SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAAESGGLTANAVYTEAY
a720      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      40      50      60      70      80      90
      370      380      390      400      410      420
m720.pep  QTAESLRAAAGRLNALVAAVINQKPLIVRQAPIDGTIHQIAHEFYGDIARAAELVRLNP
a720      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
      100      110      120      130      140      150
      430      440
m720.pep  HHHHPAFIKRGTLVNSYAKX

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1166

a720 |||||
 HIHHPAFIKRGTLVNSYAKX
 160 170

g721.seq not found

g721.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq
 1 ATGTCCAAAA ATGCACAAAA AACCCCTACTT GCCGTGTGCA GTTTCGAGGT
 51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
 151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
 201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
 251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC
 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCG AGCTGGCGGA
 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
 701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
 801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG
 851 AAGGCGTATT GAAACAGCCG GCGGCGTTGG CATTTTTCGAC CGGCTTTATT
 901 GAAAACGCCC AGCCGGTTCG TGCACTGGCA GGCTCGCAA CGGGCGGCAA
 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGACG
 1001 CAAAATGCT GGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC
 1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2434; ORF 721>:

m721.pep
 1 MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAYWLTEE
 51 NGHDVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAAGWM RWLEFTPKGM
 101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
 151 MDEVLAASA QILKPETEON PMKELLQQLF DLPDAGEEEL KAALSALVEA
 201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTQYAPI SVVQELQSKV
 251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLPQ GGLAFLTGFI
 301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
 351 ECK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq
 1 ATGTCCAAAA ATGCACAAAA AACCCCTACTT GCCGTGTGCA GTTTCGAGGT
 51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA
 151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT
 201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG
 251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAA
 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG
 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCGCG GTTGGACGGT
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC
 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGGAAGCC
 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCG AGCTGGCGGA
 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT
 701 TGAATAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC
 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC
 801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAG
 851 AAGGCGTATT GAAACAGCCG GCGGCGTTGG CATTTTTCGAC CGGCTTTATT
 901 GAAAACGCCC AGCCGGTTCG TGCACTGGCA GGCTCGCAA CGGGCGGTAA
 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGACG
 1001 CAAAATGCT GGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1167

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence <SEQ ID 2436; ORF 721.a>:

```

a721.pep
  1 MSKNAQKTLL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
 51 NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEQN FMKELLQQLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTKYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

	10	20	30	40	50	60
a721.pep	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVP	PAWYLTEENGHDVALLAN				
m721	MSKNAQKTLLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVP	PAWYLTEENGHDVALLAN				
	10	20	30	40	50	60
	70	80	90	100	110	120
a721.pep	SSRNQLVVDYEHXTLYKEKNQGPAPAGWMRWLEFTPKGMFAEVEWTDK	AAAAIAAKEYR				
m721	SSRNQLVVDYEHQTLYKEKNQGPAPAGWMRWLEFTPKGMFAEVEWTDK	AAAAIAAKEYR				
	70	80	90	100	110	120
	130	140	150	160	170	180
a721.pep	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEQN	FMKELLQQLF				
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEQN	FMKELLQQLF				
	130	140	150	160	170	180
	190	200	210	220	230	240
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTA	KPDLTKYAPI				
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTA	KPDLTKYAPI				
	190	200	210	220	230	240
	250	260	270	280	290	300
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQP	GGGLAFLTGFI				
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAEGLKQP	GGGLAFLTGFI				
	250	260	270	280	290	300
	310	320	330	340	350	
a721.pep	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKES	EGKX				
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKES	EGKX				
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

```

m722.seq
  1 GTGTTTGAAG CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
 51 TACCAAAGAG CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCAGCGGCTT GAGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

```


1168

```

401 AGCCGGGCGC GCGCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCGCGCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCGACCGGCC CGCAGGCGGC AACC GTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCGCGGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTVQV KLDGIDLDEA KRRIRLTALKE YFDTLIPDGG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TGCGCGGCTT GCGCCGCCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGGCCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCGGACG
401 AGCCGGGCGC GGCCGCCAAT GTGCGCGACG GCGAGGCGCA ACTGATGGCC
451 GCGCCGCGCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCGACCGGCC CGCAGGCGGC AACC GTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCGCGGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAAGTGTGCG CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAYV YPLRRGLGTV DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTVQV KLDGIDLDEA KRRIRLTALKE YFDTLIPDGG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

1169

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

```
m723.seq
  1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
 51  AGTGATCACG CCCGAACACC TTATTTTAC CGTTTACAAA CACAATACCG
101  TCTTCGCCCC CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151  TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTTGTAGC
201  GGTTCGCGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251  TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301  AAAAGGTTCG CTGAACCGCC CCAGATACGC GTCGATTTTC GCAGTGGCGT
351  CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401  CGGTCGGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451  CTAACCGTC GCGTATGCCA TTACTCGACC GCCTTGCCTT GCAGCATAGG
501  CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551  CTTCGCGCCA GCCGCCGTC AAGAGCAGGC CGCCGCGCCA AAATCTCTTG
601  CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651  GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701  ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTCAGCATT
751  TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801  GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTTCGGCG GTTTCGGTT
851  TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901  CGCATTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

```
m723.pep
  1  MRPKPRFRRS VIACISVIT PEHLIFTVYK HNTVFARGHF FAAIHAQLH
 51  FAFGHSTQQV EHVDFVAHAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101  KRSSEPPQIR VDFGSGVHQR GLCDLAVNQP LVVAVGELQD FQLTETRNHI
151  LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201  PSAPVLTSIT SRLSAKASAA RVCCTLSSA SSADSAFLSS SAFSKAVVSI
251  STSFRAAASS ACTASNSALM SSNDGAAVSA VSGLLLVFAM MTPCFRRRRI
301  RI*
```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

```
m724.map
  1  ATGAGTTTGAGTAAATTGGCGAAAAAACGGCACAACTGCTAAAAATATCGGCGAAACC
    -----+-----+-----+-----+-----+-----+ 60
a   TACTCAAACATTTAACCGCTTTTGTCCGTGTTGACGATTTTATAGCCGCTTTGG
    M S L S K L A K K T A Q T A K N I G E T -
    CTGCGCGCGGCCTTTCGGGGAAAAATCACGCTGGTGGTGTCTCGAGCCGATAACAGCGC
 61  -----+-----+-----+-----+-----+-----+ 120
a   GACGCGCGCCGAAAGCCCTTTTAGTGCGACCACACAGCAGGCTCGGCTATGTCGCG
    L R A A F R G K I T L V V S S E P I Q R -
    GTGCAGTTGAGCGGCTTGGCCGACGAAACCCTGCAAGACCTTGAACATTTGCAGGAATAC
121  -----+-----+-----+-----+-----+-----+ 180
a   CACGTCAACTCGCCGAACCGGCTGCTTTGGGACGTTCTGGAAGTTGTAACGTCCTTATG
    V Q L S G L A D E T L Q D L E H L Q E Y -
    GGCTTTGCCAGCCATCCGCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181  -----+-----+-----+-----+-----+-----+ 240
a   CCGAAACGGTCGGTAGGCGGGCTGCCGTGCTTCGCCATCACTATGGCGACCCGCCGTTA
    G F A S H P P D G S E A V V I P L G G N -
```

1170

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241 -----+-----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTCGGTCGTGCCGTCGATGGCGTAGTTTTTGGAAATTC
a      T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTTAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301 -----+-----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTAGCTAATTTCGTTCCGTTT
a      P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTTAACTGCAACAATACGAGGTTAATGCG
361 -----+-----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a      I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCACTGTTGACGGCGCAA
421 -----+-----+-----+-----+-----+-----+-----+ 480
      CGGTGCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACCTGCCGCGTT
a      A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481 -----+-----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAAATCG
a      G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541 -----+-----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGGCCGCGTCGAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA
a      G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCGCCAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601 -----+-----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCGTGGGCGTATGGCTGTCTAGCCGCGTTTTGGAATGGCCGCTT
a      I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661 ----- 669
      GGCCGTATC
a      P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI
Sali SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724 . pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQ GK IIEADCDVYR VNCKQYEVNA ATDAKFNAPL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTGDGVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724 . seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGGCGATTTT TAATCATGAG GGTGCAAAAA TCGTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTACCGG GTTAACTGCA
401 AACAATACGA GGTTAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

```

1171

```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQKG IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQKG					
m724	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQKG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet

g725.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
1  ATGGTGCGCA CGGTTAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
51  GCAAATCCAT ACGCTGCCTG CCGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCGGC GGCGTATGCG GACGTTATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCGCAAT CTGCGCAACG AGCAGGCGCA
201 GCGGCAAGGC GGCATCGACA GCCGCGAAAT CGGCAGCAAC GATTTAATCC
251 GCGCTGTTTC CCGCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAATAA GACCGCTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTACGAC CCGCAATCCG
551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
1  MVRTVKSUNG EADDLAQIHL TLPVWVWYTG GSKVEPASTG GVCGRYQDTA
51  EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLD DGQRLGFADS
101 RGLVPKAVRA IANHVLVQNA AVSIYAVEYA IRFNTCGLEN DRYPERTDNP
151 DDPNHIIFTKY QGTLSEFPWD FEGLDGKIYD PQSADEIPVN LTLKDKQ*

```

a725.seq not found yet

a725.pep not found yet

g726.seq not found yet

g726.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

m726.seq

```

1   ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACAT TGGGCGGCAT
51  CCCC GAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGATTAC CACGAATGGG ACGGCAAAAA
201 ATGGAAAATC AGCAAAGCCG CCGCCGCCGC CCGTTTCGCC AAACAAAAAA
251 CCGCCTTGGC ATTCCGCCTC GCGGAAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGCGCG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTATCG AAAAATCCGC CCGCCTGGCT GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGT CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CCGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:

m726.pep

```

1   MTIYFKNGFY DDTLGSIPEG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSDY HEWDGKKWKI SKAAAAARFA KQKTALAFRL AEKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDVLIE
151 KVIEKSARLA VAAGAIIGKR QQLEDKINTI ETAPGLDALE KEIEEWTLNI
201 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

a726.seq

```

1   ATGACCATCT ATTTCAAAAA CGGCTTTTAC GACGACACCT TGGGCAGCAT
51  CCCC GAAGGC GCGGTTGCCG TCCGCGCCGA AGAATACGCC GCCCTTTTGG
101 CAGGACAGGC GCAGGGCGGG CAGATTGCCG CAGATTCCGA CGGCCGCCCC
151 GTTTTAACCC CGCCGCGCCC GTCCGAATAC CACGAATGGG ACGGCAAGAA
201 ATGGGAAATC GGCGAAGCCG CTGCCGCCGC CCGTTTCGCC GAACAAAAAA
251 CCGCCACGGC ATTCCGCCTC GCGGCAAAGG CGGACGAACT CAAAAACAGC
301 CTCTTGCGCG GCTATCCCCA AGTGGAATC GACAGCTTTT ACAGGCAGGA
351 AAAAGAAGCC CTCGCGCGGC AGGCGGACAA CAACGCCCCG ACCCCGATGC
401 TGGCGCAAAT CGCCGCCGCA AGGGGCGTGG AATTGGACGT TTTGATTGAA
451 AAAGTTGTCG AAAAATCCGC CCGCCTGGCC GTTGCCGCCG GCGCGATTAT
501 CGGAAAGCGG CAGCAGCTCG AAGACAAATT GAACACCATC GAAACCGCGC
551 CAGGATTGGA CGCGCTGGAA AAGGAAATCG AAGAATGGAC GCTAAACATC
601 GGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

a726.pep

```

1   MTIYFKNGFY DDTLGSIP EG AVAVRAEEYA ALLAGQAQGG QIAADSDGRP
51  VLTPPRPSEY HEWDGKKWEI GEAAAAARFA EQKTATAFRL AAKADELKNS
101 LLAGYPQVEI DSFYRQEKEA LARQADNNAP TPMLAQIAAA RGVELDVLIE
151 KVVEKSARLA VAAGAIIGKR QQLEDKINTI ETAPGLDALE KEIEEWTLNI
201 G*

```

a726/m726 95.5% identity in 201 aa overlap

	10	20	30	40	50	60
a726.pep	MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTPPRPSEY					
m726	MTIYFKNGFYDDTLGSIPEGAVAVRAEEYAALLAGQAQGGQIAADSDGRPVLTPPRPSEY					
	10	20	30	40	50	60

1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGEAAAAARFAEQKTATAFRLLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQQLEDKLNITI
              |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          LARQADNNAPTMLAQIAAARGVELDVLEIKVIEKSARLAVAAGAIIGKRQQLEDKLNITI
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              |||||:|:|:|||||:|||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

g727.seq      not found yet
g727.pep      not found yet

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1   ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATTAT
51  CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTTGC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGGCTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1   MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51  AQALLLSAQN YARELELARA EAKKYEKKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIPFPDP SRNPNTGFRL FSPQIPNFT QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1   ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
51  CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCAGCGTGC GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCTGAA
251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1   MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51  AQALLLSAQN YARELEQARA EAKKYEKKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGGCI DGFGHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQYKSAFAKQQAVIDKMERDKAQALLLSAQN
              10      20      30      40      50      60

              70      80      90      100     110     119
a727.pep  YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENV-LTQDRKNAGGGC
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAFAAKKYEVKAHAVGMALAKKQAEVSRLKTE--RDLCKIPFPDSDRNPTGF
              70      80      90      100     110

              120     130     140
a727.pep  IDGFGHHGLQLYKRALGYGNX

m727      RLFSPQIPPNTQIPPX
              120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

g728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAATAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATCCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACG CCAGAGTTTC GAATATTATT TGA AAAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGCGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAAGCC TATCATGCGC AACAGACGTG GTATTGTGGT GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

g728.pep

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

m728.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAAATCT TGCCGGAACT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

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1175

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501  CGGGGAAAAT  TATGAAACGA  CAGGAGAATA  TCGGGTTGTT  TGGCAACCAG
551  ACGGTTCCGT  ATTTGATGCG  GCGGGGCGCG  GGAAAATCGG  GGAAGATGTT
601  TATGAGCATT  GCCTCGGGTG  TTATCAGATG  GCCCAGGTAT  ATTTGGCGAA
651  ATACCGGGAT  GTCGCGAATG  ACGAGCAGAA  GGTTTGGGAC  TTCCGCAAAG
701  AGAGCAACCG  AATTGCGTCG  GACTCGCGCA  ATTCTGTGTT  TTATCAGAA
751  ATGCGGGAAT  TGATGCCCCG  AGGGATGAAG  GCGAACAGTC  TTGTGGTCGG
801  CTATGATGCG  GACGGTCTGC  CGCAAAAAGT  CTATTGGAGT  TTCGACAATG
851  GAAAAAACG  CCAGAGTTTC  GAATATTATT  TGAAAAACGG  AAATCTTTT
901  ATTGCACAAT  CTTGACGGT  AGCATTGAAA  GCGGATGGCG  TAACGGCGGA
951  TATGCAGACC  TATCATGCGC  AACAGACGTG  GTATTTGGAT  GCGGGGCGGA
1001 TTGTCCGCGA  AGAGAAACAG  GGAGACAGAC  TGCCTGATTT  TCCTTTGAAC
1051 TTGGAAAATT  TGGAAAAGA  GGTGCGCCGT  TATGCAGAGG  CTGCGGCGAG
1101 ACGTTCGGGC  GGCAGGCGCG  ACCTTTCTCA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

m728.pep

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYM AQVYLAKYRD VANDEQKVDW FRKESNRIAS DSRNSVFYQN
251 MRELMPRGMK ANSLVVGYYDA DGLPQKVYWS FDNGKKRQSF EYYLKNNGNLF
301 IAQSSVALK  ADGVTADMQT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

	10	20	30	40	50	60
m728.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKPNNAFVAKLARLFRNA					
g728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNNAFVAKLARLFRNA					
	10	20	30	40	50	60
m728.pep	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
g728	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
	70	80	90	100	110	120
m728.pep	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV					
g728	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTAHGENYETTGEYRVV					
	130	140	150	160	170	180
m728.pep	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
g728	WQPDGSVFDAAGRGKIGEDVYEHCLGICYMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	190	200	210	220	230	240
m728.pep	DSRNSVFYQNMRELMPRGMKANSLVVGYYDADGLPQKVYWSFDNGKKRQSF EYYLKNNGNLF					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGYYDADGLPQKVYWSFDNGKKRQSF EYYLKNNGNLF					
	250	260	270	280	290	300
m728.pep	DSRNSVFYQNMRELMPRGMKANSLVVGYYDADGLPQKVYWSFDNGKKRQSF EYYLKNNGNLF					
g728	DSRDYVFYQNMRELMPRGMKANSLVVGYYDADGLPQKVYWSFDNGKKRQSF EYYLKNNGNLF					
	250	260	270	280	290	300
m728.pep	IAQSSVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m728.pep	IAQSSVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
g728	IAQSSVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					

1176

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g728      IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR
           310      320      330      340      350      360

           370
m728.pep  YAEAAARRSGRRDLSHX
           |||||
g728      YAEAAARRSGRRGLSHX
           370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

```

a728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTGTG CACTTGTATT
51  TGCTTTTGG CTGGGAACGG GTATTGCCA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAAATCCGA ATGCTTTTGT GGCGAAACTT
151 GCCCGCCTGT TCCGAAATGC CGACAGGCGG GTTGTTCATCG TGAAGGAATC
201 GATGAGGACG GAGGAAAGTC TTGCCGAGC TGTGGATGAC GGTCCGTTGC
251 AGTCGGAGAA GGATTATCTT GCACTCGCTG TCCGGCTCAG TCGTTTGAAA
301 GAAAAGGCGA AATGGTTTCA CGTAACGGAG CAGGAACATG GGGAAGAGGT
351 TTGGCTGGAT TACTATATCG GCGAGGCGG TTTGGTTGCG GTTTCGCTTT
401 CGCAACGCTC GCCGGAAGCG TTTGTTAATG CCGAATATCT GTATCGGAAC
451 GATCGTCCGT TTTCTGTAAA TGTGTACGGC GGAACGGTTC ACGGGGAAAA
501 TTATGAAACG ACAGGAGAAT ATCGGGTTGT TTGGCAACCG GACGGTTCGG
551 TATTTGATGC GTCGGGCGC GGGAAAATCG GGGAAGATGT TTATGAGCAT
601 TGCCTCGGGT GTTATCAGAT GGCCAGGTA TATTGGCGA AATATCGGGA
651 TGTCGCGAAT GATGAGCAGA AGGTTTGGGA CTTCCGCGAA GAGAGTAACC
701 GGATTGCGTC GGA CTGCGC GATTCTGTGT TTTATCAGAA TATGCGGGAA
751 TTGATGCCCC GAGGGATGAA GGCAAACAGT CTTGTGGTCG GCTATGATGC
801 GGACGGTCTG CCGCAGAAAG TCTATTGGAG TTTCGACAAT GGGAAAAAAC
851 GCCAGAGTTT CGAATATTAT TTGAAAAACG GAAATCTTTT TATTGCACAA
901 TCTTCGACGG TAGCATTGAA AGCGGATGGC GTAACGGCGG ATATGCAGAC
951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

```

a728.pep
1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGICYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKQRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGRR DLSH*

a728 / m728 96.3% identity in 377 aa overlap

           10      20      30      40      50
a728.pep  MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA
           |||||
m728      MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
           10      20      30      40      50      60

           60      70      80      90      100     110
a728.pep  DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLLALAVRLSRLKEKAKWFHVTEQEHGEEV
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLLALAIRLSRLKEKAKWFHVTEQEHGKEV
           70      80      90      100     110     120

           120     130     140     150     160     170
a728.pep  WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           ||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
m728      WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFSVNVYGGTVHGENYETTGEYRVV
           130     140     150     160     170     180

```

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGQYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
	: : : : : :					
m728	WQPDGSVFDAAAGRGKIGEDVYEHCLGQYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSLVVGADGLPQKVYWSFDNGKKRQSFEEYLLKNGNLF					
	: : : : : :					
m728	DSRNSVFYQNMRELMPRGMKANSLVVGADGLPQKVYWSFDNGKKRQSFEEYLLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGGRIVREEKQGDRLPDFPLNLEDLEKEVSR					
	: : : : : :					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDLSHX					
	: :					
m728	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

```

1  ATGAATACTA CATTGAAAAC TACCTTGACC TCTGTTGCAG CAGCCTTTGC
51  ATTGTCTGCC TGCACCATGA TTCCTCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCGGAAAC CTTCCAAAAC GACACATCGG TTTCTTCCAT CCGCGCGGTT
151 GATTGGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCACTTT GCGTACAGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATCG AGCGCAACAA CCTCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGGCTCGCGC CAAGGCAGCT TGAGCGGCgg
351 caaTGTCAGC AGCAGCTACA ATGTCTGACT GGGTGcGGca tCTTACGAAC
401 TCGATCTGTT CgGGCGCGTG CGCagcaacA GcgaagcAGC ACTGcaggGC
451 tATTTTGCCA GCGTTGCCAA CcgcGATGCG GCACATTtGa ttCtGATTGC
501 CACCGTTGCC AAAGCCTATT TCAAcgaGcG TTATGCCGAA AAAGcgatgT
551 CTTTGCGCa gcGTGTCTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTGCGGT ACAAGGCAGG CGTGATTtCC GCCGTCGCCC TGCGCCAGCA
651 GGAAGCCTTG ATTGAATCTG CCAAAGCCGA TTATGCCAT GCCGCGCGCa
701 gcCGGAACA GCGCGCAAT GCCTTGGAAC CCTTGATTAA ccGTCCGATA
751 CCCGAagaCC TGCCCGCCGG TTTGCCGTTG GACAagcAGT TTTTGTGTA
801 AAAATGCCT GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCGACA
851 TCCGCGCCGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 gcgCGCGCCg ccTTTTTCCC GTCCATCCGC CTGACCGGAA GCGTCGGTAC
951 GGGTTCTGTC GAATTGGGCG GGCTGTTCAA AAGCGGCACG GCGGTTTGGG
1001 CGTTCGCTCC GTCTATTACC CTGCCGATT TTAATTGGG AACGAACAAG
1051 GCGAACCTTG ATGTGGCAA ACTGCGCAA CAGGCACAAA TTGTGCCTA
1101 TGAATCCGCC GTCCAATCCG CCTTTCAAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGA CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGATTtGC TCGATGCGGA ACGCATCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CGCTCgacGG CGGATTGAAA CGGGATACCC AAACCGGCAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

```

1  MNTTLKTTLT SVAAAFALSA CTMIPOYEQP KVEVAETFQN DTSVSSIRAV
51  DLGWHDFAD PRLQKLIDIA LERNtSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANGSR QGSLSGGNVS SSYNVGLGAA SYELDLFGRV RSNSEAAALQG
151 YFASVANRDA AHLILIAIVA KAYFNERYAE KAMSLAQRLV KTREETYKLS

```

m729.seq

1	ATGGATACTA	CATTGAAAAC	CACCTTGACT	TCTGTTGCAG	CAGCCTTTGC
51	ATTGTCTGCC	TGCACCATGA	TTCCCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TTGCCGAAAC	GTTCAAAAAC	GATACCGCCG	ACAGCGGCAT	CCGCGCCGTC
151	GATTTAGGTT	GGCATGACTA	TTTTGCCGAC	CCGCGCCTGC	AAAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAAGTT	CGGTACCGCC	GTTATTGAAC
251	GCGAAATCTA	CCGCAAACAA	TACATGATTG	AGCGCAACAA	CCTCCTGCCC
301	ACGCTTGCCG	CCAATGCGAA	CGACTCGCGC	CAAGGCAGCT	TGAGCGGCGG
351	CAATGTAAGC	AGCAGCTACA	AAGTCGGACT	GGGTGCGGCA	TCTTACGAAC
401	TCGATCTGTT	CGGGCGTGTA	CGCAGCAGCA	GCGAGGCGGC	ACTGCAAGGC
451	TATTTGCGCA	GCAACGCCAA	CCGCGATGCG	GCACATTTGA	GCGTGATTGC
501	CACCGTTGCC	AAAGCCTATT	TCAACGAACG	TTACGCCGAA	GAAGCGATGT
551	CTTTGGCGCA	ACGTGTTTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAATTACGTT	ACAAGGCAGG	CGTGATTTCG	GCCGTGCCCC	TACGTCAGCA
651	GGAAGCCCTG	ATCGAATCTG	CCAAAGCCCA	TTATGCCCAT	GCCGCGCGCA
701	GCCGCGAACA	GGCGCGCAAT	CTTTGGCAA	CCTTGATTAA	CCAACCGATA
751	CCCGAAGACC	TGCCTGCCGG	TTTGCCGCTG	GACAAGCAGT	TTTTTGTGTA
801	AAAAC TGCCG	GCCGGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCGATA
851	TCCGTGCTGC	CGAACACCGG	CTCAAAACAG	CAAACGCCAA	TATCGGTGCG
901	GCACGCGCGG	CAATTTTTCC	ATCCATCCG	CTGACCGGAA	CCGTCCGGAT
951	GGGTTCTGCC	GAAATGGGTG	GGTTGTTCAA	AAGCGGCACG	GGCGTTTGGT
1001	CGTTCGCGCC	GTCTATTACC	CTGCCGATTT	TTACCTGGGG	TACGAACAAG
1051	GCGAACCTTG	ATGTAGCCAA	GCTGCGCCAA	CAGGTACAAA	TCGTTGCCTA
1101	TGAATCCGCG	GTCCAATCCG	CATTTCAGA	CGTGGCAAA	GCATTGGCGG
1151	CGCGCGAGCA	GCTGGATAAA	GCCATTGACG	CTTTAAGCAA	ACAAAGCCGC
1201	GCCTCTAAAG	AAGCGTTGCG	CTTGGTCGGC	CTGCGTTACA	AGCACGGCGT
1251	ATCCGGCGCG	CTCGACTTGC	TCGATGCGGA	ACGCAGCAGC	TATGCGGCGG
1301	AGGTGCGCGC	TTTGTGCGCA	CAACTGACCC	GCGCCGAAAA	CCTTGCCGAT
1351	TTGTACAAGG	CACTCGGCGG	CGGATTGAAA	CGGGATACCC	AAACCGACAA
1401	ATAA				

729. per

1	MDTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV
51	DLGWHDYFAD	PRLQKLIDIA	LERNLSLRTA	VLNSEIYRKQ	YMIERNLLP
101	TLAANANDSR	QGSLSGGNVS	SSYKVGLGAA	SYELDLFGRV	RSSEEAALQG
151	YFASTANRDA	AHLSLIATVA	KAYFNERYAE	EAMS LAQRVL	KTREETYKLS
201	ELRYKAGVIS	AVALRQKEAL	IESAKADYAH	AARSREQARN	ALATLINQPI
251	PEDLPAGLPL	DKQFFVEKLP	AGLSSEVLLD	RPDIRAAEHA	LKQANANIGA
301	ARAAFFPSIR	LTGTVGTGSA	ELGGLFKSGT	GVWSFAPSIT	LPIFTWGNTK
351	ANLDVAKLRQ	QVQIVAYESA	VQSAFQDVAN	ALAAREQLDK	AYDALSKQSR
401	ASKEALRLVG	LRYKHGVSGA	LDLLDAERSS	YAAEGAALSA	QLTRAENLAD
451	LYKALGGGLK	RDTOTDK*			

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / q729 95.7% identity in 467 aa overlap

m729.pep MDTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFKNDTADSGIRAVDLGWHDYFAD
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g729 MNTTLKTTLTSVAAAFALSACTMIPQYEQPKVEVAETFONDTSVSSIRAVDLGWHDYFAD
 10 20 30 40 50 60

1179

	70	80	90	100	110	120																							
m729.pep	PR	LQ	KL	DI	AL	ER	NT	SL	RT	AV	LN	SE	IY	RK	QY	MI	ER	NN	LL	PT	LA	AN	AN	DS	RQ	GS	LS	GG	NVS
g729	PR	LQ	KL	DI	AL	ER	NT	SL	RT	AV	LN	SE	IY	RK	QY	MI	ER	NN	LL	PT	LA	AN	AN	GS	RQ	GS	LS	GG	NVS
	70	80	90	100	110	120																							
	130	140	150	160	170	180																							
m729.pep	SS	YK	VL	GA	AS	YEL	DL	FG	RV	RS	SS	EA	AL	QGY	FA	ST	AN	RD	AA	HL	SL	IA	TV	AK	AY	FN	ER	YAE	
g729	SS	YN	VL	GA	AS	YEL	DL	FG	RV	SN	SE	EA	AL	QGY	FA	SV	AN	RD	AA	HL	LI	IA	TV	AK	AY	FN	ER	YAE	
	130	140	150	160	170	180																							
	190	200	210	220	230	240																							
m729.pep	EA	MS	LA	QR	VL	KTR	EE	TY	KL	SE	LY	KAG	VI	SA	VA	LR	QE	AL	IE	SA	KAD	YA	HA	AR	SRE	QA	RN		
g729	KA	MS	LA	QR	VL	KTR	EE	TY	KL	SE	LY	KAG	VI	SA	VA	LR	QE	AL	IE	SA	KAD	YA	HA	AR	SRE	QA	RN		
	190	200	210	220	230	240																							
	250	260	270	280	290	300																							
m729.pep	AL	AT	LI	NQ	PI	PE	DL	PA	GL	PL	DK	QFF	VE	KL	PA	GL	SE	VLL	DR	PD	IR	AA	EH	AL	KQ	AN	IG		
g729	AL	AT	LI	NR	PI	PE	DL	PA	GL	PL	DK	QFF	VE	KL	PA	GL	SE	VLL	DR	PD	IR	AA	EH	AL	KQ	AN	IG		
	250	260	270	280	290	300																							
	310	320	330	340	350	360																							
m729.pep	AR	AA	FF	PS	IR	LT	GT	VG	TG	SA	EL	GG	LF	KS	GT	GV	WS	FA	PS	IT	LP	IF	TW	GT	NK	AN	LD	VAK	LR
g729	AR	AA	FF	PS	IR	LT	GS	VG	TG	SV	EL	GG	LF	KS	GT	GV	WA	FA	PS	IT	LP	IF	TW	GT	NK	AN	LD	VAK	LR
	310	320	330	340	350	360																							
	370	380	390	400	410	420																							
m729.pep	QV	QI	VA	YES	SA	VQ	SA	FQ	DV	AN	ALA	ARE	Q	LD	KAY	DAL	SK	QS	RA	SK	EA	LR	LV	GL	RY	KH	GV	SG	
g729	QA	QI	VA	YES	SA	VQ	SA	FQ	DV	AN	ALA	ARE	Q	LD	KAY	DAL	SK	QS	RA	SK	EA	LR	LV	GL	RY	KH	GV	SG	
	370	380	390	400	410	420																							
	430	440	450	460																									
m729.pep	LD	LL	DA	ER	SS	YA	EA	GA	AL	SA	QL	TR	AE	NL	AD	LY	KAL	GG	GL	KR	DT	QT	DK	X					
g729	LD	LL	DA	ER	IS	YA	EA	GA	AL	SA	QL	TR	AE	NL	AD	LY	KAL	DG	GL	KR	DT	QT	GK	X					
	430	440	450	460																									

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

1	AT	GG	ATA	CTA	CAT	TG	AAA	AAC	CAC	CTT	GACT	TCT	GTT	GCAG	CAG	CCT	TCGC	
51	ATT	ATC	CGCC	TGC	ACC	ATGA	TTCC	CCAATA	CGAG	CAG	CCCC	AAAG	T	CGAAG				
101	TTG	CCG	AAAC	GTT	CAAAA	AAC	GAT	ACCGCCG	ACAG	CGGC	AT	CCGT	G	CGGTC				
151	GATT	TGG	GTT	GGC	ATG	ACTA	TTTT	TGCCGAC	CCG	CGC	CTGC	AAA	A	AGTGAT				
201	CGAC	ATC	GCA	CTC	GAG	CGCA	ATAC	CAGTTT	GCG	TAC	CGCC	GTAT	T	GAACA				
251	GCG	AAAT	CTA	CCG	CAAC	AA	TAC	ATGATTG	AGC	GCA	ACAA	CCT	C	TGCC				
301	ACG	CTT	GCCG	CCA	ATG	CGAA	CGAC	TCGCGC	CAAG	G	CAGCT	TGAG	C	GGCGG				
351	CAAT	GTA	AAGC	AGC	AGC	TACA	AAG	TCGGACT	GGG	T	CGGCA	TCT	T	ACGAAC				
401	TCG	ATC	TGTT	CGG	GCG	TGTA	CGC	AGCAGCA	GCG	AGG	CGGC	ACT	G	CAAGGC				
451	TATT	TCG	CCA	GCAC	CGC	CAA	CCG	CATGCG	GCAC	ATT	TGA	GCCT	G	ATTGC				
501	CAC	CGT	TGCC	AAAG	CCT	TAT	TCA	ACGAACG	TTAT	G	CCGAA	GAAG	C	GATGT				
551	CTTT	GCG	GCA	ACGT	GTTTT	TG	AAA	ACGCGC	AGGA	AA	ACCTA	CAAG	C	TGTCC				
601	GAAT	TAC	GTT	ACA	AGG	CAGG	CGT	GATTTCC	GCC	GT	CGCC	TAC	G	TGCGA				
651	GGA	AGC	CCCTA	ATC	GAAT	CTG	CCAA	AGCCGA	TTAT	G	CCCAT	GCC	G	CGCGCA				
701	GCC	GCG	GAACA	GGC	GCG	CAAT	GCCT	TGGCAA	CCCT	G	ATTAA	CCA	A	CCGATA				
751	CCC	GAC	GACC	TGCC	CGCC	G	TTT	GCCGTTG	GACA	A	GCAGT	TTTT	T	GTTGA				
801	GAAG	CTG	CCG	GCC	GTT	TGA	GTT	C	CGAAGT	ATT	G	CTCGAC	CGT	C	CCGATA			
851	TCC	GTG	CTGC	CGA	AC	ACGCG	CTCA	AA	CAGG	CAA	AC	GCCAA	TAT	C	GTCGCG			
901	GAC	GCG	CCG	CCT	TTTT	TCC	ATCC	AT	CCGC	CTG	AC	CGGAA	GCG	T	CGATAC			
951	GCAT	TCT	GCC	GAAT	TGG	GCG	GGCT	GTTCAA	AAG	C	GGCACC	GGC	G	TTTGGT				
1001	TGTT	CGC	ACC	TTCC	ATT	ACC	CTGC	CGATT	TTAC	C	TGGGG	TAC	G	AACAAG				

1180

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1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTC AAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGGATAAA GCCTATGACG CTTTAAGCAA ACAAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTCGGT CTGCGTTACA AACACGGCGT
1251 ATCCGCGCGC CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA
```

This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

```
a729.pep
1  MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51  DLGWHDYFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANDSR QGSLSGGNVS SSKVGLGAA SYELDLFGRV RSSSEAALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPA GLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVSGA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*
```

a729 / m729 98.1% identity in 467 aa overlap

a729.pep	MDTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV	DLGWHDYFAD
m729	MDTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFKN	DTADSGIRAV	DLGWHDYFAD
a729.pep	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNLLP	TLAANANDSR	QGSLSGGNVS
m729	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNLLP	TLAANANDSR	QGSLSGGNVS
a729.pep	SSKVGLGAAS	YELDLFGRV	RSSSEAALQ	GYFASTANRDA	AHLSLIATVA	KAYFNERYAE
m729	SSKVGLGAAS	YELDLFGRV	RSSSEAALQ	GYFASTANRDA	AHLSLIATVA	KAYFNERYAE
a729.pep	EAMSLAQRVL	KTREETYKLS	ELRYKAGVIS	AVALRQOEAL	IESAKADYAH	AARSREQARN
m729	EAMSLAQRVL	KTREETYKLS	ELRYKAGVIS	AVALRQOEAL	IESAKADYAH	AARSREQARN
a729.pep	ALATLINQPI	PDDLPA GLPL	DKQFFVEKLP	AGLSSEVLLD	RPDIRAAEHA	LKQANANIGA
m729	ALATLINQPI	PDDLPA GLPL	DKQFFVEKLP	AGLSSEVLLD	RPDIRAAEHA	LKQANANIGA
a729.pep	ARAAFFPSIR	LTGSVDTHSA	ELGGLFKSGT	GVWLFAPSIT	LPIFTWGTNK	ANLDVAKLRQ
m729	ARAAFFPSIR	LTGSVDTHSA	ELGGLFKSGT	GVWLFAPSIT	LPIFTWGTNK	ANLDVAKLRQ
a729.pep	QAQIVAYEAA	VQSAFQDVAN	ALTAREQLDK	AYDALSKQSR	ASKEALRLVG	LRYKHGVSGA
m729	QAQIVAYEAA	VQSAFQDVAN	ALTAREQLDK	AYDALSKQSR	ASKEALRLVG	LRYKHGVSGA

1181

	430	440	450	460
a729.pep	LDLLDAERSSYSAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
m729	LDLLDAERSSYAAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX			
	430	440	450	460

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2469>:

g730.seq

1	GTGAAACCGC	TGCGCAGACT	GACAAACCTC	CTTGCCGCCT	GCGCCGTAGC
51	GGCGGTCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	GCGCAAGACC
101	CGTTCATTAC	CGATAACACC	CAACGGCAGC	ACTACGAACC	CGGCGGCAAA
151	TACCACCTCT	TCGGcgaCCC	GCGCGGCAGC	GTTTCCGACC	GCACCGGCAA
201	AATCAACGTC	ATCCAAGACT	ATACCCACCA	GATGGGCAAC	CTGCTCATCC
251	AACAGGCGGC	AATCCAAGGC	AATCTTGGTT	ACACCGTCCG	CTTTTCCGGA
301	CACGGACACG	AAGAACACGC	CCCCTTCGAC	AACCACGCCG	CCGACAGCGC
351	AAGCGAAGAA	AAAGGCAACG	TTGACGACGG	CTTTACCGTG	TACCGGCTCA
401	ACTGGGAAGG	ACACGAACAT	CATCCCGCCG	ATGCCTACGA	CGGCCCGAAG
451	GGCGGCAATT	ACCCCAAACC	TACGGGCGCA	CGAGACGAAT	ACACCTATCA
501	CGTCAACGGC	ACAGCCCGCA	GTATCAAAC	CAATCCGACC	GACACCCGCA
551	GCATCCGGCA	ACGCATATTC	GACAACTACA	ACAACCTCGG	CAGCAATTTT
601	TCCGACCGCG	CCGATGAAGC	CAACAGAAAA	ATGTTTCGAGC	ACAATGCCAA
651	GCTCGACCGC	TGGGGCAACA	GCATGGAGTT	TGTCAACGGC	GTGCGCGCCG
701	GCGCGCTCAA	CCCCTTTATC	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC
751	ATACTGTACG	GAACGCGCTA	TGCCATAGAC	AAAGCCGCGA	TGCGCAACAT
801	CGCCCCCTTA	CCCGCCGAGG	GCAAATTCGC	CGCCATCGGC	GGCTTGGGCA
851	GCGCGGCGGG	CTTTGAAAAA	AATACGCGCG	AAGCCGTTGA	CCGGTGGATA
901	CAGGAAACC	CCAATGCCGC	CGAAACCGTC	GAAGCCCTGG	TCAACGTCCT
951	GCCGTTTGCC	AAAGTCAAAA	ACCTGACAAA	GGCGGCAAAA	CCGGGGAAGG
1001	CTGCGGTTAG	TGGGGATTTT	TCTAAATCCT	ACACCTGCTC	CTTCCACGGC
1051	AGCACCTTGG	TCAAACGGC	AGACGGCTAC	AAAGCCATTG	CCCATATTCA
1101	AGCCGGAGAC	CGCGTCCTTT	CCAAGGACGA	GGCAAGCGGA	GAAACGGGAT
1151	ACAAACCCGT	TACCGCCCGA	TACGGCAATC	CGTATCAAGA	AACCGTTTAC
1201	ATTGAAGTTT	CAGACGCGAT	CGGCAACAGC	CAAACCTGA	TTTCCAACCG
1251	CATCCACCCG	TTTATTTCCG	ACGGCAAATG	GATTAAGCGG	GAAGATTTAA
1301	AAGCGGGAAG	CCGGCTGTTA	TCCGAAAGCG	GCAAAACCCA	AACCGTCCGC
1351	AACATCGTTG	TCAAACCAAA	ACCGCTCAAA	GCCTACAATC	TGACCGTTGC
1401	CGATTGGCAT	ACCTACTTCG	TCAAGGGTAA	TCAGGCGGAA	ACGGAAGGGG
1451	TTTGGGTTCA	TAATGATTGT	CCGCCTAAAC	CAAAACCAAC	CAATCATGCC
1501	CAACAAAGAA	AAGAAGAAGC	TAAAAACGAT	TCTCATCGAA	GTGTGGGAGA
1551	TTCCAATCGT	GTCGTTTCGC	AAGGAAAGCA	ATATTTAGAT	TCCGACACAG
1601	GAAACCATGT	TTATGTAAAA	GGAGATAAAG	TGGTTATTCT	AACTCCTGAT
1651	GGAAGACAGG	TAACCTCAAT	TAAGAAGTCG	AAAGCCAATA	CGTCAAAAAG
1701	GGTAAAAAAT	GGGAAATGGA	CACCAAAATA	A	

This corresponds to the amino acid sequence <SEQ ID 2470; ORF 730.ng>:

g730.pep

1	VKPLRLRLTNL	LAACAVAAVA	LIQPALAADL	AQDPFITDNT	QRQHYEPGGK
51	YHLFGDPRGS	VSDRTGKINV	IQDYTHQMGN	LLIQQAAIQG	NLGYTVRFSG
101	HGHEEHAPFD	NHAADSASEE	KGNVDDGFTV	YRLNWEGHEH	HPADAYDGPK
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIF	DNYNLGLSNF
201	SDRADEANRK	MFEHNAKLDR	WGNMSEFVNG	VAAGALNPFI	SAGEALGIGD
251	ILYGTRYAID	KAAMRNIAPL	PAEGKFAAIG	GLGSAAGFEK	NTREAVDRWI
301	QENPNAAETV	EALVNVLPFA	KVKNLTKAAK	PGKAAVSGDF	SKSYTCSFHG
351	STLVKTADGY	KAIAHIQAGD	RVLSKDEASG	ETGYKPV TAR	YGNPYQETVY
401	IEVSDGIGNS	QTLISNRIHP	FYS DGKWIKA	EDLKAGSRL	SES GKTQTVR
451	NIVVKPKPLK	AYNLTVADWH	TYFVKGNQAE	TEGVVWHNDC	PPKPKPTNHA
501	QQRKEEAKND	SHRSVGDSNR	VVREGKQYLD	SDTGNHVYVK	GDKVVILTPD
551	GRQVTQFKNS	KANTSKRVKN	GKWT PK*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2471>:

m730.seq

1	GTGAAACCGC	TGCGCAGACT	GACAAACCTC	CTTGCCGCCT	GCGCCGTAGC
51	GGCGGCCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	GCGCAAGACC

1182

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101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCCAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCGCGC ATGCCTACGA CGGCCCGAAG
451 GGCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCGCCG
701 GCGGCTCAA CCCCTTTATC AGCGCGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGTCT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTATTATA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAAAACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTAA

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This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
  1 VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
 51 YHFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEHGEH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYNLSNFI
201 SDRADANRK MFEHNAKLDR WGNSEFING VAAGALNFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPKNFLNQKN RKQIKATIEA ANQQGKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

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g730 / m730 93.0% identity in 344 aa overlap

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g730.pep      10      20      30      40      50      60
               VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHFLGDPGRGS
m730          10      20      30      40      50      60
               VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHFLGDPGRGS

g730.pep      70      80      90      100     110     120
               VSDRTGKINV IQDYTHQMGNLLIQQAIIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
m730          70      80      90      100     110     120
               VSDRTGKINV IQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE

g730.pep     130     140     150     160     170     180
               KGNVDDGFTVYRLNWEHGEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT
m730         130     140     150     160     170     180
               KGNVDEGFTVYRLNWEHGEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT

g730.pep     190     200     210     220     230     240
               DTRSIRQRIFDNYNNLGSNFSRDEANRKMFEHNAKLDRWGNSEFVNGVAAGALNPF
m730         190     200     210     220     230     240
               DTRSIRQRISDNYNLSNFSRDEANRKMFEHNAKLDRWGNSEFINGVAAGALNPF

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1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAAKPGKAAVSGDFSYSYCSFHGSTLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAKPGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVNTARYGNPYQETVYIEVSDGIGNSQTLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNFLNQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

```

a730.seq
1   GTGAAACCGC TGCGAAGACT CATCAAGCTC CTTGCCGCCT GTGCCGTAGC
51  GCGCGCCGCA CTCATACAGC CCGCCCTCGC GCGCGACTTG GCGCAAGACC
101 CGTTCATTAC CGATAACGCC CAACGCGAGC ACTACGAACC CGGAGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGAGC GTCTCCGACC GCACCGGTCA
201 AATCAACGTC ATCCAAGACT ATACCCACCG GATGGGCAAC CTGCTCATCC
251 AGCAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTTCGGGA
301 CACGGATACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GCGGGAATT ACCCCAAACC TACGGGTGCA CGCGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCACGCA GCATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTC
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAA AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAACC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GGCGGCAAAA CCGGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT TCTGCTGCAT ACAATACAAG AACAACTAGA
1051 AAAGTTACTA CAGAAACAGA GGGGTTAAAT AGAATCAGAC AGAACCAGAA
1101 AAATAGTAAT ATACATGAGA AAAATTATGG AAGAGATAAT CCTAATCATA
1151 TTAATGTTTT ATCTGGAAT TCTATACAAC ATATACTGTA TGGAGATGAA
1201 GCAGGAGGTG GGCATCTTTT TCCTGGCAAA CCTGGTAAGA CAACATTCCC
1251 CCAACATTGG TCAGCCAGTA AAATAACTCA TGAAATTAGT GATATCGTTA
1301 CATCCCCAAA AACGCAATGG TATGCACAGA CTGGAACAGG CGGCAATAT
1351 ATTGCTAAAG GAAGACCAGC TAGGTGGGTA TCATATGAAA CGAGAGATGG
1401 AATTCGTATC AGAACAGTTT ATGAACCTGC AACAGGAAAA GTGGTAACGT
1451 CATTCCCCGA TAGAACCTCT AATCCCAAT ATAACCCTGT AAAATAA

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This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

```

a730.pep
1   VKPLRLRIKL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
51  YHLEFGDPRGS VSDRTGQINV IQDYTHRMGN LLIQQANING TIGYHTRFSG
101 HGYEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIIS DNYSNLGNSF
201 SDRADEANRKL MFEHNAKLDR WGNMSEFING VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSAAGFEK NTREAVDRWI
301 QENPNAAETV EALVNVLPFA KVNLTAAK PGKAAVSGDF SAAYNTRTTR
351 KVTTETEGLN RIRQNQNSN IHEKNYGRDN PNHINVLSGN SIQHILYGDE
401 AGGGHLFPKG PGKTTFPQHW SASKITHEIS DIVTSPKTQW YAQTGTGGKY
451 IAKGRPARWV SYETRDGIRI RTVYEPATGK VVTAFFPDRTS NPKYNPVK*

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1184

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730.pep	VKPLRRLIKLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
m730	VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
a730.pep	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
a730.pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGKNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
a730.pep	DTRSIRQIRISDNYSNLGNSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGNSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
a730.pep	DTRSIRQIRISDNYSNLGNSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGNSNFSRDEANRKMFEHNAKLDRWNSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
a730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSAAYNTRTTRKVTETETGLN					
m730	QENPNAAETVEAVFNVAATAKAKLAKAAKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	360
a730.pep	QENPNAAETVEALVNVLPFAKVKNLTKAAKPGKAAVSGDFSAAYNTRTTRKVTETETGLN					
m730	QENPNAAETVEAVFNVAATAKAKLAKAAKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	360
a730.pep	RIRQNQKNSNIHEKNYGRDNPINHINVLSGNSIQHILYGDEAGGGHLFPGKPGKTTTFPQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410
a730.pep	RIRQNQKNSNIHEKNYGRDNPINHINVLSGNSIQHILYGDEAGGGHLFPGKPGKTTTFPQHW					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIDKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731.seq
1  gatttttcgag  cgttttcatG  CGAGAACGGT  TTGTCTGTGC  GCGTCCGCAA
51  TTTGGACGGC  GGCAAAATCG  CGTTGCGGCT  GGACGGCAGG  CGTGCCGTCC
101 TCTCTTCCGA  CGTTGCCGCA  TCCGGCGAAC  GCTATACCGC  CGAACACGGT
151 TTGTTCGGAA  ACGGAACCGA  GTGGCACCAG  AAAGGCGGCG  AAGCCTTTTT
201 CGGCTTTACC  GATGCCTACG  GCAATTCGGT  CGAAACTTCC  TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2476; ORF 731.ng>:

```

g731.pep
1  DFRAFSCENG  LSVRVRLDGR  RAVLSSDVAA  SGERYTAEHG
51  LFGNGTEWHQ  KGGEAFFGFT  DAYGNSVETS  CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731.seq
1  ATGAATATCA  GGTTTTTCGC  GCTGACCGTA  CCGGTTTTGT  CTTTGGCGGC
51  CTGTGCCGTG  CCGGAGGCGT  ATGATGACGG  CGGACGCGGG  CATATGCCGC
101 CCGTTCAAAA  CCAAGCCGGC  ACGGACGATT  TTCGGGCGTT  TTCCTGCGAG
151 AACGGTTTGT  CTGTGCGCGT  CCGCCATTTG  GACAGCGGCA  AAGTCGCGTT
201 GCGGCTGGAC  GGCAGGCGTG  CCGTCTCTC  TTCCGACGTT  GCCGCATCCG

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251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CACCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSC
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

g731/m731 95.2% identity in 84 aa overlap

				10	20	30
g731.pep				DFRAFSCENGLSVRVRNLDGGKIALRLDGR		
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHLDSGKVALRLDGR					
	20	30	40	50	60	70

	40	50	60	70	80
g731.pep	RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX				
m731	RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX				
	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq
 1 ATGAATATCA GGTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCGGC
 51 CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGAGGG CATATGCCGC
 101 CCGTTCAAAA CCAAGCCGCG ACGGCAGATT TTCGGGCATT TTCCTGCGAG
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG
 301 CATCAGAAAG GCGGCGAAGC CTTTTCGGC TTTACCGATG CCTACGGCAA
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSC
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR*

a731/m731 94.4% identity in 126 aa overlap

	10	20	30	40	50	60
a731.pep	MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRAFSCENGLSVHVRRL					
m731	MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCENGLSVRVRHL					
	10	20	30	40	50	60

	70	80	90	100	110	120
a731.pep	DGGRIALRLDGRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE					
	: :					
m731	DSGKVALRLDGRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE					
	70	80	90	100	110	120

a731.pep	TSCRARX
m731	TSCRARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq
 1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg
 101 ACGGgcgGGA TAACGAagtc CTGCCGGTGC AATCCATCCG TACGATGGCG

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151 GAGGTTTACG GTCAGATTAA GGCAAACCTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCTTGCCG AGTTGAAAAC GATTCCGATG ACGgtATTGG TcaaTTCCGG
951 TTCggcttCC GCGTCGGAGA TTGtgcCGG GCGATTGCAG GACCACAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTACGGC ACAGGGGATT GTTCCCAGATG
1151 TCgaaGTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GCGGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCttgcCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAACTCTT TGGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732 . pep

```

1 MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDGRDNEV LPVQSIRTMA
51 EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGFEGGLGME IGQEDGFVKV VSPIEDTPAE RAEVKSGDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YGMGGDPLAG
301 IPAELKTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFKGVSQVT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKKKD K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732 . seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACCTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GACTGAAAG
851 CCATTCTCTG AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCTTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 TCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CCGCACTGTA

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GGCGGATTGT
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAAGT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLAG
301 IPAEKLTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKDADKPA VKEGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

	10	20	30	40	50	60
m732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
	70					
m732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGAEIKESTSGEFGGLGMEIGQEDGFVKV					
	:					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130					
m732.pep	VSPIEDTPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIEDTPAERA EVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190					
m732.pep	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKNKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGIRVSQFQERTVESVNTAAKELVKNKGKPLKGLV					
	190	200	210	220	230	240
	250					
m732.pep	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAIPEDYVYGMGGDSLAG					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
	310					
m732.pep	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAEKLTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
g732	PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVS NKDKKKDKKKX					
g732	PVS NKDKKKDKKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGTGCA AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTGCG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACGCGCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGCG GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCTGCGG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCTTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT TATTTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCGCGA GCGGATTGTT
1201 GTCGACACA TCGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACCAAGT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

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This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EYVGQIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YGMGGDSLGA
301 IPAEIKTIPT TVLVNSGSAS ASEIVAGALQ DHKRAIVGT QSFKGSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVS NKDKKKDK KDKK*

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a732/m732 99.6% identity in 494 aa overlap

	10	20	30	40	50	60
a732.pep	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYGOIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLVPQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a732.pep	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a732.pep	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
	190	200	210	220	230	240
a732.pep	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
a732.pep	LDLRDDPGGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSL					
m732	LDLRDDPGGLLTGAVGVSA AFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGGDSL					
	250	260	270	280	290	300
	310	320	330	340	350	360
a732.pep	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
m732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFGKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
	370	380	390	400	410	420
a732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
a732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
a732.pep	PVSNDKDKDKDKKX					
m732	PVSNDKDKDKDKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq

```

1  ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT
51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG
101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGAAAAACGg cgACACTTCG
151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA
201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCATTG GGA CTGCTGC

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251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
 101 KRLFPESGVF MDFLMKTGKG GKR*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSL	YYYGGYPDTVYEGLKNDDTSLGKQTEKMEK				
g733	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGA	FRQFEEKRLFPESGVFMDFLMKTGKG				
g733	YFAEAANKKMNAAPGAHAHLGLLLSRSGDKEGA	FRQFEEKRLFPESGVFMDFLMKTGKG				
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACACTTCG
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA
 201 CAAAAAATG AATGCCGCCC CGGGTGCGCA CGCCCATCTG GGAAGTCTGC
 251 TTTCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG
 301 AAAAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

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```

1  MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS
51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE
101 KRLFPESGVF MDFLMKTGKG GKR*

```

a733/m733 100.0% identity in 123 aa overlap

```

              10      20      30      40      50      60
a733.pep      MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              |||||
m733          MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK
              10      20      30      40      50      60

              70      80      90      100     110     120
a733.pep      YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEKRLFPESGVFMDFLMKTGKG
              |||||
m733          YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEEKRLFPESGVFMDFLMKTGKG
              70      80      90      100     110     120

a733.pep      GKRX
              ||||
m733          GKRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

```

g734.seq
1  ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGA CTGCGGC
51  GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCGGCG
151 AAAAGCGAAG CGTTTGCCGA GTTGGAAGCC TTTTGCAAAG GTCAGGACAC
201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CATCTTCTTA TTACGGCGGG
451 GCTGTTCGCT CCTTAATCCA ACACCTGAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

```

g734.pep
1  MMKKILAVSA LCLMTAAAOA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA
51  KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA
101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYG AQQQCGLQTV YCTSSSYGG
151 AVRSLIQHLK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

```

m734.seq (partial)
1  TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTCTGCT
51  GAACAATACC TGTGTCGCGC TGGCATACCC GAAAGCCTTG GGCGCGCTGC
101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTTAC GAGCGTTCAT
151 CAGGTCGCAC TCAACCAGTG CATCAAAAAA TACGGCGTAC AGGGACAATG
201 CGGCTTGGAA ACAGTGTATT GCACATCTTC TTCTTATTAC GGCGGAACTG
251 TCGGCTCTTT GATTCAAAAT CTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

```

m734.pep (partial)
1  SGIAEDEPTG CRSVSVLNNT CVALAYPKAL GALRVDNAVV ITSPRFTSVH
51  QVALNQCIKK YGVQGCGLQ TVYCTSSSYG GGTVRSLIQN LK*

```

m734/g734 92.4% identity in 92 aa overlap

```

              10      20      30
m734.pep      SGIAEDEPTGCRSVVSLNNTCVALAYPKAL
              : |||||
g734          VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL

```


	40	50	60	70	80	90
m734.pep	GALRVDNAVVITSPRFTSVHQVALNQCICKYGVQGQCGLETVYCTSSSYYGGTVRS LIQN					
g734	GAMRVENAVVITSPRFTSVHQVALNQCICKYGAQGQCGLETVYCTSSSYYGGA VRSLIQH					
	100	110	120	130	140	150
m734.pep	LKK					
g734	LKK					
	160					

a734.seq

1	ATGATGAAAA	AGATACTGGC	CGTATCGGCA	CTATGCCTGA	TGACTGCGGC
51	GGCACGGGCT	GCCGATACTT	ACGGCTATCT	CGCCGTTTGG	CAGAATCCGC
101	AGAATGCAAA	CGATGTTTTG	CAGGTTAAAA	CCACAAAAGA	AGATTGCAGC
151	AAAAGCGAAG	CGTTTGCCGA	GTTGGAAGCT	TTCTGCAAAG	GTCAGGACAC
201	GCTTGCGGGC	ATTGCCGAAG	ACGAGCCGAC	CGGATGCCGG	TCGGTCGTGT
251	CGCTGAACAA	TACCTGTGTC	GCGCTGGCAT	ACCCGAAAGC	CTTGGGCGCG
301	ATGCGCGTTG	AAAACGCCGT	TGTGATTACT	TCTCCGCGTT	TTACGAGCGT
351	TTATCAGGTC	GCACTCAACC	AGTGCATCAA	AAAATACGGC	GCACAGGGAC
401	AATGCGGCTT	GAAACAGATG	TATTGCACGT	CTTCTTCTTA	TTACGGGGGA
451	ACTGTGCGCT	CTTTGATTCA	AAATCTCAA	TAA	

a734.pep

1	<u>MMKKILAVSA</u>	<u>LCLMTAAARA</u>	ADTYGYLAVW	QNPQNANDVL	QVKTTKEDST
51	KSEAFAELEA	FCKGQDTLAG	IAEDEPTGCR	SVVSLNNTCV	ALAYPKALGA
101	MRVENAVVIT	SPRFTSVYQV	ALNQCIKKYG	AQGQCGLETV	YCTSSSYGG
151	TVRSLIQNLK	*			

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
g734	MMKKILAVSALCLMTAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVLAYPKALGAMRVENAVVITSPRFTSVYQV					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQQV					
	70	80	90	100	110	120
	130	140	150	160		
a734.pep	ALNQCIKKYGAQGQCGLETVYCTSSSYGGTVRSLIQNLIKX					
g734	ALNQCIKKYGAQGQCGLETVYCTSSSYGGAVRSLIQHLLKX					
	130	140	150	160		

m735.seq		g1		g2	
1	ATGAATCTCG	TGAAACTGCT	GGCGAATAAC	TGGCAACCGA	TTGCCATTAT
51	CGCGCTTGTC	GGCACGGGCT	TGGCTGTGTC	GCACCATCAA	GGCTACAAGT
101	CGGCATTGTC	GAAGCAGCAG	GGCGTCTATC	ACAAGATGGA	GCGCGACAAG
151	GCGCAAGCCC	TGCTGTTGTC	GGCTCAA AAC	TATGCGCGCG	AACTGGA ACT
201	GGCAGCGCGC	GAAGCTAAAA	AATATGAAGT	CAAGGCGCAC	GCTGTCGGGA
251	TGGCTTTGGC	GAAGAAAAAC	CGCGGAAGTC	GCCGCTGTAA	AACGGAAAAA
301	AAAAAGGAAA	TCGAAAATGT	CCTTACTCAA	GACCGTAAAA	ATGCAAGCGG

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351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG
 401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
 51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
 101 KKEIENVLTQ DRKNASGGCI DGFGSHGLQL YNRALGYGN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT
 51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
 101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
 151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
 201 GCGCGGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA
 251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAT
 301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
 351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG
 401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
 51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
 101 KKEIENVLTQ DRKNAGGGCI DGFGHHGLQL YKRALGYGN*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARAEAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAHAVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFGHHGLQLYKRALGYGNX					
m735	DGFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
 51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGCGG AAATCCGGCA
 101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
 151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTCG TCGGTATGGT
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGCGCGAACT GGGTCCCGTG
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
 401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GGCGGGCGTG
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
 551 GGCCGCAGAT GCAGAACAAAC ATTACGATAC ATTACGATGT AATCAACGGT

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```

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

```

1 MNFIRSVGAK TLGLIQSFGS ITLFLNLA KSGTAFARPR LSVRQVYFAG
51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMNN ITIHYDVI
201 LIKSAAFGVA VTLIAVHQGF HCIPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

```

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51 CTTCGGCAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA
101 CGGCTTTCGC CCGTCCGCGC CTGAGCGTGC GCCAAGTGT TTTTGCCGGC
151 GTGCTGTCGG TGCTGATTGT TGCCGTTTCG GGGCTGTTTC TCGGTATGGT
201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGAACT GGGTCCCGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCGGTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG
401 CGGTCAACCC CGTCGCCCGC GTGGTTGCCC CGCGTTTTTG GCGGGCGTG
451 TTTTCTATGC CGCTTTTGGC TTCGATTTTC AACGTCGCGG GCATTTTCGG
501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT
551 GGCCGCAGAT GCAGACAAC ATTACGATAC ATTACGATGT AATCAACGGT
601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGCGGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

```

1 MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMAVNPVAR VVAPRFWAGV
151 FSMPLLASIF NVAGIFGAYL VGVSWLGLDS GIFWSQMNN ITIHYDVI
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNLA KSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
g736	MKTGQLEAMNVMAVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVSS					
g736	GIFWPQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHC IPTSEGILRASTRTVSS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

1	ATGAATTTTA	TCCGTTCCGT	CGGGGCGAAA	ACCCTCGGCC	TTATTCAATC
51	TCTCGGCAGT	ATCACGCTGT	TTCTGCTGAA	TATTCTGGCG	AAATCCGGTA
101	CGGCTTTCGT	CCGTCCGCGC	CTGAGCGTGC	GCCAAGTGTA	TTTTGCCGGC
151	GTGCTGTCGG	TGTTGATTGT	TGCCGTTTCA	GGGCTGTTG	TCGGCATGGT
201	CTTGGGTTTG	CAGGGCTATA	CGCAGTTGTC	GAAATTCAAA	TCCGCCGATA
251	TTTTGGGCTA	TATGGTCGCG	GCTTCGCTGT	TGCGCGAACT	GGGTCCGGTG
301	TTGGCGGCGA	TTCTGTTTGC	CAGCAGCGCG	GGCGGTGCGA	TGACCAGCGA
351	AATCGGTTTG	ATGAAAACGA	CCGAACAGCT	CGAAGCGATG	AACGTGATGG
401	CGGTAAACCC	CGTCGCCCGA	GTGGTTGCGC	CGCGCTTTTG	GGCGGGCGTG
451	TTTTCCATGC	CGCTTTTGGC	TTTCGATTTT	AACGTGGCGG	GTATTTTTCGG
501	CGCGTATTTG	GTCCGGTGTA	CCTGGCTGGG	CTTGGACAGC	GGTATTTTCT
551	GGTCGCAAAT	GCAGAACAA	ATCACGATAC	ATTACGATGT	AATCAACGGT
601	CTGATCAAAT	CCGCCGCGTT	CGGCGTGGCG	GTAACGCTGA	TTGCCGTGCA
651	TCAGGGCTTC	CACTGCGTCC	CGACCTCGGA	AGGCATTTTG	CGCGCCAGCA
701	CGCGCACGGT	GGTTTCGTCC	GCCCTGACGA	TTTTGGCGGT	CGATTTTATA
751	TTGACCGCGT	GGATGTTTAC	AGATTGA		

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

1	MNFIRSVGAK	TLGLIQSLGS	ITLFLNILA	KSGTAFVRPR	LSVRQVYFAG
51	VLSVLIVAVS	GLFVGMVLGL	QGYTQLSKFK	SADILGYMVA	ASLLRELGPV
101	LAAILFASSA	GGAMTSEIGL	MKTTEQLEAM	NVMAVNPVAR	VVAPRWFAGV
151	FSMPLLASIF	NVAGIFGAYL	VGVTWLGLDS	GIFWSQMNN	ITIHVDVING
201	LIKSAAFGVA	VTIAVHQGF	HCVPTSEGIL	RASTRTVSS	ALTILAVDFI
251	LTAWMFTD*				

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNVMAVNPVARVAPRWFAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
m736	MKTTEQLEAMNVMAVNPVARVAPRWFAGVFSMPLLASIFNVAGIFGAYLVGVTWLGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHVDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVSS					

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```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVTVSS
           190      200      210      220      230      240

           250      259
a736.pep   ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

g737.seq

```

1   atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

g737.pep

```

1   MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

m737.seq..

```

1   ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

m737.pep

```

1   MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep   MNIKHLLLTSAAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQAEKAALAR
           |||||
g737       MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHGKQDKIISRQAEKAAWAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep   VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||
g737       VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

a737.seq
 1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
 51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
 101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
 151 GCCCAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCGA
 201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
 251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
 301 GTGATTTCCT CCCGCCGCGA CGACTGA

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep
 1 MNFKRLLLTAAATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
 51 AQAEEAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
 101 VISSRRDD*

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTAAATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR	AQAEEAALAR	
m737	MNIKHLTSAATALLSIS	PALAHHDGHG	DDDHGHAHQ	HNKQDKIISR	AQAEEAALAR	
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDLEHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
m737	VGGKITDIDLEHDNGRPHYD	VEIVKNGQEY	KVVVDARTGR	VISSRRDDX	
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq
 1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACCTGCC
 51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
 101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCG
 151 GCGGCCGCGC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
 201 TGATGTCAA ATCCCCGCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
 251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTTATCC CGGAATGAAC
 301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
 351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCATcgtT ACCCTGTTTG
 401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
 451 CAGTTTGCGG GCTGGGAAAA CACCCCTCTG CTCAAAACA TCATCGTTCA
 501 CAGAGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
 551 ACTACCTCAT GTGGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA
 601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
 651 TTTAGGTTTG GTCAATTCTG GCACCATCTT GACCTACATA GCCGCCATCG
 701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
 751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
 801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAACTG
 851 CCGTCGAACG CTCGCGCAAC GCGGTTTTCA CAGACTTGCC GCGCCAAAGC
 901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
 951 CGGCTGGAAC AGTTTTGCCC AACAAACCTT CCTGATCAAT GCCGAACAGC
 1001 ACACCATA CAACAACCTT CTCAGCACCT TGTTACCCCA TTCCACAAC
 1051 ATCATCTCTC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
 1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
 1151 CCCCCGCATC ACTTTTCTCT CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
 1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTCTCG
 1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
 1301 AAAAAGCCCG CAATCTCGGC ATACTGACCG CCTCGCCGC CATATTCGCA
 1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
 1401 CCCCCCGCT GACGACAGTG CAAAACCTT CAACCGGAAA ATCAACGAAC
 1451 TGCGCTATAT TTCCGCAAC AGCCCGATGC TGTCTTTTA TGCCGACTTC
 1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
 1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCCTAC TCCGCCACCT

1198

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1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAAACA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pep

```

1 MSAETTVSGA RPAAKLPIYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLFL TAGKKLFDVK IPAISFLLEA MAAFWWLOAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KIPAAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFQ SAPIFGHGW N SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
351 IILQLLAEMG ISGTLLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAEASDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWTYT RLVNSFSPA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAE EA TLKALKYRPY SATYRIALYL MRQKVAEAK
551 QWMRATQSY Y PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAACCTGCG
51 GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCCGCC
151 GCAGCCGGCC TGATTGTCTT GTTGTTCTCT ACGGCAGGAA AAAAAGTGT
201 TGATGTCAA ATCCCGCCA TCAGCTTCCT TCTGTTTGCA ATGGCGCGCT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTCAGCG CGTGGGCTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
501 CAGCGGGCAA GCGCTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCATA CTCGCCCGCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCTCATCCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGCGCG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCACCCA TTCCACAAC
1051 ATCGTCTCTC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTCGCA
1351 GGATGCTGCT ACTTGGAAGT GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pep

```

1 MPAETTVSGA HPAAKLPIYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

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1199

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51  AAGLIVLLFL TAGKKLFDVK IPAISFLLFA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNIYDNL LSNLFTSHSN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAESDG IAFKKAANLG ILTASAAIFA
451 GLLHLDWTYT RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

	10	20	30	40	50	60
m738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTVSGARPAAKLPIYILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m738.pep	TAGKKLFDVKIPAISFLLFAMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIPAISFLLFAMAAFWWLQARLMNLIYPGMNDIASWVFILLAVSAWACKSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m738.pep	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m738.pep	NLGHYLMWGILAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWGILASAYLNGQRKIPAAALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
	250	260	270	280	290	300
m738.pep	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRRTMLGIAAAVFLTALFQFSMNAILETFTGIRYETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m738.pep	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHNIYDNL LSNLFTSHSNIVLQLLAEMG					
g738	EWNKALAAFQSAPIFGHGWN SFAQQTFLINAEQHTIHDN FLSTLFTSHSNII LQLLAEMG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m738.pep	ISGTLVAATLLTGIAGLLK RPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	ISGTLVAATLLTGIAGLLK RSLTPASLFLCALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
	430	440	450	460	470	480
m738.pep	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDW TYTRLVNAFSPATDDSAKTLNRK					
g738	FLSPAESDGI AFKKAANLGILTASAAIFAGLLHLDW TYTRLVNSFSPAADDDSAKTLNRK					

1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEETLKSLKYRPHSATYRIALYL					
g738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEETLKALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738.seq
1  ATGCCCCTG AAACGACCGT ATCCGGCGCG CACCCCGCCG CCAAAC TGCC
51  GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCCGACT TTTACCACGA TGCCGCGCCG
151 GCAGCCGGCC TGATTGTCCT GTTGTTCTCT ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTACTC GCCGTCAGCG CGTGGGCTTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGG CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CCGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTACCCA TTCCACAAC
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCTTCCG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCC GCCACT GACGACAGTG CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTCTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCTATTAC CCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738.pep
1  MPAETTVSGA HPAAKLP IYI LPCFLWIGIV PFTFALRLQP SPDFYHDA
51  AAGLIVLLFL TAGKKLFDVK IPPISELLFA MAAFYWLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TLFAWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

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1201

201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
 251 TILGIAAAVF LTALFQFSMN TILETFTGIR YETAVERVAN GGFTDLPRQI
 301 EWRKALAAAFQ SAPIFGHGWN SFAQQTFLIN AEQHNHNDNL LSNLFTSHSN
 351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
 401 SMLEYPLWYV YFLIPFGLML FLSPAESDGI AFKKAANLG ILTASAAIFA
 451 GLLHLDWYTY RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
 501 SLVNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
 601 KPCK*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALRLQSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPIYILPCFLWIGIVPFTFALKLKPSDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
a738.pep	70	80	90	100	110	120
	TAGKKLFDVKIPPISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
m738	TAGKKLFDVKIPAISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
a738.pep	130	140	150	160	170	180
	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
m738	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
a738.pep	190	200	210	220	230	240
	NLGHYLMWGILAAAYLNGQRKIPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
m738	NLGHYLMWGILAAAYLNGQRKIPALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
a738.pep	250	260	270	280	290	300
	YFRSDKSNRRRTILGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
m738	YFRSDKSNRRRTMLGIAAAVFLTALFQFSMNTILETFTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
a738.pep	310	320	330	340	350	360
	EWRKALAAAFQSAPIFGHGWN SFAQQTFLINAEQHNHNDNL LSNLFTSHSNIVLQLLAEMG					
m738	EWNKALAAAFQSAPIFGHGWN SFAQQTFLINAEQHNIDNL LSNLFTSHSNIVLQLLAEMG					
	310	320	330	340	350	360
a738.pep	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
m738	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
a738.pep	430	440	450	460	470	480
	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRMVNAFSPAT DDSAKTLNRK					
m738	FLSPAESDGI AFKKAANLG ILTASAAIFAGLLHLDWYTYRLVNAFSPAT DDSAKTLNRK					
	430	440	450	460	470	480
a738.pep	490	500	510	520	530	540
	INELRYISAN SPMLSFYADFSLVNFALPEYPETQTWAEATL KSLKYRPH SATYRIALYL					
m738	INELRYISAN SPMLSFYADFSLVNFALPEYPETQTWAEATL KSLKYRPH SATYRIALYL					
	490	500	510	520	530	540

1202

	550	560	570	580	590	600
a738.pep	MRQ GKVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
m738	MRQ GKVAEAKQWMRATQSYYPYLMPRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600
a738.pep	KPCKX					
m738	KPCKX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739.seq

```

1  ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCTT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCTTGCCG CACCCAAGAA AAACCGGGTC AAACCGCGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAACA
551 CGCCGGCCAA ACCCCATAAA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDAARA ADSLTGTGTQ AENTLKETPV LPTNAPHPEP
151 RKETPEKQAA PKETPKKET PKENHTKPD TPKNTPAKPHK EILDNLFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739.seq

```

1  ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG AAAAAACCTT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCTTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCGCAG CCCAAAGAAA CGCCCAAGA
501 AAACCATACC AAACCGGACA CCGCGAAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739.pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDDAGTQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAA PKETPKENHT KPDTPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALVSTFNPNGDKTLQAE PQHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALVSTFNPNGDKTLQTE PQHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSGLPSAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTQAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHKEILDKLF					
g739	PKNTPAKPKHKEILDNLFX					
	180	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

```

a739.seq
1  ATGGCAAAAA AACC GAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCTCCTCAT
251 CCGCACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAGCACAA GCTGAAAACA
401 CACTCAAAGA AACC CCGTA CTGCCACAA ACGTCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAAA ACAGGCACAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGCCTAA ACCCCATAAA GAAATTCTCG ACAACCTCTT CTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

```

a739.pep
1  MAKKPNKPFRLTPKLLIRAVLLICITAIGA LAIGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPNGVVG QDAAQPEHHH ASSSAPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQADTAQT DRQPDDAGAQ AENTLKETPV LPTNVPRPEP
151 RKETPEKQAQ PKETPKEKET PKENHTKPD PKNTPPKPKH EILDNLFX*

a739/m739 93.9% identity in 197 aa overlap

a739.pep
10 20 30 40 50 60
MAKKPNKPFRLTPKLLIRAVLLICITAIGALVSTFNPNGDKTLQTEPQHTDSPRET
|||||:|||||:|||||:|||||:|||||:|||||
m739
MAKKPNKPFRLTPKLLIRAVLLICIAAIGALVSTFNPNGDKTLQAE PQHTDSPRET
10 20 30 40 50 60

a739.pep
70 80 90 100 110 120
EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT
|||||:|||||:|||||:|||||:|||||:|||||
m739
EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDESGSGLPSAAPKKNRVKQPADTAQT
70 80 90 100 110 120

a739.pep
130 140 150 160 170 180
DRQPDDAGAQAE NTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD
|||||:|||||:|||||:|||||:|||||:|||||
m739
DRQPDDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD
130 140 150 160 170
  
```

1204

```

              190
a739.pep      PKNTPPKPHKEILDNLFX
              |||||
m739          PKNTPPKPHKEILDKLF
              180   190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

g740.seq

```

1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTTC CCGCCAATcc gccCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATTT
201 GAAACgtcaa ACCATGTTTC TGTATTATCC GATTGTTTGG CTGGTTGTGT
251 ATTTGTTCCA CTATTTCGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

g740.pep

```

1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPQHILINGII LACEATFLFK
51 FVLFETIKHH LKQGFDLKRQ TMFLFIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

m740.seq

```

1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCGTT
51 GGCGACGCTT GCCGTTTTTC CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

m740.pep

```

1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

              10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK FVLFDTIKHH
              |||||
g740          MSRNLLVRWLA VCLIPLATL AVFAANPPED KPQHILINGII LACEATFLFK FVLFETIKHH
              10      20      30      40      50      60

              70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*
              |||
g740          LKQGFDLKRQ TMFLFIPIVL LVVYLFHYFG AF*
              70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

a740.seq

```

1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCGACGCTT GCCGTTTTTC CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATTT
201 GAAACGTCAA ACTATGTTGC TGTATTATCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

a740.pep

```

1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPQHILINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

              10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVLVCLIPLATLAVFAANPPEDKPKQHLINGIILACEATFLFKFVLFDTIKHH
|||||:|||||
m740      MSRNLLVRWLAVCLIPLATLAVFAANPPEDKQHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep  LKQEFDLKRQTMLLFIPILLIVLYLFHYFGAFX
|||||
m740      LKQEFDLKRQTMLLFIPILLIVLYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1   GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTC GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAACCG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGCGGGCA
251 AAGACAACAG CCTCAACACG GGCAAACCTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAATCAAC AACCCTGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTGGGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGGCAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAACTG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCTCCGCC GAACTCAAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACCTACCG CCTCGCCCTT
751 TTCGGCGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1   VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTLTL SAQGAETFK AGGKDNSLNT GKLKNDKISR
101 FDFVQKIEVD GQTITLASGE FQIYKQDHS VVALRIEKIN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAKQ
201 GHGKIEHLKT PEQVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1   GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCCGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTGAGG AAAACGAGA AACTGAAGCT
201 GCGGCACAA GGTGCGGAAA AAATTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CCTTAACCGC CTTTCAGACC GAGCAAATAC
401 AAGATTCGGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCA AGCAGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCCGATAT
651 CAAGCCGGAT GGAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1   VNRTAFCCLS LTTALILTAC SSGGGGVAAD IGAGLADALT AFLDHKDKGL
51  QSLTLDQSVR KNEKLKLAAG GAEKTYGNND SLNTGKLKND KVSRLFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFTQ EQIQDSEHSK KMLAKRQFRI

```

1206

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLTYTID FAAKQNGNKI
 201 EHLKSPELNV DLAAADIKPD GKRHAVISGS VLYNQAEKGS YSLGIFGGKA
 251 QEVAGSAEVK TVNGIRHIGL AAKQ*

m741/g741 61.4% identity in 280 aa overlap

	10	20	30	40	50
m741.pep	VNRTAFCCLSLT	---ALILTACSSGGGGVAAD	IGAGLADALTAPLDHKDKGLQ	SLTLDO	
g741	VNRTTFCCLSLT	AGPDSRLQRRGGGGVAAD	IGTGLADALTAPLDHKDKGLK	SLTLEA	
	10	20	30	40	50
	60	70	80	90	100
m741.pep	SVRKNEKLKLA	AQGAEKTY---GNGDSLNTG	KLKNDKVS	RFD	FIRQIEVDGQLITLES
g741	SIPQNGTLT	LSAQGAEKTFKAGGKDNS	LTGKLKNDKIS	RFD	VFQKIEVDGQTITLAS
	70	80	90	100	110
	120	130	140	150	160
m741.pep	FQVYKQSHS	ALTAFQTEQIQDSEHSG	KMVAKRQFRIG	DIAGEHTSF	DKLPEGGRATYRG
g741	FQIYKQDHS	AVVALRIEINNPDKID	SLINQRSFLVSD	LGGEHTAFNQL	PDG-KAEYHGK
	130	140	150	160	170
	180	190	200	210	220
m741.pep	AFGSDDAGG	KLTYTIDFAAKQNGNKIE	HLKSPELNVDL	AAADIKPDGKR	HAVISGSVLYN
g741	AFSSDDADG	KLTYTIDFAAKQGHGKIE	HLKTPEQNV	ELASAEKAD	ESHAVILGDT
	180	190	200	210	220
	240	250	260	270	
m741.pep	QAEKGSYSL	GIFGGKAQEVAGSAE	VKTVNGIRHIG	LAAKQX	
g741	GEEKGTYR	LALFGDRAQE	IAGSATVKIG	KEKVHEIGI	ADKQX
	240	250	260	270	280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2537>:

a741.seq
 1 GTGAACCGAA CTGCCTTCTG CTGCCTTTCT TTGACCGCCG CCCTGATTCT
 51 GACCGCCTGC AGCAGCGGAG GCGGCGGTGT CGCCGCGGAC ATCGGCGCGG
 101 TGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAAGTTTG
 151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAACGAGA AACTGAAGCT
 201 GCGGCGACAA GGTGCGGAAA AAACCTATGG AAACGCGGAC AGCCTCAATA
 251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAA
 301 ATCGAAGTGG ACGGGCAGCT CATTACCTTG GAGAGCGGAG AGTTCCAAGT
 351 GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC
 401 AAGATTCGGA GCATTCAGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
 451 GGCGATATAG CGGGTGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
 501 CAGGGCGACA TATCGCGGGA CGGCATTCGG TTCAGACGAT GCCAGTGGAA
 551 AACTGACCTA CACCATAGAT TTCGCGGCCA AGCAGGGACA CGGCAAAATC
 601 GAACATTTGA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT
 651 CAAGCCGGAT AAAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
 701 ACCAAGCCGA GAAAGGCAGT TACTCTTAG GCATCTTTGG CGGGCAAGCC
 751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAACG GCATACGCCA
 801 TATCGGTCTT GCCGCCAAGC AGTAA

This corresponds to the amino acid sequence <SEQ ID 2538; ORF 741.a>:

a741.pep
 1 VNRTAFCCLS LTAALILTAC SSGGGGVAAD IGAVLADALT APLDHKDKSL
 51 QSLTLDQSVR KNEKLKLAQ GAEKTYGNGD SLNTGKLKND KVS

a741/m741 95.6% identity in 274 aa overlap

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQGAEKTYGNGDSLNTGKLNKDKVSRFDFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPPEGGRATYRGTAFGSD					
m741	SHSALTAFQTEQIQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPPEGGRATYRGTAFGSD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAKQGHGKIEHLKSPELNVDLAASDIKPKDKRHAIVISGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAKQGNKGKIEHLKSPELNVDLAAADIKPDGKRHAIVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQKX					
m741	YSLGIFGGKAQEVAGSAEVKTVNGIRHIGLAQKX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

```

m742.seq
1   ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCGACAGCA GTGTGCTTAC
51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCGTGAT TTTTCGGGCA
101 TTATTTTGCC CTGTGAAAAT CAGAAACTG CCCCCTTCAG TTCAACGCCT
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTAAGTGCCG ACAAATACAA CCTTTTCTCA GGATTCAAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAATATGC
351 GGCGGGTTTG TCGGGTGAGG ATGCGGTAGG CTTTTTGACT GAAAAAACG
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGATG AAACGCGCAA GGAATACCGG GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA ACAGTATCGC AGCCGCCGTG
551 CCGCAGAACG CAAAGCCGGT TTTGACAAGT GTATGAGTGA CCCTTTCGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGCG TTGATGCCGA
651 CAAGGCGGAA TTTGTGCGTA AAGCCCTTGC GAAGGAGGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCT AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTCGGGCGG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGGTGATGAA
901 AAGATACGTT CGGAATATCT AGAAATCTAC GAACGCCGCT ACAGAGTACG
951 TCCGAATACG GGGGCAACGC ACGCGGTGTA TGCGGGAAGT TGTCAAGAGG
1001 AGCCGGACGG CGATTGTCTG TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAC GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACACCGGTA
1201 TATGTCGATG TATATGAGCT GGACGAAAAA GGCAACAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCCCT CTTTACCCTG TTTTCCGGT ACGGTGCCGG
1301 TTTGGAAAAA CGTCAAAGTG GCAGACGACC ATGTTCCCTG CTTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAACC CATTTCCTGA CTGCCAGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCACCT TTTGGGCGGG CTGCACTACA

```


1208

```

1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTGCTCG ATTTCCGCTA TGTTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATTCCA GTGCAGACCC GTACAACTTC AGCAATTTC
2051 CACCCGTGCA CATATTCCGT TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAACAA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
  1  MVGIAEADA GDSSVLTLGG MYQKSREVPD FSGIILPCEN QKTAPFSSTP
 51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNDGW QLNAEVSYTK
101  NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEKLKA
151  YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSDPFA
201  LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAAQRFN NSLYDSSFNR
251  KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FFGVYAYGDE
301  KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEP DGDLS SPLVRGHKEP
351  DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401  YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKT VKV ADDHVPALYN
451  YAKYLNNTKT HSLTASTRFN VTGRHLHLLG LHYTRYETSQ TKDMPVRYGQ
501  PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551  FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRNLNASF ALFYLEQKNR
601  TVVDFGYVPG AGGKQGSFQT VAKPIGKVVV RGAEFELSGE LNEDWKVFAG
651  YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHIPNT
701  GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751  GRTYFENNYN RTRGANNFYG EPRTVSMKLD WQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
  1  ATGGTTTACG GCATTGCCGA AGCCGATGCG GGCGACAGCA GTGTGCTTAC
 51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101  TTATTTTGTC CTGTGAAAAT CAGAAAACCTG CCCCCTTCAG TTCAACGCCCT
151  GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201  TTGGTCGCGG TTGAGTGCTG ACAAATACAA CCTTTTCTCA GGTTTCAAAC
251  ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAAGTGTC TTATACCAAG
301  AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAAA ACGAACATGC
351  GGCGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAACG
401  AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451  TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501  TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTC
551  CCGCAGAACG CAAAGCCGGT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601  CTGGACTTTA TCTGTCAAGG TTCTTGCGGG GATCCGGGTG TTGATGCCGA
651  CAAGTCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701  ATGCGGCACA ACGTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751  AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTTGC GGCATACCAA
801  AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851  TGTTCGGGCG GGAGCATGAT TTCTTTGTCT GCTATGCCTA CGGCGATGAA
901  AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951  TCCGAATACA GGGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAGGGGG
1001 AGCCGGACGG TGATTTGTCT TCTCCTTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAAACCGA GCCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

```

a742.pep

1	MVYGIAEADA	GDSSVLTGG	MYQKSREVPD	FSGIILSCEN	QKTPAFSSPT
51	ACNRPLQLPR	NTYLGEDWSR	LSADKYNLFS	GFKHVFDPNGW	QLNAEVSYTK
101	NESDAKVGQF	FLKNEHAAAGL	SDEDAVGFLT	EKNEVIFPEF	KDKALEKLKA
151	YRDETAKEYR	ERKDDFVKNR	FDNTAFEQYR	SRRAERKAG	FDECMSAPFA
201	LDFICQGSWG	DPGVDADKSE	FVDKALAKEG	IFNNAAQRFP	NSLYDSSFN
251	KATANRRYS	MPLRHRTKDDR	QWGIKDLDTG	TYGLFGREHD	FFVGYAYGDE
301	KIRSEYLEIY	ERRHRVREPN	GATHGVYAGS	CQGEPDGDL	SPLVRGHKEP
351	DWQAYDEKGN	RTVYAEECRN	AKKIKTEPKL	DAEGKQVYYY	DEYSGSRTPV
401	YVDVYELDEK	GNKIQETNPD	GTPAFTGFSG	TVPVWKTVMK	ADHHPALYN
451	YAKYLTNTNK	HSLTAGTRFN	VTGRLHLLGG	LHYTRYETSP	TKDMPVRYQG
501	PASDFQNTASS	IKADQDHYTA	KMQGHKLTPY	AGITYDLTPQ	QSIYGSYTKI
551	EKQQDNVDVS	AKTVLPPLVG	TNYEYWGKGA	FLQGRNLASF	ALFYLEQKNR
601	TVVDFGYVPG	AGGKQGSFQT	VAKPIGKVVS	RGAEFELSGE	LNEDWKVFAG
651	YTYNKSRYKN	AAEVNAERLA	KNTGADPYNF	SNFTPVHIFR	FGTSEHIPNT
701	GLTVGGGVSNA	QSGTSSSLYN	RQGGYGLIDG	FVRYELGKHA	KLSLIGTNLN
751	GRTYFENNYN	RTRGANNFYG	EPRTVSMKLD	WOF*	

	10	20	30	40	50	60
a742.pep	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILSCENQKTAPFSSTPACNRPLQLPR					
m742	MVYGIAEADAGDSSVLTGGMYQKSREVPDFSGIILPCENQKTAPFSSTPACNRPLQLPR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a742.pep	NTYLGEDWSRLSADKYNLFSGFKHVFNDNGWQLNAEVSYTKNESDAKVGQFFLKNEHAAGL					
m742	NTYLGEDWSRLSADKYNLFSGFKHVFNDNGWQLNAEVSYTKNESDAKVGQFFLKNEYAAGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a742.pep	SDEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
m742	SGEDAVGFLTEKNEVIPFEPKDKALEKLKAYRDETAKEYRERKDDFVKNRFDNTAFEQYR					
	130	140	150	160	170	180
	190	200	210	220	230	240
a742.pep	SRRAAERKAGFDECMSPFALDFICOGSWGDPGVDDADKSEFVDKALAKEGIFENNAAORF					

m742	SRRAAERKAGFDKCMSDFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAAQRFP	190	200	210	220	230	240
a742.pep	NSLYDSSFNRKATANRRYSYMPLRHTKDDRQWGIKLDLTGTYGLFGREHDFVGYAYGDE	250	260	270	280	290	300
m742	NSLYDSSFNRKATANRRYSYMPLRHTKDDRQWGIKLDLTGTYGLFGREHDFVGYAYGDE	250	260	270	280	290	300
a742.pep	KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEPPDGLSSPLVRGHKEPDWQAYDEKGN	310	320	330	340	350	360
m742	KIRSEYLEIYERRYVRPNTGATHGVYAGSCQGEPPDGLSSPLVRGHKEPDWQAYDEKGN	310	320	330	340	350	360
a742.pep	RTVYAEECRNAAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD	370	380	390	400	410	420
m742	RTVYAEECRNAAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD	370	380	390	400	410	420
a742.pep	GTPAFTGFSGTVPVWKTVKVADDDHVPALYNYAKYLNTNKTSLTAGTRFNVTRGLHLLGG	430	440	450	460	470	480
m742	GTPAFTGFSGTVPVWKTVKVADDDHVPALYNYAKYLNTNKTSLTAGTRFNVTRGLHLLGG	430	440	450	460	470	480
a742.pep	LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTTPYAGITYDLTPQ	490	500	510	520	530	540
m742	LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTTPYAGITYDLTPQ	490	500	510	520	530	540
a742.pep	QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFQGRNLNASFALFYLEQKNR	550	560	570	580	590	600
m742	QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFQGRNLNASFALFYLEQKNR	550	560	570	580	590	600
a742.pep	TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN	610	620	630	640	650	660
m742	TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN	610	620	630	640	650	660
a742.pep	AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPTGLTVGGGVSAQSGTSSLYNI	670	680	690	700	710	720
m742	AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSFHIPTGLTVGGGVSAQSGTSSLYNI	670	680	690	700	710	720
a742.pep	RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD	730	740	750	760	770	780
m742	RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD	730	740	750	760	770	780
a742.pep	WQFX						
m742	WQFX						

a742/ p25184
sp|P25184|PUPA_PSEPU FERRIC-PSEUDOBACTIN 358 RECEPTOR PRECURSOR
>gi|94923|pir||S15169

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi|45723 (X56605)
 pseudobactin uptake protein [*Pseudomonas putida*]Length = 819
 Score = 152 bits (381), Expect = 6e-36
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADDDHV-PALYNYAKYLTNTKTHSLTAGTRFNVGTGRLLHLLGGLHYTRYETSQTKDM 494
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y
 Sbjct: 511 QTPKPGDDEIIPGI----QYNISNRQSGYFVASRFNLTDLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTPYAGITYDLTPQQSIYGSYTKIFKQQ 554
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q
 Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKPQ 609

Query: 555 DNVDVSAKTVLPPLVGTNYEVGWKGAFLOGRNLNASFALFYLEQKNRTVVDFGYVPGAGGK 614
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG
 Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGFELEGRLNANIALYMKRDNLAESTNEVVPDSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674
 S + + ++G + ELSGE+ W VF GY++ ++
 Sbjct: 669 IAS-----RAVDGAETKGVDELSEVLPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +
 Sbjct: 708 ADGKRLTPQLPMDTFREWNTYRLPGWEKLTLLGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783
 RY + + +L N+ + Y Y G+ YG PR ++ L + F
 Sbjct: 768 TSLMARYRINESLAATLNVNNIFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq
 1 ATGAATCAAA ATCATTTTTTC ACTTAAAAATT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
 151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
 351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
 401 TGACCGTCAA TGTTCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
 451 TCTCCGAGTA CCGATTGGC GGTATTGAC CATATTGAAG TTGTACGGGG
 501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
 551 TGATCCGTAA GTGA

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep
 1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSRLD DKAHVHLEEA
 101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
 151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq
 1 ATGAATCAAA ATCATTTTTTC ACTTAAAAATT CTGACCGTTA TGCTGTTATC
 51 GGCTTACGGT GGTTCCTTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
 101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTGCG
 151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
 201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
 251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
 301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

1212

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351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGC GGTTTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRMSTATGM RIAGKDTPQS VSVITRSLD DKAHVHLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

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              10      20      30      40      50      60
a743.pep      MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
              |||
m743          MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT
              10      20      30      40      50      60

              70      80      90      100     110     120
a743.pep      IDRMSTATGMRIAGKDTPQSVSVITRSLDDKAVHGLEEAMKNTTGVNVVRDSSLQTRFL
              |||
m743          IDRMSTATGMRIAGKDTPQSVSVITRSLDDKAVHGLEEAMKNTTGVNVVRDSSLQTRFL
              70      80      90      100     110     120

              130     140     150     160     170     180
a743.pep      SRGFYIDQIGEDGITVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
              |||
m743          SRGFYIDQIGEDGMTVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
              130     140     150     160     170     180

a743.pep      TVNLIRKR
              |||
m743          TVNLIRKX

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g744.seq not found yet

g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

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m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTGGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTGGGA TGAATTATGT GAACCAAATA TTTGTTTTT AATCGGAGAA
151 AAGGGAAC TG GAAAGACAGC ATATGCTGTT TATTTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTC AGATTTTACA
301 AGTATTGGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AAATGAATAT TATTATGGCG CTTTGATCC GGAAATTGTA
451 CAAGCAATAA CTTTAAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACCTTTA
551 CAGAAAGTAA ATTCCAAGCA AATTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATGTA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTAAATAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAAT ACCAACTTC
851 AAGATAATTC AGTATTTTGA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTTCCAT
1001 GGAATGCTCC TAATTACAT GATGAGTATA AAAATTTAAC TTCATTATAT
1051 AGCTTCCTAA GAAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAA GTGATTATCA
1251 AAATTTCTCG AAATTTTTTG AATTTTAAA CGGGAAGAT AGATTTAAAT

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1213

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1301 ATAGTGATTT TTTAAAAGCA TTTGAACGTT TGAAAAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTTATTT GACTTGAATG TTATTGCTTA TTAGATAAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTTA AAGATAGAAA TTATGCAAAT
1501 ATTTCTCCTA AAATAAAAAC TGAAACTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTTGATGTTG GTACTCCATT TAAGACAAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

m744.pep

```

1 MKPLKLTLEFG FVDAANYRRR ENKDLFNRIK VKGEYLDELK EPNISFLIGE
51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLKK ARHLTVSDFT
101 SIWKVILYLL ISNQIKKEN GILSSIFNKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQO ITFTESKFQA NLGFIERKFK
201 DALSQLKLKD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVVLLIRPDI FDSLGLQONQ TKLQDNVSVL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLRKSYYRP RDILQMLTLL QKNKKSKEYD VVAEDFDNTS FOREYSIYLL
401 GEIKDHLLFY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVEIPKEMS TANEFLQFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEFKNK Q*

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g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

m745.seq

```

1 ATGTTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGGG
51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTGCGCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TGCGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTTG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTTC GCCTCTTGTT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTTGTTT
451 GCATTATGGA AAGCAAACCC CTTAAAGGCA TCTGATTTGT GA

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This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

m745.pep

```

1 MFWQLTVVSV TAVIALGTIF INKKTSKQKA TLDVILNDYQ DAQFVEADNH
51 ISPYIRGTAV DDNNARIDLY EIIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREEERKD TIFRELEILV
151 ALWKANPLKA SDL*

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a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

g746.seq

```

1 ATGTCCGAAA ACAAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
51 ACGGCGCAAC CGCCGCGGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGTT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGCGCA AACCAGCGCA ACGGAAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAAATCCGC CGCCGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAACACGTA GGCGCGCCGC TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGGA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCAGAGCA GGCAAAACAA
451 CGCGCTGCCG AAAAAGTGTC GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCAGAAAC TGCTGCCGAA AAAACCAAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAAGCGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAAA ACACGAAACG

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1214

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751 GCGCAAAAAA CCGACAAAGC GGACAAAACC AAAACCGCCG AGAAGGAAAA
801 ATCCGGCAAG GCGGGCAAAA AAGCCGCCAT TCAGGCAGGT TATGCCGAAA
851 AAGAACGCGC CTTGAGCCTC CAGCGCAAAA TGAAGGCGGC GGTATCGAT
901 TCGACCATCA CCGAAATCAT GACCGACAAC GGCAAAAGTTT ACCGCGTCAA
951 ATCAAGCAAC TATAAAACG CAAGGGATGC CGAACGCGAT TTGAACAAC
1001 TGCGCGTGCA CGGCATCGCC GGCCAGGTAA CGAATGAATA G

```

This corresponds to the amino acid sequence <SEQ ID 2552; ORF 746.ng>:

g746.pep

```

1 MSENKQNEVL TGYEQLKRRN RRRLVTASSL VAASCILLAA ALSSDPADSN
51 PAPQAGETGA TESQTANTAQ TPALKSAAEN GETAADKPQD LAGEDKPSAA
101 DSEISEPENLV GAPLVLINDR LEDSNIKGLE ESEKLQQAET AKTEPKQAKQ
151 RAAEKVSATA DSTDTVAVEK PKRTAEPKPQ KAERTAEAKP KAKETKTAEK
201 VADKPKTAAE KTKPDTAKSD SAVKEAKKAD KAEGKKTAEK DRSDGKKHET
251 AQKTDKADKT KTAKEKESGK AGKKAATQAG YAEKERALS QRMKAAGID
301 STITEIMTDN GKVYRVKSSN YKNARDAERD LNKLVRHGIA GQVTNE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2553>:

m746.seq

```

1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51 ACGGCGCAAC GCGCGCCGCC TCGTAACGGC AAGTTGCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 CCGGGCGAAA GAAGCGCGT AGAAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGC CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGAGCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGCG AACTGCCGAC
451 AGTACGGATA CGGTAGCGCT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAGC CAAGCCCAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCGACAAAC CGAAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAGCGGA CAAGACCAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAAA GCGGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGCGGCGCG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATTT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2554; ORF 746>:

m746.pep

```

1 MSENKQNEVL SGYEQLKRRN RRRLVTASCL VAASCILLAA ALSSGPAEQT
51 AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINERL EDSNIKGLEA SEKLQQAETA KTAPKQAKQ AAEKVPATAD
151 STDTVAVEKP KRTAETKPKQ AERTAKAPK AKETKTAEKV ADKPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADTK
251 TAEKEKSGKK AAIQAGYAEK ERALSQRKM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

m746/g746 89.9% identity in 346 aa overlap

```

          10      20      30      40      50
m746.pep  MSENKQNEVLSGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQT---AGETSG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746      MSENKQNEVL TGYEQLKRRNRRRLVTASSLVAASCILLAAALSSDPADSNPAPQAGETGA
          10      20      30      40      50      60

          60      70      80      90     100     109
m746.pep  VENKAAGAAQTPALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER
          :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g746      TESQTANTAQTALPKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR
          70      80      90     100     110     120

```

1215

```

      110      120      130      140      150      160      169
m746.pep LEDSNIKGLEASEKLQQAETA KTAPKQAKQRAAEKV PATADSTDTVA VEKPKRTAETKPQ
          |||
g746      LEDSNIKGLEESEKLQQAETA KTEPKQAKQRAAEKVSATADSTDTVA VEKPKRTAEPKPQ
          |||
          130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep KAERTAKAKPKAKETKTAEKVADKPKTAAEKT KPDTAKSDSAVKEAKKADKAESKKTAEK
          |||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKT KPDTAKSDSAVKEAKKADKAEGKKTAEK
          |||
          190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep DRSDGKKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALS LQRKMKAAAGID
          |||
g746      DRSDGKKKHETAQKTDKADKTKTAEKEKSGKAGKKA AIIQAGYAEKERALS LQRKMKAAAGID
          |||
          250      260      270      280      290      300

      290      300      310      320      330
m746.pep STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||
          310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1  ATGTCCGAAA ACAACAAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGCGCAAC CGCCGCCGCC TCGTAACGGC AAGTTGCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCCGGCGAAA CAAGCGGCGT AGAAAAACAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCCTT AATCCGCCG CCGACAAACC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCCGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
351 TTTGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAAGC CAAGCCCAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAAG AAGCGAAAAA
651 AGCCGCAGAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAAGCGGA CAAGACCAA
751 ACCGCCGAGA AGGAAAAATC CGGTAAAAA GCGCCATTC AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGGCGGCGG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAAAT CAAGCAACTA TAAAAACGCA AGGGATGCCG AACCGGATT
951 GAACAAATTG CGCGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pap
1  MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINDRL EDSNIKGLEA SEKLQQAETA KTAPKQAKQR AAEKV PATAD
151 STD T VAVEKP KRTAETKPQK AERTAKAKPK AKETKTAEKV ADKPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADKTK
251 TAEKEKSGKK AATQAGYAEK ERALS LQRKM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pap  MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
          |||
m746      MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
          |||
          10      20      30      40      50      60

```


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```

          70      80      90      100      110      120
a746.pep  AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSNIKGLEA
          70      80      90      100      110      120
m746      AAGAAQTPALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSNIKGLEA

          130      140      150      160      170      180
a746.pep  SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK
          130      140      150      160      170      180
m746      SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKQAERTAKAKPK

          190      200      210      220      230      240
a746.pep  AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA
          190      200      210      220      230      240
m746      AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA

          250      260      270      280      290      300
a746.pep  QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY
          250      260      270      280      290      300
m746      QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALS LQRMKAAGIDSTITEIMTDNGKVY

          310      320      330
a746.pep  RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          310      320      330
m746      RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX

```

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

m747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTCCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGACG GTGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2558; ORF 747>:

```

m747.pep
1   LTPWADAYAD LRGKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCCGCGA TGTCAGCAAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAAACAA TCTGCAAACC
201 CCGTGAGATT GTTTTGACG GCGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACGCAA CGTTCTATAG TCAATTAAAA
301 TCAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2560; ORF 747.a>:

```

a747.pep
1   LTPWADAYAD LRGKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPYYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

1217

Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

```

          10      20      30      40      50      60
a747.pep  LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR
          |||||
m747      LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR
          10      20      30      40      50      60

          70      80      90     100
a747.pep  HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX
          |||||
m747      HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX
          70      80      90     100

```

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

```

Query: 1  LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKGWSVGIGLNVGKQLTDSVGLEFDPYYR 60
          + PW++  DL + K+ T          +D+++  GW  G+G N+GK+L +S +E P+Y+
Sbjct: 174 INPWSEVKFDLNSRYKLNTGVNLLKKDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

```

```

Query: 61  HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95
          +T + E +  GD  + ++  EYG RV  F
Sbjct: 234 QRTYKESGEFSVTTKSGDVSILTIPKTSIREYGLRVGIKF 272

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

```

1  ATGAGTCAAA ACCAACCCGC ACAACCGACC AAACGCAATC TGTCAAAAC
51  CGCCCTTGCC GTCGCGCAA TCGGCGCAAT CGGAGGTTAT TTCGCGCGCA
101  AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA ACACTCGCCC
151  CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGTATCG TTACGCCGCG
201  GCAGGCGTTT TCCATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251  AGCAGCTGGA AAACCTGTTC CGCACACTGA CCGCCCGCAT CGAGTTTCTC
301  ACCCAAGGCG GAGAATACCA AGACGGCGAC GACAACTCC CGTCAGCCGG
351  CAGCGGCATT TTGGGTAAAG CCTCAACCC CGACGGATG ACCGTTACCG
401  TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451  AAAACGGTTC ATTTGCAGGA AATGCGCGAC TTCCCAACG ATAAGCTGCA
501  AAAAAGCTGG TGCAGCGCG ATTTGAGCCT GCAAATCTGC GCCTTACCCC
551  CCGAAACCTG CCAAACCGCC CTGCGCGACA TCATCAACA CACCGCCCAA
601  ACCGCCGTCA TCCGCTGGAG TATCGACGGG TGGCAGCCTA AATCCGAACC
651  CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCGAGAC GGCACGGGCA
701  ACCCAAGGT TTCCGATCCC AAAACCGCCG ACGAGGTTT ATGGACGGGG
751  GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGGAAAA ACGGCAGCTA
801  TCAGGCAGTC CGCCTTATCC GCCGCTTTGT CGAGTTTGG GACAGGACGC
851  CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGGAAAAA CAGCGGGGCG
901  CCGATGGACG GCAAAAAGA AGCCGACCAA CCGGATTTG CCAAAGACCC
951  CGAGGGTGAT ATCAGCCCCA AAGACAGCCA TATGCGCCTG GCGAATCCGC
1001  GCATCCCCGA ATTCTCAAA AAACACTGCC TCTCCGCGC CGCTACAGC
1051  TATTCTCGCG GACCCGCCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101  CGTCTGCTAT CAGGCAAATC TTGCCGACGG TTTCATCTTC GTGCAAAACC
1151  TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201  TATTCTTCG TCTTGCCCGG CGTGGGAAAA GCGGATTCT TGGGACAAGG
1251  GCTGCCGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

```

1  MSQNQPAQPT KRNLFKTALA VGAIGAIGGY FGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPROAF SIMCAFDVTA QSAKQLENLF RTLTARIEFL
101  TQGGHEYQDGD DKLPASAGSI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151  KTVHLQEMRD FPNDKLQKSW CDGDLQLQIC AFTPETCQTA LRDIKHTAQ
201  TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251  VAANSLDEPE WAKNGSYQAV RLIRRFVEFW DRTPLEQTD IFGRRKYSGA
301  PMDGKKEADQ PDFAKDPEGD ITPKDSHMRL ANPRDPEFLK KHCLFRAYS
351  YSRGPASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEYISPFGGG

```

1218

401 YFFVLPGVGK GGFLGQGLPG V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2563>:

m748.seq

```

1   ATGAGCAAAA AACAAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CGCGATCGCA GCCGGAGCAG TCGGCGCAAT CGGAGGTTAT CTCGGCGGCA
101 AAAAACAGGG CGAAACCGCC GAACGCACCG CCGAAAGCCA AACTCGCCC
151 CAAGCCTATC CCTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGCGGTTT TCGATTATGT GCGCCTTCGA CGTAACCGCG CAAAGTGCCA
251 AGCAGCTGGA AAACCTGTTC CGCAGCTGA CCGCCCGCAT CGAGTTTCTC
301 ACCCAAGGCG GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAAG CCTTCAACCC CGACGGGTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCCTG TTTGACGGCC GGTTCGGACT CAAAGACAAA
451 AAACCGGATC ATTTGCAGGA AATGCGCGAC TTCTCCAACG ATAAGCTGCA
501 AAAAAGCTGG TGGCAGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTGCGCGACA TCATCAAACA CACCGTCCAA
601 ACCGCCGTTA TCCGTGGAG TATCGACGGG TGGCAGCCCA AATCCGAACC
651 CGGCGCGATG GCGGCGCGCA ACCTGTTGGG CTTCAGGGAC GGCACGGGCA
701 ACCCAAAGT TTCCGATCCC AAAACTGCCG ACGAGGTTT GTGGACGGGG
751 GTGGCCGCCA ACAGCCTCGA CGAACCGGAG TGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT CGAGTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAACCGAC ATTTTCGGGC GCGCAAATA CAGCGGTGCG
901 CCGATGGACG GCAAAAAAGA AGCCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGGTGAT ATCAGGCCA AAGACAGCCA TATACGCCTG GCGAATCCGC
1001 GCGATCCCGA ATTCTCAAA AAACACCGCC TCTTCCGCG CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTCG GGCTGGTGTT
1101 CGTCTGCTAT CAGGCAAACC TTGCCGACGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGG CGAACCGCTG GAAGAATACA TCAGCCCTT CGGCGGCGGC
1201 TATTCTTCG TCTTGCCCGG CGTGAAAAA GCGGCTTTT TGGGGCAAGG
1251 GCTGCTGGGC GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2564; ORF 748>:

m748.pep

```

1   MSKKQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKKQGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQAF SIMCAFDVTA QSAKQLENLF RLTARIEFL
101 TQGGYQDGD DLKPPAGSGI LGKAFNPDGL TVTVGVGSSL FDGRFGLKDK
151 KPIHLQEMRD FSNKDLQKSW CDGDLQLQIC AFTPETCQAA LRDIKHTVQ
201 TAVIRWSIDG WQPKSEPGAM AARNLLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRHFEVFW DRTPLQEQTD IFGRKYSQA
301 PMDGKKEADQ PDFAKDPEGD ITPKDSHRL ANPRDPEFLK KHRLFRFRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNNGEPL EYISPFGGG
401 YFFVLPGVEK GGFLGQGLLG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae*

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPT RRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSPQAYPCYGEHQ					
g748	MSQNQPAQPTKRNLFTALAVGAIGAIGGYFGKKQGETAERTAESQHSPQAYPCYGEHQ					
	10	20	30	40	50	60
m748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGYQDGDGDLKPPAGSGI					
g748	AGIVTPRQAFSIMCAFDVTAQSAKQLENLFRTLTARIEFLTQGGYQDGDGDLPSAGSGI					
	70	80	90	100	110	120
m748.pep	LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLQLQIC					
g748	LGKAFNPDGLTVTVGVGSSLFDGRFGLKDKKTVHLQEMRDFPNKDLQKSWCDGDLQLQIC					
	130	140	150	160	170	180
m748.pep	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
g748	AFTPETCQAALRDIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
m748.pep						

	: : : :
g748	AFTPETCQTALRDIKHTAQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP
	190 200 210 220 230 240
m748.pep	KTADEVLWTGVAANSLDEPEWAKNGSYQAVRLIRHFEVFWDRTPLQEQTDFGRRKYSGA
	250 260 270 280 290 300
g748	KTADEVLTGVAANSLDEPEWAKNGSYQAVRLIRRFVEFWDRTPLQEQTDFGRRKYSGA
	250 260 270 280 290 300
m748.pep	PMDGKKKEADQPDKFDPEGDITPKDSHIRLANPRDPEFLKKHRLFRRAYSYSRGLASSGQ
	310 320 330 340 350 360
g748	PMDGKKKEADQPDKFDPEGDITPKDSHMLANPRDPEFLKKHCLFRRAYSYSRGPASSGQ
	310 320 330 340 350 360
m748.pep	LDVGLVFVCYQANLADGFIFVNLLNGEPLEEYISPFGGGYFFVLPGVGKGGLGQGGLLG
	370 380 390 400 410 420
g748	LDVGLVFVCYQANLADGFIFVNLLNGEPLEEYISPFGGGYFFVLPGVGKGGLGQGGLPG
	370 380 390 400 410 420
m748.pep	VX VX
q748	

a748.sec

1	ATGAGCAAAA	ACCAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAC
51	CGCATCGCA	GCTGGAGACG	TCGGCCGAAT	CGGAGGTTAT	CTCGGCGGCA
101	AAAAACGGG	CGAAACCGCC	GAACGCACCG	CCGAAAGCCA	ACTACTCGCCC
151	CAAGCCTATC	CTGCTACGG	GCAACATCAG	GCAGGCATCG	TTACGCCGCA
201	GCAGGCGTTT	TCGATTATGT	GCGCCTTCGA	CGTAACCGCG	CAAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTT	CGCAGCGCTA	CGCCCCGCAT	CGAGTTTCTG
301	ACCCAAGGCG	GCGAATACCA	AGACGCGCAC	GCAAAACTTC	CAGCTAGCCG
351	CAGCGGCATT	TGGGCAAGC	CCTTCAACCC	CGACGGGTAT	ACCGTTACCG
401	TGGGGTGCGG	CATGCAAGCT	TTTGACGGCC	GGCTCGGGACT	CAAGAGCAAA
451	AAACCGATT	ATTTCAGGA	AATGCGGCAC	TTTCTCAAAG	ATAAGTGCGA
501	AAAAAGCTGG	TGCGACGGCG	ATTTGAGCCT	GCAAACTCTG	GCCTTCACCC
551	CCGAAACCTG	CCAAAGCCGC	CTGCGGACCA	TCATCAAAAC	ACCGTCCAAA
601	ACCGCCGTTA	TCGCGTGGAG	TATCGACGGA	TGGGACGCTA	AATCCGAAAC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCCGCGAC	GGCACGGGCA
701	ACCCCAAAGT	TTCCGACCCC	AAAACTGGCG	ACGAGGTTTT	GTGGCAGGGG
751	GTGGCCGCCA	ACAGCCTCCA	GCAACGGGAG	TGGGCGAAAA	ACGGCAGTGA
801	TCAGGCAGTC	CGCCTTATCC	GCCACTTTGT	TGAGTTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAAACGAC	ATTTTCGGCG	GGCGCAAAAT	CAGCGGCGCG
901	CCGATGGACG	GCAAAAAAG	AGCCGACCAA	CGGAGATTTG	CCAAAGACCC
951	CGAGGGGAAT	ACACGCGCCA	AAGACAGCCA	TATAGCCTTG	CGCAATCCGC
1001	GCGATCCCGA	GTTCTCTTAA	AAACACCGCC	TCTTCCGCGC	CGCCTACAGC
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTCG	GGCTGGTGTG
1101	CGTCCTGCTAT	CAGGCAAAAC	TGCGGACGGG	ATTACATCTC	GTGCAAAACC
1151	TCCTCAACGG	CGAAGCCGTG	GAAGAATACA	TCAGCCCCCT	CGGCGCGCGC
1201	TATTTCTCTG	CTTGCCCGGG	CGTGAAAAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGCG	GTATAA			

a748.ppt

1	MSKNQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKRGETA	ERTAESQHSP
51	QAYPCYGEHG	AGVTPPQQA	STMCAPDFTA	QSAQOLENLF	RTLTAIRLEFL
101	TQGGYEQDGD	DKLPPAGSGI	LGKAFFNDVL	TVTVGVGSSL	FDGFRGLKDK
151	KPIHLQEMRD	FSNDKLQKSW	CDGDLSLQIC	AFTPETCQAA	LRDIIKHTVQ
201	TAIVRWSIDG	WQPKSEPGAM	AARNLLGFRR	GTGNPKVSDP	KTAEVLWGTG
251	VANSLSDEPE	WAKNGSYQAV	RLIRHFVEFW	DRTLPLQEOTD	IFGRRKLSWA
301	PMDGKKEADQ	PDFAKDPEN	TTPKDSHRL	ANPRDPEFLK	KHRLFRFRAYS
351	YSRGLASSGO	LDVGLVFVCI	QANLADGFIF	VQNLLNGEPL	E EYISPFGGG
401	YFVFLPGVEK	GGFLGOGLLV	V*		

Computer analysis of this amino acid sequence gave the following results:

1220

Homology with a predicted ORF from *N meningitidis*

ORF 748 shows 99.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. meningitidis*:

a748/m748 99.0% identity in 421 aa overlap

	10	20	30	40	50	60
a748.pep	MSKNQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKRGETAERTAESQHSFPQAYPCYGEHQ					
m748	MSKKQPAQPTRRTLFKTAIAAGAVGAIGGYLGKKQGETAERTAESQHSFPQAYPCYGEHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
a748.pep	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTAIEFLTQGGEYQDGDCLKPPAGSGI					
m748	AGIVTPQQAFSIMCAFDVTAQSAKQLENLFRTLTAIEFLTQGGEYQDGDCLKPPAGSGI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a748.pep	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLIC					
m748	LGKAFNPDGLTVTVGVGSSSLFDGRFGLKDKKPIHLQEMRDFSNDKLQKSWCDGDLSQLIC					
	130	140	150	160	170	180
	190	200	210	220	230	240
a748.pep	AFTPETCQAALRDIIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
m748	AFTPETCQAALRDIIKHTVQTAVIRWSIDGWQPKSEPGAMAARNLLGFRDGTGNPKVSDP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a748.pep	KTADEVLTWGVAANSLEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQTDIFGRRKYSGA					
m748	KTADEVLTWGVAANSLEPEWAKNGSYQAVRLIRHFVEFWDRTPLEQTDIFGRRKYSGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
a748.pep	PMDGKKEADQPDFAKDPEGNTTPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ					
m748	PMDGKKEADQPDFAKDPEGDITPKDSHIRLANPRDPEFLKKHRLFRAYSYSRGLASSGQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
a748.pep	LDVGLVFVCYQANLADGFI FVQNLLNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
m748	LDVGLVFVCYQANLADGFI FVQNLLNGEPL E EYISPFGGGYFFVLP GVEKGGFLGQGLLG					
	370	380	390	400	410	420
a748.pep	VX					
m748	VX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

g749.seq

```

1  ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCCGCGCCG GCCCGGTCCG
101 GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTCGGTAT CGCCGTCAAC
151 GACAATGCTT GCGAACCGAT GAATCTGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AGGGCGTGAT GGTGGTGGAC GAACGCGAAA ATATCGCCCC GGGGCTTTCC
301 GACAAAATGA CCGTAAccct GCTGCCGGGC GAATACGAAA TGACCTGCGG
351 CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401 AAGACACGCG CAACGAAGCG GATTGGAAA AACTGCCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG CGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCCTGTTTGC CGCCACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGTGTG AAGACGACTT
651 CAAAGACGGT GCGAAAAGAT CCGGGTTTAC CGGCTTCCAC CGTATCGAAC
701 ACGCCCTTTG GGTGGAAAAA GACGTATCCG GCGTGAAGGA AACC GCGGCC
751 AAACGTATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC

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1221

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801 GttccctCCG GGCAAAGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TGCGGACGGA TCTAAAAAAA TCGTCGATT
951 GTTCCGTCGG TTGATTGAGG CCAAAAAACA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGCACCAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

g749.pep

```

1 MRKFNLTLALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGI AVN
51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQFLA
151 DYKAYVQGEV KELAAKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DATEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

m749.seq

```

1 ATGAGAAAAAT TCAATTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCCGCTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTCAAC
151 GACAATGCCT GCGAACCGAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCCT GTTGCCGGGC GAATACGAAA TGAATTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAAACTTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTAC CGGCTTTCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGAT CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 TGGCGGCGAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATT
951 GTTCCGTCGG CTGATCGAGG CCAAAAAACA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

m749.pep

```

1 MRKFNLTLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSI AVN
51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

10 20 30 40 50 60
m749.pep MRKFNLTLALSVMALGLTACQPPEAEKAAPAAASGEAQTANEGGSVSI AVNDNACEPMELT
|||||
g749 MRKFNLTLALSVMALGLTACQPPEAEKAAPAAASGETQSANEGGSVGI AVNDNACEPMNLT
10 20 30 40 50 60

```

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNSGRKLEWEILKGVMMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNSGRKLEWEILKGVMMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPOPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRVHYERIEPIAELFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDTNFKQVNEILAKYRTKDGFTYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDTNFKQVNEILAKYRTKDGFTYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

1	ATGAGAAAT	TCAATTGAC	CGCATTGTC	GTGATGCTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGGCGGTT	CGGTCAGTAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCAGAT	GGAACGTACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCACCTT	GTTGCCGGGC	GAATACGAAA	TGACTTGCGG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAATCTGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAACGT	ATTGAAGAAG
851	TGGCGGGCAG	TAAAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTCGATTT
951	GTTCCGTCGG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTTG	GAAAAAACCG
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAA			

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

1	MRKFNLTALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTAN	EGGSVSIAVN
51	DNACEPMELT	VPSGQVVFNI	KNNSGRKLEW	EILKGVMMVD	ERENIAPGLS
101	DKMTVTLLPG	EYEMTCGLLT	NPRGKLVVTD	SGFKDTANEA	DLEKLSQPLA
151	DYKAYVQGEV	KELVAKTKTF	TEAVKAGDIE	KAKSLFADTR	VHYERIEPIA
201	ELFSELDPVI	DAREDDFKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKEIAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	GEEDRYSHTD

1223

301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNL	TALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT			
m749	MRKFNL	TALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	AVNDNACEPMELT			
	10	20	30	40	50	60
a749.pep	VP	SGQVVFNIKNN	SGRKLEWEILKGV	MVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT		
m749	VP	SGQVVFNIKNN	SGRKLEWEILKGV	MVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT		
	70	80	90	100	110	120
a749.pep	NPRGKLVV	TDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE				
m749	NPRGKLVV	TDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE				
	130	140	150	160	170	180
a749.pep	KAKSLFAD	TRVHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK			
m749	KAKSLFAD	TRVHYERIEPIAELFSELD	PVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK			
	190	200	210	220	230	240
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
a749.pep	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDG	FETYDKLG				
m749	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDG	FETYDKLG				
	310	320	330	340	350	360
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380	389			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

```

1  GTGAAACCGC GTTTTATG GGCAGcctGC GCCGTCTGC CGGCCGCCTG
51  TTCGCCCCGAA CCTGCCGCCG AAAAACTGT ATccgCCGCA TCCCAAGCCG
101 CATCCACACC TCTGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC
151 GTTGTGCCGA AGAATCCCGA ACgcgtcgcc gtgtAcgaCt ggGCGGCGTt
201 ggaTACGTG ACCGAGCCGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG
251 TCGCGTGGGA CTATTGCGAG CCTGCATTG ACAAGGCGGC AACGGTGGGG
301 ACGCTGTTG AGCCCGATTG CGAATCCCTG CACCGCCACA ATCCGCAGTT
351 TGTCATTACC GCGGGGCCGG GTGCGGAAGC GTATGAACAG TTGGCGAAAA
401 ACGCGACCAC CATAGATTG ACGGTGGACA ACGGCAATAT CCGCACCAGC
451 GCGGAGAAGC AGATGGAGAC CCTGTCGCGG ATTTTCGGTA AGGAAGCGCG
501 CGTGGCGGAA TTGAATGCGC AGATTGACGC GCTGTTCCGC CAAAAGCGCG
551 AAGCCGCCAA AGGCAAAGGA CGCGGGCTGG TGCTGTCCGT TACAGGCAAC
601 AAGGTGTCCG CTTTCGGCAC GCAATCGCGG TTGGCAAGTT GGATACACGG
651 CGACATCGGC CTGCCGCCG TGGACGAATC TTTACGCAAC GAAGGGCACG
701 GGCAGCCCGT TTCCTTCGAA TACATCAAAG AGAAAAACCC CGGCTGGATT
751 TTCATCATCG ACCGCACCGC CGCCATCGGG CAGGAAGGGC CGGCTGCCGT

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q750 . pep

1	VKPRFYWAAC	AVLPAACSPE	PAAEKTVSAA	SQAASTPVAT	LTVPTARGDA
51	VVPKNPERSA	VYDWAALDTL	TEPGVNVGAT	TAPVRVDYLO	PAFDKAATVG
101	TLFEPDCELS	HRHNPQFVIT	GGPAQAEAYEQ	LAKNATTIDL	TVDNGNRTS
151	GEKQMETLSR	IFGKEARVAE	LGNADIALFA	QKREAAKGGK	RGVLVSVTGN
201	KVSAGTQSR	LASWTHGDIG	LPPVDES LRN	EGHGQPVSE	YIKEKNPGWI
251	FIIDRTAAIG	QEGPAAEVIL	DNALVCGTNA	WKRKQIIVMP	AANYIVAGGA
301	ROLIOAAEOL	KAAFEKAEPV	AAO*		

m750.seq

1	GTGAAACCGC	GTTTTATTG	GGCAGCCTGC	GCCGTCCTGC	TGACCGCCTG
51	TTCCGCCGAA	CCTGCCCGCC	AAAAAAGTGT	ATCCGCCGCA	TCCGATCTG
101	CCGCCACGCT	GACGTCGCC	ACCGCGCGTG	GCGATCCGCT	TGTGCCGAAG
151	AATCCCGAAC	GCCTGCCCGT	GTACGACTGG	CGCGCGTTGG	ATACGCTGAC
201	CGAATTGGGC	GTGAATTGTG	GCGCAACCAC	CGCGCCGGTG	CGCGTGGATT
251	ATTTGCAGCC	TGCATTGTAG	AAGGCGGCCAA	CGGTGGGGAC	GCTGTTCCGAG
301	CCGGATTACG	AAGCCCTGCA	CCGCTACAAT	CCTCAGCTTG	TCTATTACCG
351	CGGGCCGGGC	GCGGAAGCGT	ATGAACAGTT	AGCGAAAAAC	GCGACCACCA
401	TAGATCTACG	GGTGGAACAA	GGCAATATCG	GCACACGCGG	GCAAAAGCGAG
451	ATTGGAGAGT	TGGCGCGGAT	TTCCTGCAAG	GAAGCGCGCG	CGCGGGAATT
501	GAAGGCGCAG	ATTGACGCGC	TGTTCCGCCA	AACGCGCGAA	GCCGCCAAAG
551	GCAAAGGACG	CGGGCTGGTG	CTGTCCGGTA	CGGGCAACAA	GGTGTCGCCC
601	TTCCGCCACG	AGTCGCGGTT	GGCAAGTTGG	ATACACGGCG	ACATCGGCCT
651	ACCGCTTGTA	GACGAATCTT	TACGCAACGA	GGGGACGGGG	CAGCGCTGTT
701	CCTTCGAATA	CATCAAAGAG	AAAAAGCCCG	ATTGGATTTT	CATCATCGAC
751	CGTACCGCCG	CCATCGGGCA	GGAAGGCGCG	CGGCGTGTGC	AAGTATTGGA
801	TAAACGCGCT	GTACCGGGCA	CGAACGCTTG	GAAGCGCAAG	CAATCATCGC
851	TCATGCCTGC	CGCGAACTAC	ATTGTCGCGG	GCGGCGCGCG	GCAGTTGATT
901	CAGGCGCGGG	AGCAATTGAA	GCGGCGGCTT	AAAAAGGCAG	AACCCGTTGC
951	GGCGGGGAAA	AAGTAG			

m750.pep

1	VKPRFYWAAC	AVLLTACSPE	PAAEKTVSAA	SASAATLTVP	TARGDAVVPK
51	NPERVAVYDW	AALDTLTTEL	VNVGATAPFV	RVDYLQPAFD	KAAATVGTLFE
101	PDYEALHRYN	PQLVTITGGP	AEAYEQLAKN	ATTIDLTVDN	GNIRTSGEKQ
151	METLARIIFGK	EARAELKKAQ	IDALFAQTR	AARKGKRGVL	LSVTGNKVS
201	FGTQSRSLAS	IHGDI GLPPV	DESLRNEGHG	QPVSEFYIKE	KNPDWIFIID
251	RTAAIGQEGP	AAAEVDLNAL	VRGTNAWKRK	QIIVMPAANY	I VAGGARQLI
301	AAEAEOLKAAF	KKAEPEVAAGK	K*		

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 750 shows 93.8% identity over a 322 aa overlap with a predicted ORF (ORF 750) from *N. gonorrhoeae*

m750/g750 93.8% identity in 322 aa overlap

	10	20	30	40	50
m750.pep	VKPRFYWAACAVLLTACSP	EPAAEKTVSAASASA----	ATLTVPTARGDAVV	PKNP	ERVA
g750	VKPRFYWAACAVLPAACS	EPAAEKTVSAASQAAST	PVATLTVPTARGDAVV	PKNP	ERVA
	10	20	30	40	50
	60	70	80	90	100
m750.pep	VYDWAALDTLT	ELGVNVGATTAPVR	VDYLQPAFDKAAT	VGTLFEPDYEAL	HRNYPQLVIT
g750	VYDWAALDTLT	EPGVNVGATTAPVR	VDYLQPAFDKAAT	VGTLFEPDCESL	HRNYPQFVIT
	70	80	90	100	110
	120	130	140	150	160
m750.pep	GGPGAEAYEQLAKN	ATTIDLTVDNGNI	RITSGEQMETLAR	IFGKEARAAELKA	QIDALFA

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g750      GGPGAEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLSRIFGKEARVAELNAQIDALFA
           130         140         150         160         170         180

           180         190         200         210         220         230
m750.pep  QTREAAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      QKREAAKGKGRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESLRNEGHGQPVSF
           190         200         210         220         230         240

           240         250         260         270         280         290
m750.pep  YIKEKNPDWIFIIDRTAAIGQEGPAAVEVLNDAVLRGTNAWKRKQIIVMPAANYIVAGGA
           | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      YIKEKNPGWIFIIDRTAAIGQEGPAAVEVLNDAVLCGTNAWKRKQIIVMPAANYIVAGGA
           250         260         270         280         290         300

           300         310         320
m750.pep  RQLIQAAEQLKAAFEKAEPVAAGKKX
           | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g750      RQLIQAAEQLKAAFEKAEPVAAQX
           310         320

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a750.seq
1 GTGAAACCGC GTTTTTATTG GGCAGCCTGC GCCGTCCTGC TGACCCGCTG
51 TTCGCCCGAA CCTGCCCGCC AAAAACCTGT ATCCGCCGCGT TCCGCACTCG
101 CGCCACACAT GACCGTGC CGATAGCCGT TGTGCCGAAG
151 AATCCCGAAC GCGTCGCCGT GTACGACTGG CCGGCGTTGG ATACGCTGAC
201 CGAATTGGGT GTGAATGTGG GCGCAACCAC CGCGCCGGTG CCGCTGGATT
251 ATTTGCAGCC TGCAATTGAC AAGCGCGCAA CGGTGGGGAC GTGTTTCGAG
301 CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351 CGGGCCGGGG GCGGAAGCGT ATGAACAAGT GGGCAAAAAA GCGACCACCA
401 TAGATCTGAC GGTGGACAAC TTCAATATCC GCACCAGCGG CGAAAGCAGT
451 ATGGAGACCT TGGCGCGGAT GTTTCGGAA G AAGCGCGCG CGCGCGAATT
501 GAAGGCGCAG GTTAGCGCGC TGTTCCGCCA AACGCGCGAA GCCGCCAAG
551 GCAAAAGGAC CGGGCTGGTG CTGTTCGGTTA CGGGCAACAA GGTGTCGCCC
601 TTCGGCACGC AGTCGCGGTT GCGAAGTTGG ATACACGGCG ACATCGGCTT
651 ACCGCTGTGA GACGAATCTT TACGCAACGA GGGGCACGGG CAGCCTGTTT
701 CCTTCGAATA CATCAAAGAG AAAAACCCCG ATTGGATTTT CATCATCGAC
751 CGTACCGCGC CCATCGGGCA GGAAGGCGCG CGCGCTGTGC AAGTATTGGA
801 TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG AACAATCATC
851 TCATGCTCTG CGCGAACTAC ATTGTCGCGG GCGGCTCGCG GCAGTTGATT
901 CAGGCGGGCG AGCAGTTGAA GGAGGCGTTT GAAAAGGCGA AACCCGTTGC
951 GGCGGGGAAA GAGTAG
```

a750.pep

1	VKPRFYWAAC	AVLLTACSP	PAAEKTVSAA	SASAATLTVP	TARGDAVVPK
51	NPERVAVYDW	AALDTLTTEL	VNGVATTAPV	RVDYLQPAFD	KAATVGTLFE
101	PDYEALHRYN	PQLVITGGPG	AEAYEQLAKN	ATTIDLTVDN	GNIRTSGEKQ
151	METLARIFGK	EARAELKQA	IDALFAQTRN	AAKGKGKGLV	LSVTGNKVSA
201	FGTQSRLASW	IHGADILGPPV	DESLRNEHGK	QPVSFYEYKE	KNPDIWFID
251	RTAAEIQEGEP	AAAEVLDNAL	VRGTNAWKRR	QIIVMPAANY	IVAGGSRQLI
301	QAAEOLKEAF	EAEKPEVAGK	E*		

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

	10	20	30	40	50	60
a750.pep	VKPRFYWAA	CAVLLTACS	PEPAAEKT	VSAA	SASAATLT	VP
m750	VKPRFYWAA	CAVLLTACS	PEPAAEKT	VSAA	SASAATLT	VP
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AAALDTL	TELGVN	GATTAP	VRVDYL	QPAFDK	AAATVG
m750	AAALDTL	TELGVN	GATTAP	VRVDYL	QPAFDK	AAATVG
	AAALDTL	TELGVN	GATTAP	VRVDYL	QPAFDK	AAATVG

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	70	80	90	100	110	120
	130	140	150	160	170	180
a750.pep	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
m750	AEAYEQLAKNATTIDLTVDNGNIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a750.pep	AAKGKGRGLVLSVTGNKVS AFGTQSRLASWIHGDI GLPPVDESLRNEGHGQPVSF EYIKE					
m750	AAKGKGRGLVLSVTGNKVS AFGTQSRLASWIHGDI GLPPVDESLRNEGHGQPVSF EYIKE					
	190	200	210	220	230	240
	250	260	270	280	290	300
a750.pep	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWKRKQIIVMPAANYIVAGGS RQLI					
m750	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWKRKQIIVMPAANYIVAGG ARQLI					
	250	260	270	280	290	300
	310	320				
a750.pep	QAAEQLKEAFKAEPVAA GKEX					
m750	QAAEQLKA AFKKAEPVAA GKXX					
	310	320				

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

```

m751.seq..
1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAATTGGTTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTCGTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTCAG AAAAAGTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CGGAGGTGCC AAAAGCAGGT ACAAAGAAT TTGATGACTA TGTA AAAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAATCTAA
951 ACCCATACTG GTAGAACCAA ACAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2580; ORF 751>:

```

m751.pep..
1  MAWSMFATTQ ADRAVRSATA PKEMWFHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAQNR NSTNGSGVIA
101 VMNPPTGKYK SDSNNKIKDF LWLGSSLVSE LMYVGYDQLN NKVFQGYLPK
151 TNSEKLNQDI YREVQKMGNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFIGNKWIPF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKEFDDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKT KDNE KYEKEAF*

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a751.seq not found yet

a751.pep not found yet

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g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC
651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTCGATTTT CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTGAAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTCACTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAAAGC
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTT GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTTGCTCCT CAGGATTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

m752.pep

```

1  MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51  DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQWFWCIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSQALE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILLHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTIFYIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALEYVAP QDLLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1  ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51  GCAGCATCTC ACTGAAAGAA TGACGCAAAT TGCCAAGCTG CTGAATTCTT
101 CCGCAAACAA TCCTGATATA GACATTCCTG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTC ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTTCTG CATTCCCGAC TCTTTGCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTGTC ACCGCATTGC

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651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCCTGCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTCATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTTG GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTGTCTCCT CAGGATTTAT TGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDTRM KWRVAVKESRK KIQKPIDFPF
101 EHQWFECIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
151 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDLHRIATSN AIENKAEPGO FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFIH PVVQAIILHE LIGYIHPFGD
301 GNGRTARALF YWFMKNGYW LFEYISISRL LKNAPAQYAK SYLYAETDDL
351 DLTYFYIYQC DIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
451 SGNALFYVAP QDLLERLEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTTAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTTGC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TCGCCAGTT ATTTCTTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAIT WLWYQSPTHR QVPIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESD RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSQHM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

1229

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```

m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTGT GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTTGATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCAGTG CACACCTCAA AAATTTTTCG TACTCTATC ATGACGAATA
951 CGATGTTCGT CTTGCACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATTG
1051 AACCTGACTA ACCACGGTAA GAAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```

m754.pep
1  MMKSILTVSG NRMRKPRITY LDVWANDER I GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVS VSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLS EDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLD T SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKPTY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*

```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```

m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTACTCCGAT ATTTAAACCA
101 TCTTGCTAG ACATGGATTT GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTT ACTCCTGTAT TTCAAACATT AAGTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTGGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA

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1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

m755.pep..

```

1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
51 REGISEAHGT IAIQELTARF DWFYSCISNI KFYRLES DLN AQFIADGVYQ
101 AKQAF LQRVE QLRISL TEAG LSDEQINQVL EKQKFELESP NLKLN*
```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

m756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCCGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCGA AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCTGTC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

m756.pep

```

1 MTANFAQTLV EIQDSLRYRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGDML QDMPPKIRSA TLVALTTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVYPYGA E LVSDGNFTAV LSDIGD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

a756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCCGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTTGCGA AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCTGTC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

a756.pep

```

1 MTANFAQTLV EIQDSLXRVV STVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGDML QDMPPKIRSA TLVALTTLLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAESQERIT SAILKGARGA DVFQIGRRSY
151 SREDISEANR RAERVYPYGA E LVSDGNFTAV LSDIGD*
```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLXRVVSTVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

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```

              70      80      90      100      110      120
m756.pep      TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a756           TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD
              70      80      90      100      110      120

              130      140      150      160      170      180
m756.pep      RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVVPYGAELVSDGNFTAV
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a756           RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVVPYGAELVSDGNFTAV
              130      140      150      160      170      180

m756.pep      LSDIGDX
              |||||||
a756           LSDIGDX

```

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

```

m757.seq
1  ATGAAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51 TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTA AAAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAAATA AAGGGCTGAA TGACCAAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCGGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCGCAC AATGCTGCGT GATACCGCGG ACCAAATCGA AATGGCGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGTTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2596; ORF 757>:

```

m757.pep (lipoprotein)
1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51 AANKGLNDQK TGLTLPEHVV PIDNAEGKNL LHD FSDGLTI LTVDTDKADK
101 ITAVRVVWNT DAMPKAEKL SKAAAALIAA TAPEDRTMLR DTGDQIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPVS VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

```

m758.seq
1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51 TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAACCT GGTGGAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCG
151 GATTTGCGCG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCCGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451 CTGCTGGCGG CGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA

```


1232

This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151  LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1  ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101  AGGGCAAACCT GGTGGAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151  GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201  CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251  CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTTGCA CACGCCCCGC
301  CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351  CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401  TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTTGAA TCCGCCGACC
451  CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501  ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1  MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGEYGP
 51  DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101  RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151  LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

m758.pep	10	20	30	40	50	60
	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGEYGPDLAEVAAFHQ					
	10	20	30	40	50	60
m758.pep	70	80	90	100	110	120
	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAGSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAGSVGIGGSQT					
	70	80	90	100	110	120
m758.pep	130	140	150	160		
	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1  ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51  TCTTTTGGCC GTTCCCCTCG CTTACTCATC CATTGTCCGC AACGATGTCG
101  ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTCAACCGTA
151  GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201  GGTTCCTCAAC GGCAATCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251  CCGCCATCGC CACCCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301  AACGTCGGCT ACGGTTCCAT ACAATTCGGC AACGACACCC AAAATCCAGA
351  AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGACT
401  ACGACTACCA CCTTCCCCGC CTCAACAAAC TGGTTACCGA AATCTCACCT
```

451	ACCGCACTCA	GCAGCGTACC	CTTGCTTGGA	AACGGCCAGC	CAAAGGCCAA
501	TGCTTACCTC	GATACCGACC	GCTTCCCCTA	CTTTGTACGA	CTCGGCTCAG
551	GCACGCAACA	AGTCCGCAAA	GCAGACGGCA	CGCGTACACG	AACCGCCCCG
601	GCATACCAAT	ACCTGACCGG	CGGCACGCCG	CTGAAAGTAT	TGGGGTTCCA
651	AAACCACGGC	TTACTCGTCG	GCGGCAGCCT	GACCGACCAA	CCCCTTAACA
701	CCTACGCAAT	CGCCGGAGAC	AGCGGTTCCC	CCCTGTTTGC	CTTCGACAAG
751	CATGAAAACC	GCTGGGTGCT	TGCGGGCGTA	CTCAGCACCT	ACGCCGGCTT
801	CGATAATTTT	TTCAACAAAT	ACATCGTCAC	GCAACCCGAA	TTCATCCGTT
851	CCACCATCCG	CCAATACGAA	ACCCGGCTGG	ATGTCGGGCT	GACCACCAAC
901	GAATCATAT	GGCGCGACAA	CGGTAATGGC	AACAGCACCC	TGCAAGGGCT
951	CAACGAACGC	ATCACCTTGC	CCATTGCAAA	CCCTTCGCTT	GCCCCACAAA
1001	ACGACAGCAG	GCACATGCCG	TCTGAAGATG	CCGGCAAAAC	GCTCATCCTA
1051	TCCAGCAGGT	TCGACAACAA	AACACTGATG	CTGGCAGACA	ATATCAACCA
1101	AGGCGCAGGC	GCATTGCAGT	TCGACAGCAA	CTTCACCGTC	GTCGGTAAAA
1151	ACCACACATG	GCAAGGTGCA	GGCGTTATCG	TAGCCGACGG	CAAACGCGTC
1201	TTCTGGCAAG	TCAGCAACCC	CAAAGGCGAC	CGGCTCTCCA	AACTGGGCGC
1251	AGGCACGCTT	ATCGCCAACG	GACAAGGCAT	CAACCAGGGC	GACATCAGCA
1301	TCGGGGAAGG	CACTGTCGTA	CTCGCCCAAA	AAGCTGCTTC	AGACGGCAGC
1351	AAACAAGCAT	TCAACCAAGT	CGGCATCACC	AGCGGCAGGG	GCACGGCCGT
1401	CCTCGCCGAC	AGCCAGCAAA	TCAAACCCGA	AAACCTCTAT	TTGGGCTTCA
1451	GGGGCGGACG	GCTCGACCTC	AACGGCAACA	ACCTTGCCCT	TACCCATATC
1501	CGCCATGCGG	ACGGCGGCGC	GCAAATCGTC	AATCACAACC	CTGACCAAGC
1551	CGCGACACTG	ACGCTGACCG	GCAACCCCGT	CCTCAGTCCC	GAGCATGTCT
1601	AGTGGGTGCA	ATGGGGCAAC	CGTCCGCAAG	GCAACGCGGC	GGTTTACGAA
1651	TACATCAACC	CGCACCGBAA	CCGTGCGACC	GACTACTTCA	TACTCAAACC
1701	CGGCGGCAAC	CCGCGCGAAT	TTTTTCCGTT	AAATATGAAA	AACTCAACAA
1751	GCTGGCAATT	TATCGGCAAC	AACAGGCAAC	AGGCCGCCGA	ACAAGTCGCC
1801	CAAGCCGAAA	ATGCCCCGCC	CGACCTGATT	ACCTTCGGCG	GATACTTGGG
1851	TGAAAACGCG	CAAACGGGCA	AAGCCGCGCC	GAGTTACAGC	AAAACCAATG
1901	AAGCAGCCAT	AGAAAAAACC	CGCCATATCG	CAAATGCCGC	CGTATACGGC
1951	CGGCCCGAAT	ACCGTTACAA	CGGCGCACTC	AACCTGCACT	ATCGTCCCAA
2001	ACGCACCGAC	AGCACGCTGT	TGCTCAACGG	CGGCATGAAC	CTTAACGGGG
2051	AAGTCTTGAT	TGAGGGCGGC	AATATGATTG	TGTCAGGCAG	GCCCGTACCC
2101	CATGCCCTACG	ACCACCAGGC	CAAACGCGAA	CCCGTTCTTG	AAAACGAATG
2151	GACCGACGGC	AGCTTCAAGG	CTGCACGGTT	CACCCTGCGA	AACCATGCCC
2201	GACTGACGGC	AGGGCGCAAT	ACCGCGCATC	TGGACGGCGA	CATAACGCCA
2251	TACGATCTGT	CCGGCATCGA	CCTCGGCTTT	ACCCAAGGCA	AAACACCGGA
2301	ATGCTACCGC	TCCTACCATA	GCGGCAGCAC	CCACTGCACA	CCCAACGCCG
2351	TTTTAAAAGC	CGAAAACTAT	CGTGCACTAC	CTGCAACGCA	AGTACGCGGC
2401	GACATTACCC	TTAACGACCG	TTCAAGAGTC	CGCCTGGGCA	AAGCACACCT
2451	GTACGGCAGC	ATCCGTGCCG	GCAAAGACAC	CGCAGTCCGC	ATGGAAGCAG
2501	ACAGCAACTG	GACACTTTCC	CAGTCCAGCC	ACACCGGCGC	ACTGACGCTT
2551	GACGGCGCAC	AAATTACCCT	GAACCCCGAT	TTCCGCAATA	ATACACACAA
2601	CAACCGCTTC	AACACACTGA	CCGTCAACGG	CACACTTGAC	GGGTTCGGCA
2651	CATTCCGATT	CCTGACCGGC	ATCGTCCGAA	AACAAAATGC	CCCCCCCCTC
2701	AAACTGGAAG	GGGACAGCCG	CGGCGCATT	CAAATCCACG	TCAAAAACAC
2751	CGGACAAGAA	CCTCAAACAA	CCGAATCGCT	TGCACTTGTT	AGCCTCAATC
2801	CGAAACACAG	CCACCAAGCC	CGATTACACC	TCCAAAACGG	CTATGCCGAT
2851	TTGGGTGCCT	ACCGCTACAT	CCTCCGCAAA	AACAACAACG	GATACAGCCT
2901	GTACAACCCG	CTCAAAGAGG	CCGAACCTCA	AATTGAAGCC	ACGCGTGCGG
2951	AACATGAGCG	CAACCAACAG	GCATACAACC	AATTACAGGC	AACCGACATC
3001	AGCAGACAGG	TTCAACATGA	CTCTGACGCG	ACCAGGCAGG	CACTACAGGC
3051	CTGGCAGAAC	AGTCAAACCG	AACTTGCCCG	CATCGACAGC	CAAGTCCAAT
3101	ATCTGTCCGC	CCAATTGAAA	CAGACAGACC	CGCTGACCGG	CATTCTGACG
3151	CGTGCCCAAA	ACCTGTGTGC	CGCACAAGGA	TACAGTGCCG	ATATCTGCCG
3201	TCAGGTTGCC	AAAGCCGCCG	ACACGAACGA	CCTGACACTC	TTCGAAACCG
3251	AACTGGATAC	GTATATAGAA	CGTGTAGAAA	TGGCCGAATC	CGAACTTGAC
3301	AAAGCACGGC	AAGGCGGCGA	TGCGCAAGCC	GTCGAAACAG	CCCGGCACGC
3351	CTACCTGAAC	GCACTCAACC	GTCTGTCCCG	ACAAATCCAC	AGTTTGAAAA
3401	CCGGCGTTGC	CGGCATCCGT	ATGCCGAACC	TGGCCGAATC	GATCAGCCGG
3451	TCGGCCAACA	CCGCCGTTTC	CGAACAGGCC	GCCTACAATA	CCGGCCGGCA
3501	ACAGGCGGGA	CGCCGCATCG	ACCGCCACCT	TACCGATCCG	CAGCAGCAAA
3551	ACATCTGGCT	GGAAACCGGT	ACGCAACAAA	CCGACTACCA	TAGCGGCACA
3601	CACCGTCCCT	ACCAACAAAC	TACCAACTAT	GCACATATCG	GCATCCAAAC
3651	CGGCATCACC	GACCGTCTCA	GTGTCGGTAC	GATTTTAAAC	GATGAGCGCA
3701	CAAACAACCG	TTTTGATGAA	GGCGTATCCG	CCCGAAACCG	CAGCAACGGC

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3751 GCACATCTGT TCGTCAAAGG GGAAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CCGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCGCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCGG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCGCCAC AACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

```

m759.pep
  1 MRFTHTFPC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
 51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQY YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDREFPYFVR LSGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLFAFDK
251 HENRWVLAVG LSTYAGFDNF FNKYIVTQPE FIRSTIRQYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNDNRHMP SEDAGKTLLI
351 SSREFDNKTL LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAGTL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGGRDL NGNNLAFTHI
501 RHADGGAQIV NHNPDAQATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHNRNRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLNNGGMN LNGEVLIEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENEWTDG SFKAARFTLR NHARLTAGRN TAHLDGDITA
751 YDLSGIDLGF TQGTPECYR SYHSGSTHCT PNAVLAENY RALPATQVRG
801 DITLNRSEL RLGAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALT
851 DGAQITLNPD FANNTHNRF NTLTVNGTLD GFGTFRELTG IVRKQNAAPL
901 KLEGDSRGAF QIHVKNTGQE PQTTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQO AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCQAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEIISR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQQT DYHSGT
1201 HRPYQQTNY AHIGIQTGIT DRLSVGTILT DERTNNRFDE GVSARNRNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRSNGN RYVLDGAEIN SPAQIQTWH AGIRLDKTV
1351 LGQAKLTAPF SSDYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

```

g760.seq (partial)
  1 AACAACCGCA ACACCCGTTA CGCCGCATTG GGCAAACCGG TGATGGAAGG
 51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCG GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGACGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCC GGTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

```

g760.pep (partial)
  1 NNRNTRYAAL GKRVMGVET EISGAITPKW QIHAGYSYLH SQIKTAANPR
 51 DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

1235

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

```
m760.seq
1   ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51  TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCCGGCCTGC GCGTGTTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGGCCTG CCCGCGCAGA
401 TGCAGAGTAT CAACGGCACG CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACC GGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGTTTTTG
751 GGCGCGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCCT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTAAAATGC ACAGCCACGA CGTGTTCCGC
901 GATTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCCGAT CGGAAAGCCG ATTCCAATTA TACGTTTGGG GGCAGCAAA
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAAGCCT TTGCGGTTGA CGCAAGTTAC AGCCGTCGGT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCCGA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAAGCGT CGCTTTAGAT
1201 GGTTTCCGCG CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCTC TGGAAGGTTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GGCGCGGTTT
1451 AACTATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCCTC CCAACTTAC
1501 ACACCGCAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACC GC CGCA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCCG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAAACCGT TACGCCGCAT TGGGCAAAAC
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAATCCA TGCAGGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTTCG GCGACGAAGG CATCTTCCTG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAGGC
1951 GGTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAACT
2001 GAAGCTGCAA ATCAACGCCG ACAACATCTT CAACCGCCAT TACTACGCCC
2051 GCGTCGGCAG CGAGAGCACC TTAAACATTC CCGGTTCCGA GCGCAGCTG
2101 ACGGCAAACC TCGGTTACAG TTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

```
m760.pep
1   MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKQ QRSYNAIATE
51  KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQVQKDRNV DTFDQLARKT
101 PGLRVLNSDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAEAD
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQQR LAPPYNGLPAD ANNKLPSLPQ HVFVGADWNK FKMHS HDVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNYTFA GSKLNNTGQA DVAGLGTDIK
351 QKAFAVDASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSKVALD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTKFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTP KKLKQ INADNIFNRH YYARVGSEST FNIPGSESRSL
701 TANLRYSF*
```

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m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760.pep	YKGSYMDRLNTRV	SFYRMKDKNAA	PLDSNNKKTRYA	ALGKRVMEGVETE	ISGAMTPKW	
				:		
g760				NNRNTRYAALGKRV	MEGVETEISGAIT	PKW
				10	20	30

	590	600	610	620	630	640
m760.pep	QIHAGYSYLHSQIK	TASNSRDEGIFLL	MPKHSANLWTTYQ	VTSGLTIGGGVNA	MSGITSS	
g760	QIHAGYSYLHSQIK	TAAANPRDDGIFL	LVPKHSANLWTTY	QVTPGLTVGGGVN	AMSGITSS	
	40	50	60	70	80	90

	650	660	670	680	690	700
m760.pep	AGIHAGGYATFDAMA	AYRFTPKLKLQIN	ADNIFNRHYYARV	GSESTFNIPGSE	RSLSLTANL	
g760	AGMHAGGYATFDAMA	AYRFTPKLKLQIN	ADNIFNRHYYARV	GGTNTFNIPGSE	RSLSLTANL	
	100	110	120	130	140	150

	709
m760.pep	RYSFX
g760	RYSFX

g761.seq not found yet

g761.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761.seq

1	ATGAAAATAT	CATTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCCGACAC	CAGCGTACTC
151	AAAGGCTACA	TCAACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTTTCC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGGCGTGC GC	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAAACG	TCGCCATCCG	TCTCACCGGC	GAAGTCGGGC	GCGCCAATTTC
651	GTTCCGCAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATTA
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCCG	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGACTG	CCTTACCGCA	TGGGGTTCGC	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAAC
1001	ACGCCTGGCA	GCAGACCGAG	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTGA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCGATTTC	AAATTCGTCC
1301	TCGGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACCTACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCCGCGG	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGGCGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCTTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCGACCG AAAACCTCTA CGGCGAAATC GGCGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAATCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTAAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m761.pep
  1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
 51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVS K YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVYDRFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLT L
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPAPYG RGGYLSIDTL
501 SSAVFNADPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a761.seq
  1 ATGAAAATAT CATTTCATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
 51 CTTCCCTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGCAA AGCATTTTCC TGCGCGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCTCCG TGCTTTATGG GCGTACCAAC GCGGCGGTG TCATCAACAT
501 GGTACGAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCGTG GGCAAACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTACCGGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAACG CGACAACGGC TTGAAGTGGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCGGACTG CTTACCGCA TGGGGTTTCG CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCCAATGGCA GCTCGCCAC CGCACGGCGG CGCAGGATTT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC
1001 ACGCTGGCA GCAGACCGAC AACAAAACCC TGTCGTCAA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTGTAA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGGAACACC GCAACCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CAAAACCGC CACAAAGCCG ACTCCTACGG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCCCGATTG AAATTCGTCC
1301 TCGGCGGCCG TTACGACAAA TACACCTTTA ATTCGGAAAA CAACTCACC
1351 GGCAGCAGC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCCG TCCACACACT TTACGCCTCG TATAACAAAG
1451 GCTTCGCGCC TTATGGCGGA CGCGGCGGCT ATTTGAGCAT CGATACGTTG
1501 TCTTCGCGCG GTTCAACGC CGACCCCGAG TACACCCGCC AATACGAAAC
1551 CGGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CTAACCAAT CGAACGCTT AATATCCGCT ACCGCCCGCA TCCAAAAAAC
1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCG GCGGCGTGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCGTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
1  MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
51  KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVS K YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYRFLG PYRMGFARND FVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTD NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KEVLGGRYDK YTFENSENKL
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFAFYGG RGGYLSIDTL
501 SSAFVNADPE YTRQYETGVK SSWLDLRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRSLGVMQA KVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLFNQ KYWRSDSMGP NPRGYTARVN
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

	10	20	30	40	50	60
m761.pep	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m761.pep	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m761.pep	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVS KYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVS KYANFKQSRNI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m761.pep	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNMVSPSITVKLDNG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m761.pep	LKWTGQYTYDNVERTPDRSPTKSVDYRFLGPYRMGFARND FVKDKLQVW RSDLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPTKSVDYRFLGPYRMGFARND FVKDKLQVW RSDLEYAFND					
	250	260	270	280	290	300
	310	320	330	340	350	360
m761.pep	KWRAQWQLAHRTAAQDFDHFYAGSENGNLIK RNYAQQTDNKTLSNLTNLNGDYTIGRFE					
a761	KWRAQWQLAHRTAAQDFDHFYAGSENGNLIK RNYAQQTDNKTLSNLTNLNGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

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```

m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRQLQILTQNRHKADSYGIFV
          |||||||
a761      NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRQLQILTQNRHKADSYGIFV
          370      380      390      400      410      420

          430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
          |||||||
a761      QNIFSATPDLKFVLGGRYDKYTFNSENKLTGSSRQYSGHSFSPNIGAVWNINPVHTLYAS
          430      440      450      460      470      480

          490      500      510      520      530      540
m761.pep  YNKGFPYGGRRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
          |||||||
a761      YNKGFPYGGRRGGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDDRLSTTLSAYQIERF
          490      500      510      520      530      540

          550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
          |||||||
a761      NIRYRPDPKNNPYIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
          550      560      570      580      590      600

          610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYNSRNKEVTTLPGFARVDAM
          |||||||
a761      RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
          610      620      630      640      650      660

          670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
          |||||||
a761      LGWNHKNVNVTFAAANLLNQKYWRSDSMPGNPRGYTARVNYRFX
          670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTCT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LFLLFIFNEF TKSIYMAIIY PILYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLVSNF ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTTTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

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301 AGTTTATGG ACTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCT
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

a762.pep

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
 51 LFLLFIFNFV TKSIYMAIIY PILYFFTICK YYPYSRKVII LLSLALSIYF
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762.pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLFLLFIFNFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762.pep	TKSIYMAIIYPILYFFTICKYYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFFTICKYYYPYSRKVIIILSLALSIYFSFMDFYFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762.pep	PLHLYIPIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIINFFSLLVSNFILSFINKX					
	130	140				

g763.seq not yet found

g763.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

m763.seq

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
 201 GGCGCAGCAA CATTCCGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG
 251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCCATGTA
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCG CCATCGATT CTTCCACCCG
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
 601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAG CCGGTTACGA
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
 701 AAAACCAATT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
 1201 TTGGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCC
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAAACGG TATTTGCGGA
 1401 ATAA

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763.pep

```

1  MTLNLNMIMO DYGISVCLTL TPYLQHELF SAMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEI AVLAEK QTYENQLNDY TDLD SKQIEA
251 IDTANLLARY LPKLERYS LD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763.seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTGCCACTA
151 TCCTTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGGGCTG ATTTTCAAGC GTCCCATTA CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGATTTCCT TCCCCATGTA
301 TCCGCCAATG CCAGTACCA GCGCCAGCCG CCATCGATT TTTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAACCTTA TTTGACGTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG
551 AAAAGAGAGC TTATGCCAG CAGSTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACAGTGT GAACGACTAC ACCGGCCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGTAT CTGCCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCCAC CGTTTCTGCC CATGTGCGCT ATCAGAATAA
951 CCTTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGAAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGCTGG AAGTAATACG GCGCGGCGAG GAAGTCGCC
1301 AAGCAGAACA GAAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGAAACGG TATTTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763.pep

```

1  MTLNLNMIMO DYGISVCLTL TPYLQHELF SAMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFQASHY QRDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYA QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEI AVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYS LD EWQRIALSNN HEYRMQQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKGMSVGVQ LNLPLYTGGE
351 LSGKIHEAEA QYGAAEAQLT ATERHIKLA V RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQQYGIR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

          10      20      30      40      50      60
m763.pep  MTLNLNMIMQDYGISVCLTLTPYLQHELF SAMKSYFSKYI LPVSLFTLPLSLSPSVSAFT
          |||
a763      MTLNLNMIMQDYGISVCLTLTPYLQHELF SAMKSYFSKYI LPVSLFTLPLSLSPSVSAFT
          10      20      30      40      50      60

```

1242

	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFOASHYQRDAVRARQQQAKAAFLPHVSANASYQRQPPSISSTRETQ					
a763	LPEAWRAAQHSADFOASHYQRDAVRARQQQAKAAFLPHVSANASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEIIVLAEKQTYENQLNDY					
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEIIVLAEKQTYENQLNDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TDLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQALQSSGQALRAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNLYTSSAQNNDYHYRGKGMSVGVQLNLPLYTGELSGKIHEAEA					
a763	QNSRYPTVSAHVGYNLYTSSAQNNDYHYRGKGMSVGVQLNLPLYTGELSGKIHEAEA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAQAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

1243

g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

```
m764.seq
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTA CTGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCA GTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GGCGTTTTTG CCCGCGCATT TGGAAC TGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GGCGGCGCGT TTTATTATGG CGTTTGC GCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GGCGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGG GGCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CCGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCCG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAAA
1351 ACGGGTAAAC GGCGGGTGCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG
```

This corresponds to the amino acid sequence <SEQ ID 2620; ORF 764>:

```
m764.pep
1  MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEQAF LPAHLELDT P
51  VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKT VS GGRSKTIQPL
101 ETAVVKAVHV RDQHV KQGE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVS VGAIE QKKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWN DLESTRG QMRQIQAAIA QAEQNRV LNT QNLKRD LDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVKIESF PYTRYGYLTG
401 KVKSVSHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTA EIK
451 TGKRRVLDYL LSPLQTKLDE SFRER*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

```
a764.seq (partial)
1  ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51  GCGCAATGTT TGGGCGGTGC GCGACCA GTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GGCGTTTTTG CCCGCGCATT TGGAAC TGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GGCGGCGCGT TTTATTATGG CGTTTGC GCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTCCGGCAA AACGGTGTCT GGCGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CGCGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GGCGCAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CGGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GGCGCAGGAG CAGAAGCTGG TTTCGGTGGG GGCGATCGAG CAGCAGAAAA
```

1244

```

701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTGAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

a764.pep (partial)

```

1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAFLE PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVQKQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QQKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

m764.pep	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
a764	10	20	30	40	50	60
	MFFSALKSFLSRYITVWRNVWAVRDQLEPPKRTAEQAFLEPAHLELTDTPVSAAPKWAAR					
m764.pep	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVVKAVHVRDQHVQKQE					
a764	70	80	90	100	110	120
	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVVKAVHVRDQHVQKQE					
m764.pep	130	140	150	160	170	180
	TLAELEAVGTDSDDVVQSEQALQAAQLSKRLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
a764	130	140	150	160	170	180
	TLAELEAVGTDSDDVVQSEQALQAAQLSKRLRYEAVLAALESRTVPHIDMAQARSLGLSDAD					
m764.pep	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAEQSAKAQEQLKLSVGAIEQQKTADYRRL					
a764	190	200	210	220	230	240
	VQSAQVLAQHQQYQAWAAQDAQLQSAALRGHQAEQSAKAQEQLKLSVGAIEQQKTADYRRL					
m764.pep	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
a764	250	260	270	280	290	300
	RADNFISEHAFLEQQSKSVSNWNLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
m764.pep	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVIAPDD					
a764	310	320	330	340	350	360
	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
m764.pep	370	380	390	400	410	420
	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT					

1245

```

a764      |||||
          DKMDVEVLVLNKDIGFVEQGQDAVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
          370      380      390      400      410      420

          430      440      450      460      470
m764.pep  AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
          |||||
a764      AVVSLDKHTLNIDGK
          430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTTG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTACGG TCGTTGCTGA TGTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAAGATT ATATGAAAC GGTGAGTTA AACAAAGTCTG
251 CCGGCAATGT CGATAACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTCAGG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2624; ORF 765>:

```

m765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG
51  ACAVVADVYG HDSATMNAAA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDDEIAAI MGHEMTHALH EHGKKNVGQQ ILTNTAAQIG TQIILDKKPD
201 TNPVLVGLGM DILGTYGLTL PYSRSLEEEA DEGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITS THPTNNARIE NLKRLLPVLM PVYEQSVRNK
301 GRVNKKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTTG GATTCAGACG GCATTTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTCGG CAGTAATCTC GGTATTGGGG
151 GCTTGTACGG TCGTTGCTGA TGTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCGAAGATT ATATGAAAC GGTGAGTTG AACAAAGTCTG
251 CCGGCAATGT CGATACTACA TCCAAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCGGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACGCGTGGG
401 CAATGCCCGG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAACTT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGA AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGTGTACAG
751 GTTTGGGAAA AAATGAATCA GGAACACGAC CAAACCGGCT TTATTTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2626; ORF 765.a>:

```

a765.pep
1  MLRCRPKSVL DSDGIFLKFN FLRSKPKYEI SFLPSFKRIL CLSAVISVLG

```

1246

```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FRRMLPYADA ANNTGHHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTGGEIAAI MGHMETHALH EHGKKNVGOK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSLSEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAITs THPTNNARIE NLKRLLPVTM PVYEHsVRNK
301 GRVKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

```

              10      20      30      40      50      60
m765.pep      MLRCRPKSVLSDSGIFLKFNFLRSKPKEISFLPSFKRILCLSAVISVLGACAVVADVYG
              |||||
a765           MLRCRPKSVLSDSGIFLKFNFLRSKPKEISFLPSFKRILCLSAVISVLGACTVVADVYG
              10      20      30      40      50      60

              70      80      90      100     110     120
m765.pep      HDSATMNAAAAKDYMKTVELNKSAGNVDTTsRTARRVQAVFRRMLPYADAANNTSHKFDW
              :|||
a765           QDSATMNAAAAKDYMKTVELNKSAGNVDTTsRTARRVQAVFRRMLPYADAANNTGHKFDW
              70      80      90      100     110     120

              130     140     150     160     170     180
m765.pep      KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDDEIAAIMGHEMTHALHEHGKNKVGQQ
              |||||
a765           KMTVFKNDELNAWAMPGGKMAFYTGIVDKLKLTDGEIAAIMGHEMTHALHEHGKNKVGQK
              130     140     150     160     170     180

              190     200     210     220     230     240
m765.pep      ILTNAAQIGTQIILDKKPDNTPELVGLGMDILGTGTLTPYSRSLSEEADEGGMMLMAQ
              |||
a765           ILTNAAQIGTQIILDKKPDNTPELVGLGMDILGMYGITLTPYSRSLSEEADEGGMMLMAQ
              190     200     210     220     230     240

              250     260     270     280     290     300
m765.pep      AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVTMPVYEQSVRNK
              |||||
a765           AGYHPAAAVRVWEKMNQENDQNGFIYAITSTHPTNNARIENLKRLLPVTMPVYEHsVRNK
              250     260     270     280     290     300

              310
m765.pep      GRVKNKRRRX
              |||||
a765           GRVKNKRRRX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

g767.seq

```

1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTTGGCG TACATTGCCA TCATTTTCGAT CCTTTGTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTACGAACA
351 AAAATCCGT TTGGAAAACA GGGCTGTTCG CGGGAAATGG GCTTTATCTC
401 AAAAAGGTTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCCCAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

g767.pep

```

1  MKFKHLPLLL LSAVLSAQAY ALTEGEDYLV LDKPIPEQP GKIEVLEFFG
51  YFCVHCHHFD PLLKLKAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANS AV FKA VYE QKIR LENRAVAGKW ALSQKGF DKG KLMRAYDSPE
 151 AAAVALKMQK LTEQY GIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq

```

1  ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCA AGAACAGTCG GGTAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAACTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGGAACA GGTCTGGTTC CGGAAATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCCTATGA TTCCCCGAA
451 GCTGCCGCCG CCGCATTA AATGCAGAAA CTGACGGAAC AATACCGCAT
501 CGACAGACG CGACCGTTA TTGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep

```

1  MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQS GKIEVLEFFG
51  YFCVHCHHFD PLLKLGLKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVNLS
101 GLKYQANPAV FKA VYE QKIR LENRSVAGKW ALSQKGF DKG KLMRAYDSPE
151 AAAAALKMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL SAVLSAQAYALTEGEDYLV LDKPIPQEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
g767.pep	PLLLKLGKALPSDYLRTHEV VVWRPEMLGLARMAAAVKLSGLKYQANS AVFKAVYE QKIR					
m767	PLLLKLGKALPSDYLRTHEV VVWQPEMLGLARMAAAVNLSGLKYQANPAV FKA VYE QKIR					
	70	80	90	100	110	120
g767.pep	LENRAVAGKW ALSQKGF DKG KLMRAYDSPE AAAVALKMQK LTEQY GIDST PTVIVGGKYR					
m767	LENRSVAGKW ALSQKGF DKG KLMRAYDSPE AAAAALKMQK LTEQY RIDST PTVIVGGKYR					
	130	140	150	160	170	180
g767.pep	VIFNNGFDGG VHTIKELVAK VREERKRQTP AVQKX					
m767	VIFNNGFDGG VHTIKELVAK VREERKRQTP AVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq

```

1  ATGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCA AGAACAGTCG GGCAAAATTG AGGTTTGGGA ATTTTTCGGC
151 TATTTCTGCG TACATTGCCA TCATTTTCGAT CCTTTGTTAT TGAAATTGGG
201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC
251 AGCCTGAAAT GCTCGGTCG GCAAGAAATGG CTGCTGCGGT CAAGCTGTCA
301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTAAAGCAG TTTACGAACA
351 AAAAATCCGC TTGGAACA GGTCTGGTTC CGAAATATGG GCTTTGTCTC
401 AAAAAGGCTT TGACGGCAAA AACTGATGC GCGCCTACGA CTCTCTGCG

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```

451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAATGGCTT TGACGGCGGT GTTCATACGA TTAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
  1 MKLKHLPLLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQKS GKIEVLEFFG
  51 YFCVHCHHFD PLLKLKGKAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
 101 GLKYQANPAV FKAUYEQKIR LENRSVAEKW ALSQKGFDDG KLMRAYDSPA
 151 AAAAASKMQQ LTEQYRIDST PTVVVGKYYR VIFNNGFDGG VHTIKELVAK
 201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

	10	20	30	40	50	60
a767.pep	MKLKHLPLLLSAVLSAQAYALTEGEDYLVLDKPIPKQSGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLPLLLSAVLSAQAYALTEGEDYLVLDKPIPEQSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
a767.pep	70	80	90	100	110	120
	PLLLKLKGKALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEKIR					
m767	PLLLKLKGKALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEKIR					
	70	80	90	100	110	120
a767.pep	130	140	150	160	170	180
	LENRSVAEKWALSQKGFDDGKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKYYR					
m767	LENRSVAGKWALSQKGFDDGKLMRAYDSPEAAAAALKMQKLTEQYRIDSTPTVIVVGKYYR					
	130	140	150	160	170	180
a767.pep	190	200	210			
	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
  1 ATGAATATCA AACAATTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
  51 TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATTGATC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATATACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
  1 MNIKOLITAA LIASAAFATQ AAPQKPVSAQ QTAQHSVWI DVRSEQEFSE
  51 GHLHNAVNIQ VDQIVRRIYE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
  1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
  51 TGCCGCGCAG GCAGCCCGCG AAAAACCCTG ATCCGCGGCC CAAACCGCGC
 101 AACATCCGGC CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
 151 GGGCATTGTC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCCG
 201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNI VDIQVRIHE AAPDKDPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAA	PQKPVSAQAQHS	AVWIDVRSE	QEFSEGLHNAVNI	P	
m768	MNIKHLITAAALIASAAFAAQ	AAPQKPVSAQAQHS	AVWIDVRSE	QEFSEGLHNAVNI	P	
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	VDQIVRRIYEAAPDKDTPVN	LYCRSGRRAEALQELKKAG	YTNVANHGGYEDLLKGMKX			
m768	VDQIVRRIHEAAPDKDTPVN	LYCRSGRRAEALQELKKAG	YTNVANHGGYEDLLKGMKX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
 51 TGCCGCGCAG GCAGCCCCGC AAAAACCCTG ATCCGCGGCC CAAACGCGC
 101 AACATTCAGC CGTTTGGATC GATGTCCGCA GCGAACAGGA ATTTAGCGAA
 151 GGTCAATTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
 201 CATACACGAA GCCGCGCCCG ACAAAGACAC GCCGGTCAAC CTCTACTGCC
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTC AAGAACTGAA AAAAGCAGGC
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE
 51 GHLHNAVNI VDIQVRIHE AAPDKDPVN LYCRSGRRAE AALQELKKAG
 101 YTNVANHGGY EDLLKGMK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAAALIASAAFAAQ	AAPQKPVSAQAQHS	AVWIDVRSE	QEFSEGLHNAVNI	P	
m768	MNIKHLITAAALIASAAFAAQ	AAPQKPVSAQAQHS	AVWIDVRSE	QEFSEGLHNAVNI	P	
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	VDQIVRRIHEAAPDKDTPVN	LYCRSGRRAEALQELKKAG	YTNVANHGGYEDLLKGMKX			
m768	VDQIVRRIHEAAPDKDTPVN	LYCRSGRRAEALQELKKAG	YTNVANHGGYEDLLKGMKX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTATTATT TGTGGGAAGA CATTATGCC
51  TGCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 CCGAAGaAAC ACCgtgCGAA CCGGATTTGA GAAGCCGTCC CGAGTTCAGG
151 CTTTATGAAG CGGAGGTCAA ACCGATCGAC AGGGAAGAAG TACCGGGGCA
201 GGTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 AAAATCCCGA ATTGTTGTCT CGTGCCATGT ATTCCGCAGT GGTCTCAAAC
301 AATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 GCAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 AGGGCAGGGT GAAGGAGGCG GTTCCCATTT ACCGGGAATT GATTGCCGCC
451 CAACCCGACG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 AGACAGGCAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 AAGATCTGCC GCCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 TTGCGCGAAC GCGATGCGTG GAAGGTAAAC GCGGGTTTCA GCGTTACCCG
651 CGAACACAAT ATCAACCAAG CCCCAGAAAC GCAGCAGTAC GGCAATTGGA
701 CTTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 GAGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACGG CGGGCGGCGA
801 CGTGTCGGGC AGGGTTTATC CGGGGAATAA GAAATTCAAC GATATGACGG
851 CAGGTGTTTC CGCGGGCATC GGTTTTGCCG ACCGGCGTAA AGATGTCGGG
901 CTGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 CGCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 AAACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC GCGCCGGGCG
1051 CGTTCCGACA ATACCCATTG GCAAATTTCC AATTGCTGGG TGTTTTACCG
1101 GAATGCGCGC CAATATTGGA CGGGCGGTTT GGATTTTAC CCGGAGCGCA
1151 ACCCCGCCGA CCGTGGCGAC AATTTCAACC GTTACGGCCT GCGCTTTGCC
1201 TGGGGCGCAG AATGGGGCGG CAGCGGCCTG TCTTCGCTGT TCCGCCTCGG
1251 CGTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTTCAGC AGTTTTAAAG
1301 GGGAAAGGCG CAGGGATAAA GAATCGGACA CATCCTTGAG CCTTTGGCAC
1351 CGGCAATTGC ATTTCAAAGG CATCACGCCG CGCTGACGC TGTGCAACCG
1401 CGAAACGTGG AGCAACGATG TGTTTAACGA ATACGAGAAA AACAGGGCGT
1451 TTGTCGAGTT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1   LIMVIFYFYF CGKTFMPARN RWMLLPLLAS AAYAEETPCE PDLRSRPEFR
51  LHEAEVKPID REKVPQVRE KGVVLQVDGE TLLKNPELLS RAMYSAVSVN
101 NIAGIRVILP IYLQARQDK MLALYAQGIL AQAEGRVKEA VSHYRELIAA
151 QPDAPAVRMR LAAALFEDRQ NEAAADQFDR LKTEDLPPQL MEQVELYRKA
201 LRERDAWKVN GGFSVTREHN INQAPKQQY GNWTFPKQVD GTAVNYRFGA
251 EKKWSLKNWV YTTAGGDVSG RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 LAVFHERRTY GNDAYSANG ARLYFNRWQT PRWQTLSSAE WGRLLKNTRRA
351 RSDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 WGEWGGGSL SSLFRLGVAK RHYEKPFFS SFGERRRDK ESDTSLSLWH
451 RALHFKGITP RLTLSHRETW SNOVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1   TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
201 GCGGGA AAAA GGAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGCGC CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTAAC GGAATTGAT TGCCGCCCAA
451 CCGGACGCGC CCGCGTCCG TATGCGTTTG GCGGCAGCAT TGTGTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCG CAGCTGATG GAGCAGGTGC AGCTGTACCG CAAGGCATTG
601 CGCGAACGCG ATGCGTGGAA GGTAATGGC GGCTTCAGCG TCACCCGCGA
651 ACACAATATC AACCAGCCG CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GTTGACGCGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CCGCTGGTAC ACGACGGCGG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CCGCATCGGT TTTGCCGACC GCGCGAAAGA TGCCGGGCTG
901 GCAGTGTTCC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCTTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGCG CCGGGCGCGT
1051 TCGGACAATA CCAATTGCA AATTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TCGCGGCCAA TATTGGATGG GCGGTTTGGG TTTTACCAGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC

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1251

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1251  GGCGAAACGG  CATTATGAAA  AACCCGGCTT  TTTCAGCGGT  TTAAAGGGG
1301  AAAGGCGCAG  GGATAAGAA  TTGAACACAT  CCTTGAGCCT  TTGGCACCAG
1351  GCATTGCATT  TCAAAGGCAT  CACGCCGCGC  CTGACGTTGT  CGCACCGCCA
1401  AACGCGGAGT  AACGATGTGT  TCAACGAATA  CGAGAAAAAT  CGGGCGTTTG
1451  TCGAGTTTAA  TAAACGTTC  TGA

```

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

m769.pep

```

1  LIMVIFYFCG  KTFMPARNRW  MLLLPLLSA  AYAETPREP  DLRSRPEFRL
51  HEAEVKPIDR  EKVPQVREK  GKVLQIDGET  LLKNPELLSR  AMYSAVVSNN
101 IAGIRVILPI  YLQQAQQDKM  LALYAQGILA  QADGRVKEAI  SHYRELIAAQ
151 PDAPAVRMRL  AAALFENRQN  EAAADQFDRL  KAENLPPQLM  EQVELYRKAL
201 RERDAWKVNG  GFSVTRHNI  NQAPKRQQYG  KWTFFPKQVDG  TAVNYRLGAE
251 KKWSLKNWY  TTAGGDVSGR  VYPGNKKFND  MTAGVSGGIG  FADRRKDAGL
301 AVFHERRTYG  NDAYSYTNGA  RLYFNWQTP  KWQTLSSAEW  GRLKNTRRAR
351 SDNTHLQISN  SLVFYRNARQ  YWMGGLDFYR  ERNPADRGDN  FNRGLRFAW
401 GQEWGGGSL  SLLRLGAAKR  HYEKPGFFSG  FKGERRRDKE  LNTSLSLWHR
451 ALHFKGITPR  LTLSHRETRS  NDVFNEYEKN  RAFVEFNKTF  *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

```

g769.pep      10      20      30      40      50      59
LIMVIFYFYFCGKTFMPARNRWMLL-PLLSAAYAETPCPEDLRSRPEFRLHEAEVKPI
|||||
m769          10      20      30      40      50
LIMVIFY--FCGKTFMPARNRWMLLPLLSAAYAETPREPDLRSRPEFRLHEAEVKPI

g769.pep      60      70      80      90     100     110     119
DREKVPQGVREKGVQLQVDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQD
|||||
m769          60      70      80      90     100     110
DREKVPQGVREKGVQLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQD

g769.pep     120     130     140     150     160     170     179
KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAAALFEDRQNEAADQFD
|||||
m769          120     130     140     150     160     170
KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAADQFD

g769.pep     180     190     200     210     220     230     239
RLKTEDLPQLMEQVELYRKALRERDAWKVNGGFSVTRHNNINQAPKQQYGNWTFPKQV
|||||
m769          180     190     200     210     220     230
RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNNINQAPKRQQYKWTFFPKQV

g769.pep     240     250     260     270     280     290     299
DGTAVNYRFGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV
|||||
m769          240     250     260     270     280     290
DGTAVNYRLGAEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA

g769.pep     300     310     320     330     340     350     359
GLAVFHERRTYGNDAYSANGARLYFNWQTPRWQTLSSAEWGRGLKNTRRARSNDNTHLQI
|||||
m769          300     310     320     330     340     350
GLAVFHERRTYGNDAYSYTNGARLYFNWQTPKWQTLSSAEWGRGLKNTRRARSNDNTHLQI

g769.pep     360     370     380     390     400     410     419
SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWQEWGGGSLSSLFRLGVA
|||||
m769          360     370     380     390     400     410
SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWQEWGGGSLSSLRLGAA

g769.pep     420     430     440     450     460     470     479
KRHYEKPGEFFSFKGERRRDKESDTSLSLWHRALHFKGITPRLTLSHRETWSNDVFNEYE
|||||

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1252

```

m769      KRHYEKPGFSSGFKGERRRDKE LNTSLSLWHRALHFKGITPR LTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep  KNRA FVEFNKTFX
          |||||
m769      KNRA FVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AACACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAGAAACACCC GCGCGAACC GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGGCAGGT
201 GCGGGAAAAA GGAAGTTT TGCAGATTGA CGGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGTGCGCCAA
451 CCCGACGCGC CCGCCGTCG TATGCGTTTG GCGCGGCGAT TGTGAAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCCTG AAGGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAAGCGG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGGCGG CCGGCGACGT
801 GTCCGCGAGG GTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCCTTTCCGG CCGCATCGGT TTTGCCGACC GCGCGAAAGA TGCGGGGCTG
901 GCAGTGTTC ACGAACGCC CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA GCCTTTTATT TCAACCGTTG GCAAACCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACGGC CCGGGCGCGT
1051 TCCGACAATA CCCATTGCA AATTTCCAAT TCCTGGTGT TTTACCGGAA
1101 TCGCGGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACCGTT ACGGCCTGCG CTTTGCCTGG
1201 GGGCAGGAAT GGGGCGGCG CCGCCTGTCT TCCTGTTGC GCCTCGGCGC
1251 GGGGAAACGG CATTATGAAA AACCCGGCTT TTTAGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCGCGA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CCGGCGTTTG
1451 TCGAGTTTAA TAAACGTTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKRQYQG KWTFFPKQVDG TAVNYRLGAE
251 KKWSLKNGWY TTAGGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRYTG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GR LKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 GQEWGSGSL SLLRLGA AKR HYEKP GFSSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDFNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

m769/a769 99.8% identity in 490 aa overlap

```

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQVREKGKVLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

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1253

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|||||
m769      EKVPGQVREKGVQLIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
              70      80      90      100     110     120

              130      140      150      160      170      180
a769.pep   LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
|||||
m769      LALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
              130      140      150      160      170      180

              190      200      210      220      230      240
a769.pep   KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQQYGKWTFFPKQVDG
|||||
m769      KAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQQYGKWTFFPKQVDG
              190      200      210      220      230      240

              250      260      270      280      290      300
a769.pep   TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
|||||
m769      TAVNYRLGAEEKKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
              250      260      270      280      290      300

              310      320      330      340      350      360
a769.pep   AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRCLKNTRRARSNDTHLQISN
|||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRCLKNTRRARSNDTHLQISN
              310      320      330      340      350      360

              370      380      390      400      410      420
a769.pep   SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSGLSLLRLGAAGR
|||||
m769      SLVFYRNARQYWMGGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGGSGLSLLRLGAAGR
              370      380      390      400      410      420

              430      440      450      460      470      480
a769.pep   HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTSLSHRETRSNDVFNEYEKN
|||||
m769      HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTSLSHRETRSNDVFNEYEKN
              430      440      450      460      470      480

              490
a769.pep   RAFVEFNKTFX
|||||
m769      RAFVEFNKTFX
              490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCGG
51  CAGCGGCCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTCGACGA TCCCACGTT
151 CAAGGGGTTG CCGTGTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTCA AGCGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTTACAGCG
401 ATAAAAATCGT CCAAGGATCG CCGAAAAATT CCTTAAGCGC GGTTTCCTGT
451 TCGGCAGCG GCATACCGCA AACCGACGGG GTGCAAGCGG ATACTTCCGG
501 CAAACTGCTT GCCGGCGCCT GCATTATTC CAACCCGATA AAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1  MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDR I EVEGFDDPDV
51  QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTFGA FKSQRIVRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FGSGIPQTDG VQADTSGKLL AGACIIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1  ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51  CAGCGGCCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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1254

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101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCTCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

m770.pep

```

1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR IVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSQIVRY YDPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

	10	20	30	40	50	60
g770.pep	MNRLLLLSAAV	LPTACGSGET	DKIGRASTV	FNMLGKNDR	IEVEGFDDPD	VQGVACYISYA
m770	MNRLLLLSAAV	LLTACGSGET	DKIGRASTV	FNILGKNDR	IEVEGFDDPD	VQGVACYISYA
	10	20	30	40	50	60
	70	80	90	100	110	120
g770.pep	KKGGLKEMVN	LEEDASDASV	SCVQTASSIS	FDETAVRKPK	EVFKRGTF	GAFAKSRQIVRY
m770	KKGGLKEMVN	LEEDASDASV	SCVQTASSIS	FDETAVRKPK	EVFKHGASFA	FAKSRQIVRY
	70	80	90	100	110	120
	130	140	150	160	170	180
g770.pep	DPKRKA	FAYLVYSDK	IVQGS	PKNSLSAVSC	FGSGIPQTDG	VQADTSGKLLAGACIISNPI
m770	DPKRKT	FAYLVYSDK	IIQGS	PKNSLSAVSC	FGGGIPQTDG	VQADTSGNLLAGACMISNPI
	130	140	150	160	170	180
g770.pep	KNPDKRX	:	I			
m770	ENLDRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

a770.seq

```

1 ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
51 CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGGAAG GATTTCGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTCA AACACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTTC CAACCCGATA GAAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

a770.pep

```

1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR IVEGFDDPDV
51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKHGASFA FKSQIVRY YDPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

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1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPKR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDDPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKEVFKHGASF AFKSRQIVRY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKEVFKHGASF AFKSRQIVRY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRKTFAYLVYSKIIQGSFKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRKTFAYLVYSKIIQGSFKNLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPKRXX					
m770	ENLDKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

1	ATGGATTAT	TATCGGTTT	CCACAAATAC	CGTCTGAAAT	ATGCGGTGGC
51	GGTGCTGACG	ATGCTGCTTT	TGGCGGCAGT	CGGGCTGCAC	GCTTCCGTAT
101	ATCGCACCTT	CACGCCGAA	AACATCCGCA	GCCGCCTCCA	ACAAAGCATT
151	GCCCATACCC	ACCGGAAAAT	CTCGTTTGAT	GCGGATATAC	GGCGCAGGCT
201	TCTGCCCCGC	CCGACCGTCA	TCCTGAAAAA	CCTGACCATT	ACCGAACCCG
251	ACGGCGGCCG	GGTCGCCGTT	TCCGTCAAAG	AAACCAAAAT	CGGATTGAGC
301	TGGAAAAACC	TGTGGTCGGA	TCGGATACAG	GTTGAAAAAT	GGGTGGTTTC
351	GGGTGCCGAT	CTTGCCCTGA	CGCGCGACAG	AAACGGCGCT	TGGAACATCC
401	AAGACCTGTT	CGACGGCGCG	AAACACTCCG	CCTCAGTCAA	CCGCATTATC
451	GTCGAAAACA	GCACCGTCCG	CCTCAATTTT	CTGCAGCAAC	AGCTTATCCT
501	GAAGGAAATC	AGCCTCAACC	TGCAATCCCC	CGATTTCGTC	GGGCAGCAGT
551	TGATAAGTTC	GGGCATACTG	GTTTGGAGAA	AGCTGTCCGT	CCCGTGGAAA
601	AGCAGGGGGC	TGTTCCCTTC	AGACGGCATC	GGCACGCCCG	AAATCTCACC
651	GTTCCATTTT	GAAAGTTCCA	CTTCGCTGGA	CGGACACGGC	ATCACCATT
701	CCACCACCGG	CAGCCCTTCT	GTCCGCTTCA	ACGCCGGCGG	AGCGGATGCC
751	GCCGGCCTCG	GCCTGCGTGC	AGACACTTCC	TTCCGCAACC	TCCACCTGAC
801	CGCGCAAATC	CCCGCACTGG	CACTCAAAAA	CAACAGCATC	AAAACCGGCA
851	CGGTCAACGG	CACGTTTACC	GCCGGCGGCG	AATATGCCCG	ATGGGACGGT
901	TCGTTCAAAC	TCGACAAAGC	CAACCTGCAC	TCCGGCATCG	CCAACATCGG
951	CAACGCCGAA	ATCTCCGGCA	GCTTCAAAAC	ACCGCGCCTT	CAAACCAATT
1001	TCTCCCTCGG	CTCGCCGTTG	GTTTGGAGTC	GGGACAACGG	GCTGGACGCC
1051	CCGCGCCTGC	ACATATCGAC	CCTTCAGGAT	ACCGTCGACC	GCCTGCCGCA
1101	ACCCCGTTTC	ATCAGCCGGC	TCGACGGTTC	GCTGTCCATA	CCGAATCTGC
1151	AAAATTGGAA	TGCCGAATTA	AACGGCACAT	TCGACCGCCA	ACCCGTTGCC
1201	GCAAAATTCA	AATATACGCG	GGAAGCGCGA	CCGCACCTGG	AAGCCGCCGC
1251	CGCGCTGCAA	AAATTAACCC	TCGCCCCCTA	TCTTGACGAA	TTTCGGCAAC
1301	AAAACGGCAA	AATATTCCCC	GACATCCTCG	GCAGGCTGTC	CGGCAACGTC
1351	GAGGCACACC	TCAAAATCGG	CAGCATCCAA	CTCCCCGGCT	TGCAACTGGA
1401	CGATATGGAA	ACCTACCTCC	ACGCCGACAA	AGACCATATC	CGGCTCAGCC
1451	GTTTCAAGTC	AGGGCTTTAC	GGCGGCCATA	CCGAAGGCGG	CATCAGCATC
1501	GCCACACACC	GTCCCGCCAC	TTACCGCCTG	CAACAGAATG	CAAGCAACAT
1551	CCAAATCCAA	CCGTGCTGTC	AAGACCTGTT	CGGCTTCAC	AGCTTCAGCG
1601	GCAACGGCGA	TGCGGTCATC	GACCTGACCG	CAAGCGGCGA	AAACCGCAAA
1651	CAGCTTATCC	GCTCGCTGCA	AGGCAGCCTG	TCGCTGAATA	TTTCCAACGG
1701	CGCGTGCCAC	GGCATCGATA	TGGACAGCAT	TTTAAAAAAC	GGCCTTTCCG

1256

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1751 GGAAATCTCT GGGCAGCACA CCCTTCTACC GATTACAGCT CAACAGCGAA
1801 ATTTTCAGACG GCATCAGCCG CCACATCGAT ACCGAACTCT TCTCCGACAG
1851 CCTCTATGTT ACCAGCAACG GCTATACCAA TCTGGATACG CAGGAATTGT
1901 CTGAAGATGT CCTTATCCGC AACGCCGTCC ATCCGAAAAA CAAACCGATT
1951 CCCCTGAAAA TCACCGGTAC GGTGGACAAG CCGTCCATTA CCGTCGATTA
2001 CGGCAGGCTG ACCGGCGGCA TCAATTCGCG CAAAGAGAAA CAGAAAATCC
2051 TCGAAGACAC CCTGTGGAA CAATGGCAGT GGCTCAAACC TAAAGAACCG
3051 TAA

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

g771.pep

```

1 MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQQSI
51 ANTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRII
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQQFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSPTS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALKNNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPV VWSRDNGLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNNNAEL NGTFDRQPVA
401 AKFKYTRREGA PHLEAAAAAQ KLNLAAPYLDE FRQONGKIFP DILGRLSGNV
451 EAHLKIGSIQ LPGLQLDDME TYLHADKDH IALSFRKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTASGENRK
551 QLIRSLQGS LSLNISNGAWH GIDMSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHD TELFSDSLYV TSNGYTNLDT QELSEDVLIR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDTLLE QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

m771.seq

```

1 ATGGATTTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAAAGCATT
151 GCACACACAC ACCGAAAAAT CTCGTTTGAT GCGGACATTC AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGCAGGA CTGCCCCTGA CGCGCGACGG GAAAGGTGTT TGGAAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTTT CTGACGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTTCGTC GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AAACGGCATC GGCCCGCCCG AAATCTCACC
651 GTTCCATTTC GAAGCTTCCA CTGCTGGA CGGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGCGCG AGCGGATGCC
751 GCCGCGCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAATC CCCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CGCTCAACCG CGCATTTACC GCGGCGCGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTGCGCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCGGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACG TGAAAATCGG AAAAGTCCAA CTTCCTCGGC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAAAGT AGGGCTTTAC GCGCGCCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCACCAC TTACCGCTCG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CCGGTCATC GACCTGACCG CGGGCGGCGA AACC CGAAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCTCG TCGCTAAATA TTTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAAATGTC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACAG
1801 CTCAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCCTGAA AATCACCGGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCCAT TACGGCAGGC TGACCGGCGG CATCAATTCT CGCAAGAGAG
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

```

This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

```
m771.pep
1 MDLLSVFHKY RLKYAVAVLT ILLAAVGLH ASVYRTFTPE NIRSRLQQSI
51 AHTRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS
101 WKNLWSDQIQ IEKWVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFSLNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTV
401 AKFRYTHEDA PHLEAAVALQ KNLNTPYLLD VRQQNGKIFP DTLAKLSGDI
451 EAHKIGIKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGSGNGDAVI DLTAGGETRK
551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
601 LNSEISDGI RHIDTELFSD SLYVTSNGYT NLDQELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGIN S RKEKQKILED TLEQWQWLK
701 PKEP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

```
m771/g771 90.3% identity in 704 aa overlap
10 20 30 40 50 60
g771.pep MDLLSVFHKYRLKYAVAVLTMLLLAAVGLHASVYRTFTPENIRSRLQQSIATHRKISFD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQQSIATHRKISFD
10 20 30 40 50 60

70 80 90 100 110 120
g771.pep ADIRRRLLPRPTVILKNLTITEPDGGRVAVSVKETKIGLSWKNLWSDRIQVEKWVVSAD
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 ADIQRRLPRPTVILKNLTITEPDGQTAVSVQETKIGLSWKNLWSDQIQIEKWVVSAAE
70 80 90 100 110 120

130 140 150 160 170 180
g771.pep LALTRDRNGAWNIDLDGAKHSASVNRIIVENSTVRLNLFQQLILKEISLNQSPDSS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQEQILKEINLNQSPDSS
130 140 150 160 170 180

190 200 210 220 230 240
g771.pep GQQFESSGILVWRKLSVPWKSRLGLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 GQPFESSGILVWGKLSVPWKSRLGLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS
190 200 210 220 230 240

250 260 270 280 290 300
g771.pep VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG
250 260 270 280 290 300

310 320 330 340 350 360
g771.pep SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWVRDNGLDAPRLHISTLQD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD
310 320 330 340 350 360

370 380 390 400 410 420
g771.pep TVDRLPQPRFISRLDGSLSIPNLQNWNAELNGTFDRQPVAAKFKYTREGAPHLEAAVALQ
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 TVNRLPQPRFISRLDGSLSVNLQNWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ
370 380 390 400 410 420

430 440 450 460 470 480
g771.pep KLNLAAPYLDEFQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m771 KLNLTPLYLDDVRQNGKIFPDITLAKLSGDI EAHKIGKVLPLGLQLDDMETYLHADKHI
```

1258

	430	440	450	460	470	480
	490	500	510	520	530	540
g771.pep	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQLLDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	
g771.pep	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMDSILKNGLSGKISG----STPFYRFT					
m771	DLTAGGETRKLIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRT					
	550	560	570	580	590	600
	600	610	620	630	640	650
g771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	660	670	680	690	700	
g771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKPEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

a771.seq

```

1   ATGGATTAT TATCGGTCTT CCACAAATAC CGTCTGAAAT ATGCGGTAGC
51  CGTGCTGACG ATACTGCTTT TGGCGGCAAT CGGGCTGCAC GCTTCCGTAT
101 ATCGCATCTT CACACCTGAA AACATCCGAA GCCGCCTCCA ACAAAGCATT
151 GCCCATACGC ACCGGAATAA CTCGTTTGAT GCGGATATAC AGCGCAGGCT
201 TCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCG GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGCCGAA CTGCCCCTGA CGCGCGACGG GAAAGGTGTT TGGAAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAAC GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTTCGTC GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC GTTTCCTTTC AGACGGCATC GGCACGCCCA AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTCGCTGGA CGGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCGGCGCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAATC CCTACGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCA ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTGCGCGCTC GTATGGACGG AAAACAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCGCTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCC GACACCCTCG CCAAGCTGTG CGGCGACATC
1351 GAGGCGCACC TGAAAATCGG AAAAGTCCAA CTTCCCGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAAGTC AGGGCTTTAC GGCGGCCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTCATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCCAACGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAACTGCG CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACAG
1801 CTCAACAGCG AAATTTCAGA CGGCATCAGC CGCCACATCG ATACCGAAT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGT ACGGTGGACA AACCTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGCGG CATCAATTCT CGCAAAGAGA
2051 AACAGAAAAT CCTCGAAGAC ACCCTGCTGG AACATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

1259

a771.pep

```

1  MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQOSI
51  ANTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKVVVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQNWNAEL NGTFDRQTVA
401 AKFRYTHEDA PHLEAAVALQ KLNLTPLYDD VRQONGKIFP DTLAKLSGDI
451 EAHLKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTGGISI
501 ANTRPATYRL QQNASNIQIQ PLLQDLFGFH SFGNGDAVI DLTAGGETRK
551 ELIRSLQGS LSLNISGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDQTQELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK
701 PKEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

	10	20	30	40	50	60
a771.pep	MDLLSVFHKYRLKYAVAVLTILLLAAGLHASVYRIFTPENIRSRLQOSIAH	THRKISFD				
m771	MDLLSVFHKYRLKYAVAVLTILLAAVGLHASVYRTFTPENIRSRLQOSIAH	THRKISFD				
	70	80	90	100	110	120
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKVVVSSAE					
m771	ADIQRRLPRPTVILKNLTITEPGGDQTAHSVQETKIGLSWKNLWSDQIQIEKVVVSSAE					
	130	140	150	160	170	180
a771.pep	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILKEINLN	LQSPDSS				
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNFLQEQILKEINLN	LQSPDSS				
	190	200	210	220	230	240
a771.pep	GQPFESSGILVWGKLSVPWKSRLFLSDGIGTPKISPFHF	EASTSLDGHG	ITISTTGSPS			
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHF	EASTSLDGHG	ITISTTGSPS			
	250	260	270	280	290	300
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	310	320	330	340	350	360
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
	370	380	390	400	410	420
a771.pep	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQTVA	AKFRYTHEDAPHLEAAVALQ				
m771	TVNRLPQPRFISRLDGSLSV PNLQNWNAELNGTFDRQTVA	AKFRYTHEDAPHLEAAVALQ				
	430	440	450	460	470	480
a771.pep	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQLDDMETYLHADKGHI				
m771	KLNLTPLYDDVRQONGKIFPDTLAKLSGDI	EAHLKIGKVQLPGLQLDDMETYLHADKGHI				

1260

```

          490      500      510      520      530      540
a771.pep  ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI
          |||
m771      ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI
          490      500      510      520      530      540

          550      560      570      580      590      600
a771.pep  DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRT
          |||
m771      DLTAGGETRKEIIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRT
          550      560      570      580      590      600

          610      620      630      640      650      660
a771.pep  LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG
          |||
m771      LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG
          610      620      630      640      650      660

          670      680      690      700
a771.pep  TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
          |||
m771      TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPKEPX
          670      680      690      700

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

```

g772.seq
1  GTGTTTCGGCA CGGTCTTGCG GACTGATGCC GACTGCCTGC AAATCATCGT
51  CGTCGGCAAG TTCTTTCAGG TTGTTGCGTA TGGTTTTCGG GCGTTGGCGG
101 AAGGCGAGTT TCACCAAGTTT GCGGAAATGA TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGCAC CACTGCGGAA TCGATTTTCG
201 GCGCGGGATC GAACGATTTCG GCGGGCACGT CAATCAGCAG CTCCATATCG
251 AAAAAATATT GCAGCATCAC ACCAAGCGA CCGTAGTCGT TGCTTTTCGG
301 CCGGCAACC ATGCGCTCGA CCACTTCTTT TTGCAACATA AAGTGCATAT
351 CGCGGACATC GTCCGCCACC TCCGCCAGTT TGAACAAAAG CGGCGTGGAG
401 ATGTTATACG GCAGGTTGCC GACGATTTTC TTTTTCCTG AGATGCCGTT
451 GAAATCAAAC TGCAACACGT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TCGAGGCGGT TCAGCTTTT CGCCAAAGGT TCGGTAATG CCGCCAAACC
601 CCGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCC GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTCTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGCAGGATC AGACTCTGTT TGGGCGGGGC GTAACCCCTT
801 CCAAATCAGG ACGACACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

```

g772.pep
1  VFGTVLRTDA DCIQLIIVVGK FFQVVAYGFA ALAEGEFHQF GEMIEIVRLA
51  DTVFHRNHAH HCGIDFRRGI ERFRHVNQQ LHIEKILQHH TQATVVVAFR
101 RGNHALDHFF LQHKVHIGDI VRHLRQFEQK RRGDVIRQVA DDFLFA*DAV
151 EIKLQHVAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNCRQT
201 RADFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSSSVETP
251 PFRAAGSDSV WAGRNPFQIR TTHRAVLVVS SCVLEHKCVY SIRLMSAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

```

m772.seq
1  ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51  CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGGCGAGTT TCACGAGTTT GGCAAAATGC TCGAAATCGT CCGCCTTGCC
151 GATGCGGTGT TTCACCGGAA TCATACGGAC GACGGCGGAA TCCACTTTCG
201 GCGCAGGGTC GAACGATTTCG GCGGTACGT CAATCAGCAT TTCCATATCG
251 AAAAAATATT GCAGCATCAC GCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CCGGCAACC ATACGCTCGA CCACTTCTTT TTGCAACATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAAG CGGTGTGGAA
401 ATGTTGTACG GGAGGTTGCC GACGATTTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTAGACGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TCGAGGCGGT TCAGCTTTT CGCCAAAGGT TCGGTAATG CCGCCAAACC
601 CCGGCCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC

```

1261

```

701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep

```

1 MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GKMLEIVRLA
51 DAVFHRNHTD DGGIHFRRRV ERFGRYVNQH FHIEKILQHH AQAQVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLYVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVVGKFFQVVAYGFAALAEGEFHFQFGEMIEIVRLADTVFHRNHAH					
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
g772.pep	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	DGGIHFRRRVVERFGRYVNQHFIHIEKILQHHQAQVVAFRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
g772.pep	VRHLRQFEQKRGRGDVIRQVADDFLFAFXDAVEIKLQHVAFVNHQFIRKRQRQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLFAFCAVEIKLQYIAFVNHQFIRKRQRQTAYDVAVD					
	130	140	150	160	170	180
g772.pep	FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
g772.pep	HRVSSSVETPPFRAAGSDSVWAGRNPFQIRTTTHRAVLYVSSCVLEHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLYVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	299

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

```

1 ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTCAGA TTGTTCGTA TGGTTTTCGG CGGTGCGTGG
101 AAGGCGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGCGCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTCG GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC TTCGCCACCC TCCGCCAGCT TGAACAAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTTC TTTTTCGCTG CGATGCCGTT
451 GAAATCAAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTTACAGCGG CATACGATGT CGCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTTT CGCCAAAGGT TCGGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGGCG ACGCCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCTG CCCGAAACGC
701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CCTTTTCGGT TGAAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTCG TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

1262

This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

a772.pep

```

1  MFGAVLRIDA DCLQIIVACK LFQIVAYGFA ALVEGEFHEF GEMLEIVRLA
51  DTVFHRNHAD DGRIFHRRGV ERFGHVNQH FHIEEILQHH AQAQVVAFR
101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RTDFNHDIIR LRAHGVDNIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

	10	20	30	40	50	60
a772.pep	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGEMLEIVRLADTVFHRNHAD					
m772	MFGAVLRIDADCLQIIVACKLFQIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a772.pep	DGRIFHRRGVVERFGRHVNQHFIHIEEILQHHQAQAVVAFRRGNHTIDHFFLQHKVHIDDI					
m772	DGGIHFRRRVERFGRYVNQHFIHIEKILQHHQAQAVVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a772.pep	VRHLRQLEQKRRGNVVGQVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a772.pep	FDNVQAVQLFRQRFGNRRQTRTDFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVDNIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
	250	260	270	280	290	299
a772.pep	HRVSFSVETPPFRAVESDSIWEGRNSFQIRTAHRVLYVSSCVLKHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRVLYVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

m773.seq

```

1  ATGGGATTGG GTGCAACGAC TTTTGTGCGT TCGGGTGCTA TAGGCGGAGG
51  TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG
101 CAGGTATGAC CGGTGGTTAT ACACAGGCC T CAGAAGGAAG CCGGCAATTG
151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG
201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG
251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATTGGG AAACCTGGCA
301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA
351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG
401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT
451 GCAAGGTAC CTAATAATT TAAACATT T GATTATTTG ATCGTGGTAC
501 AGGCACGGCA ATCAGTGCCA AAACCTCTGA TACGCAAACT ACGGCACGCC
551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG
601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA
651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA
701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA
751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA

```

1263

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

m773.pep

```

1  MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TQASEGSRQL
51  FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLA VWGLET LITRKLGNLA
101 TGVKTS LTPK TADVQRNLS QSEVGIKWGK GIEGQGM PWE DYVGKGLSAN
151 ARLPKNF KTF DYFDRGTGTA ISAKTLDTQT TARLSKPEQL YSTMKG YIDK
201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEQRLQL QRVVEY GKSQ
251 NITVKITEIE *
```

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

g774.seq

```

1  ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC
51  CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA
101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAATGTTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC
251 CTTCGGGCAG GACATACGTC CAAAAACTCG ACGACCGCAA ATTGAAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC
351 CGCACAAAAA CTCTACAATC AGGCACTCAA ACACTATCAA AACGGCAGGT
401 TTTCTGCCGC AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TACGCAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

g774.pep

```

1  MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTQENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDDRKLKE
101 HYLNTGGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESIVIEGGRY ANRFKDSPTA PEVIFKIGEC
201 QYRLQOKDIA RATWRS LIQT YPGSPA AKRA AA AVRKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

m774.seq

```

1  ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC
51  CTGTGCTTCC GTTTCACCCG TTCCGGCAGG CAGCCAAACC GAAATGTCGA
101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA
151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAGT
201 GGAAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT
251 CTTCGGGCAG GGCATACGTC CAAAAACTCG ACGACCGCAA GTTGAAGAG
301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTGAAAC
351 CGCACAAAAA CTCTACAATC AGGCACTCAA ACACTATAAA AGCGGCAAGT
401 TTTCTGCCGC TGCCTCCCTG TTGAAGGGCG CGGACGGAGG CGACGGCGGC
451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT
501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT
551 TCAAAGACAG CCCAACCGCG CCTGAAGCCA TGTTCAAAAT CGGCGAATGC
601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GCGCGAGCCT
651 GATACAGACC TATCCCGGCA GCCCGGCGGC AAAACGCGCC GCCGCAGCCG
701 TGCGCAAACG ATAG
```

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

m774.pep

```

1  MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ
51  DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDDRKLKE
101 HYLNTGGGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG
151 SIAQRSMYLL LQSRARMGNC ESIVIEGGRY ANRFKDSPTA PEAMFKIGEC
201 QYRLQOKDIA RATWRS LIQT YPGSPA AKRA AA AVRKR*
```

Computer analysis of this amino acid sequence gave the following results:

1264

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIIWLSVSASCASVLPVPEGSRT	EMPTQENASDGIPYPVPTLQDRLDYLEGKI				
m774	MKIKLPLFIIWLSVSASCASVSPV	PAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGKI				
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGR	TYVQKLDDRKLKEHYLNTEGGSASAHTVETAQN				
m774	VRLSNEVETLNGKVKALEHAKTHSSGR	AYVQKLDDRKLKEHYLNTEGGSASAHTVETAQN				
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGG	DGGSIAQRSMYLLQSRARMGNCSVIEIGGRY				
m774	LYNQALKHYKSGKFSAAASLLKGADGG	DGGSIAQRSMYLLQSRARMGNCSVIEIGGRY				
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQ	QKDIARATWRSLIQTYPGSPA	AKRAAAVRKR			
m774	ANRFKDSPTAPEAMFKIGECQYRLQ	QKDIARATWRSLIQTYPGSPA	AKRAAAVRKR			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

```

1  ATGAAGACCA AATTACCGCT TTTATCATT TGGCTGTCCG TATCCGCCGC
51  CTGTTCTTCC CCGTTTCCC GCAATATCA GGATATGCGG CTCGAACCGC
101 AGGCAGAGGC AGGTAGTTCG GACGCTATTC CCTATCCCGT TCCCACTCTG
151 CAAGACCGTT TGGATTATCT GGAAGGCACA CTCGTCCGCC TGTCGAACGA
201 AGTGGAAACC TTAACGGCA AAGTCAAAGC ACTGGAGCAT GCGAAAACAC
251 ACCCTTCCAG CAGGGCATA GTCCAAAAAC TCGACGACCG CAAGTTGAAA
301 GAGCATTACC TCAATACCGA AGGCGGCAGC GCATCCGCAC ATACCGTCGA
351 AACCGCACA AACTCTACA ATCAGGCACT CAAACACTAT AAAAGCGGCA
401 GGTTTTCTGC CGTGCCTCC CTGTTGAAAG GCGCGGACGG AGGCGACGGC
451 GGCAGCATCG CGCAACGCAG TATGTACCTG TTGCTGCAAA GCAGGGCGCG
501 TATGGGCAAC TCGCAATCCG TCATCGAAAT CGGAGGGCGT TACGCCAACC
551 GTTTCAAAGA CAGCCCAACC GCGCCTGAAG CCATGTTCAA AATCGGCGAA
601 TGCCAATACA GGCTTCAGCA AAAAGACATT GCAAGGCGCA CTTGGCGCAG
651 CCTGATACAG ACCTATCCCG GCAGCCCGGC GGCAAAACGC GCCGCCGCAG
701 CCGTGCGCAA ACGATAG

```

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

```

1  MKTKLPLFII WLSVSAACSS PVSRIQDMR LEPQAEAGSS DAIPYPVPTL
51  QDRLDYLEGT LVRLSNEVET LNGKVKALEH AKTHPSSRAY VQKLDDRKLK
101 EHYLNTEGGS ASAHTVETAQ NLYNQALKHY KSGRFSAAAS LLKGADGGDG
151 GSIAQRSMYL LLQSRARMGN CESVIEIGGR YANRFKDSPT APEAMFKIGE
201 CQYRLQQKDI ARATWRS LIQ TYPGSPA AKR AAAAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSAACSSPVSRIQDMR	LEPQAEAGSSDAIPYPVPTLQDRLDYLEGT				
m774	MKIKLPLFIIWLSVSASCAS-VSPV	PAGSQTEMSTRENASDGIPYPVPTLQDRLDYLEGK				
	10	20	30	40	50	

1265

```

a774.pep      70      80      90      100     110     120
               LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKLD DRKLKEHYLNTEGGSASAHTVETAQ
m774          60      70      80      90      100     110
               IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLD DRKLKEHYLNTEGGSASAHTVETAQ

a774.pep      130     140     150     160     170     180
               NLYNQALKHYKSGRFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCSVIEIGGR
m774          120     130     140     150     160     170
               NLYNQALKHYKSGKFSAAASLLKGADGGDGGGSIQRSMYLLQLSRARMGNCSVIEIGGR

a774.pep      190     200     210     220     230     239
               YANRFKDSPTAPEAMFKIGECQYRLQKQDIARATWRS LIQTYPGSPA AKRAAAAVRKRX
m774          180     190     200     210     220     230
               YANRFKDSPTAPEAMFKIGECQYRLQKQDIARATWRS LIQTYPGSPA AKRAAAAVRKRX

```

g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
551 CCCCCTCGCA GTACACGTTT GCCGTTGCCA TGCCCCGACAC GTCCATGTCC
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TGCGGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTCG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AA AEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTC SR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSIV LNDVQGD TTI NNHHTHTNH SDADGKALSM
151 RLTPRPLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCP PH ROEGVLIRIT APDVWTVGMI
301 SAKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAAACATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTCAGAC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTCG
551 CCCCCTCACA ATATACGTTT GCCGTTGCCA TGCCCCGACAC GTCCATGTCC
601 CCGGTTATCG AAAAGGGGGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TGCGGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTCG
701 TCGCGCACCT TGTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

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1266

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTGAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
  1 MARRSKTFEE AAAEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
 51 YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTHNN SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPRMRPADE DIVLIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

a790/m790 98.2% identity in 342 aa overlap

	10	20	30	40	50	60
a790.pep	MARRSKTFEEAAAEEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
m790	MARRSKTFEEAAAEEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a790.pep	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII					
m790	GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
a790.pep	LNDVQGDTTINNHHTHTHNSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
m790	LNDVQGDTTINNHHTHTHNSDADGKALSMRLTPRPLLSDRQAAAFARTGKLTGSFDLFA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a790.pep	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMRPADE DIVLIELSDKRLVVAHLVID					
m790	SVVAPSQYTF AVAMPDTSMS PVIEKGDLLVVEPRMCPADEDIALIELSDKRLVVAHLVID					
	190	200	210	220	230	240
	250	260	270	280	290	300
a790.pep	IAGRMLIYQTRPSEALDLPESVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI					
m790	IAGRMLIYQTRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI					
	250	260	270	280	290	300
	310	320	330	340		
a790.pep	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAC					
m790	SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
  1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTACTTGTTT
 51 TGGTTTGTGTT TTTGGTTTTT GTGTATTGG AGTGGGCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGCT CTTTGGAATC TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GCGCGGAAT TACAAAAATC GGCATTTC
251 CCGAGGTGTT CCGGAATGCG GTTATTGCC CCGAGGATAA ACGCTTTTAC
301 CCGCATTGGG GGGTGGATGT TTGGGGTGT GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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1267

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401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAAC TGCATTATGAG CGGTTTGTTT GGAATTCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTCCGAT CGCGGCAGCA GCTACGCGG TGCGGAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTTGG ATGTTACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTGCGCTTG
1151 ACAGGCCGCG CTGGGGTTT GCGGCCGAG CGGTCGATAA TGAGAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGT ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGT ACGCGCAACA GTATATCCGG
1651 CGTTTCCGCT TCAGGCCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGCGAGGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTCTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG CGAGTTGCG CGCCAAATG CAACCTTGG TGGCAGGGCA
1851 AAATGCCCTT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGGT ACGACCAACG ACAATAAAGA
2001 TGCGTGGTTT TCGGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAAATGC CTGAAGGTGT GGTACAGCAG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG GCCCGCAACC TTCCCGACGG GCAAAAAGAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

g791.pep

```

1 MVNYYSAMIK KILTTCFGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QLSLSDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFKVYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSESDV EETVSQYLSG
351 LYTVDKMVPA VVLDTTKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELP ASLSMALGTG ETTPKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRDIAAGKTG TTNDNKDAWF VGFPDPVVT A VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGQKKG MKMPEGVVS NGEYMKERM VTDPLMLDN
751 SGIAPQPSRR AKEDDEAAVE NEQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

m791.seq

```

1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTT GTGTATTTGG AGTGGGTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AACTGCCCGT CTTTGGATTC TTTGCAGCAT
151 TACCAGCCTA AATGCCGTT GACTATTTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGAGCAGC GCGCGAATT TACAAAAAT GGCATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGT GCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

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1268

```
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTC AATAAGATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTC GGAAAATCGA
801 TCAGAGTGCG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGGAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGG CGGTCAATAA TGA AAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGCGGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTACAGACA AACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCCACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CGCGCTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACGGTT CGGTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGCTGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGACGGA TGTGGTCCGT GTTGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TCGGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGCG CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGGC AGGCGGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

m791.pep

```
1 MVNYYSAMIK KILTTCTFGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFKVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMVPV VLDVTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQ ALGSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRLLRAQ QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKG MKMPEGVVS NGEYMKERM VTDPLGLTDN
751 SGIAPQPSRR AKEDDGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*
```

g791/m791 97.3% identity in 805 aa overlap

```
10 20 30 40 50 60
g791.pep MVNYYSAMIKKILTTCTFGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
|||||
m791 MVNYYSAMIKKILTTCTFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
10 20 30 40 50 60

70 80 90 100 110 120
g791.pep SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGVGNVVS
|||||
m791 SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGVGNVVS
70 80 90 100 110 120
```

1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAMLGLPKAPSAYNPVNPRAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAMLGLPKAPSAYNPVNPRAKLRQKYILNNMLE					
	190	200	210	220	230	240
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKGEDAYTQGFVKVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKGEDAYTQGFVKVYTTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMPVA					
m791	RADHQKVATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMPVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
g791.pep	VVLDTVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIRRGAVIRVKNNGGRW					
m791	VVLDTVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW					
	370	380	390	400	410	420
	430	440	450	460	470	480
g791.pep	AVVQEPLQAGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPLQAGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
	550	560	570	580	590	600
g791.pep	GVGYAQQYIRRFGRFPSELPAFLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQQYIRRFGRFSSELPAFLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
	610	620	630	640	650	660
g791.pep	DRDGRRLRAQMQLVAGQNAFQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLRAQMQLVAGQNAFQAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFGFNPDPVTVAVYIGFDKPKSMGRAGYGGTIAVPVWVDYMRFALKGKQKKG					
m791	TTNDNKDAWFGFNPDPVTVAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKKG					
	670	680	690	700	710	720
	730	740	750	760	770	780
g791.pep	MKMPEGVVSSNGEYYMKERMVTDPLMLDNGSIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYYMKERMVTDPLTLDNGSIAPQPSRRAKEDDGGAAEGGRQAADDEV					
	730	740	750	760	770	780
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```
1 ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51 TGGTTTGGTT TTTGGGTTTT GTGTATTTGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAGTCCGTT CTTTGGATTG TTTGCAGCAT
151 TACCAGCTTA AAATGCCGTT GACTATTAT TCGGCGGATG GGGAAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGGAATT TACAAAAATC GGCGATTTC
251 CAGAGGTGTT GCGGAATGCG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTG GCCCGCGCTG CCGTCGGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC AGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTTG AGCAGTGAAG AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTC AATCAGATTA CTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTGA ATGAGGAAGT GCATTACGAG CGGTTTGTTC GGAAAAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCCTAT ACGCAGGGTT TTAAGGTTA TACCACGGTC
901 CCGCGCCGATC ATCAGAAAGT GGCACCGGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TCGGAAAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CCGCAGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGTTTC AAGAGCCGTT GCTGCAGGG GCTTTGTTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCC GGGGAAAGGG
1501 CCGAACCGTT CGGTTTGAC ACCTAAAAAT TCAGACGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGTCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCCGGGCA
1851 AAATGCCGCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAAACGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 AATTAATGAA GGAACGTATG GTAACCGATC CGGCTTGAC GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CCGCGCAGAA GCGCGACGGC AGCGGCGGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAC GCGGTGCTT CCGAGTAATA CTGTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2680; ORF 791.a>:

a791.pep

```
1 MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51 YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVDVWGV ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVKVYTTV
301 RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRV QAMRQPGSTF KPFVYSAALS KGMTASTVNV DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIT LRQALTASKN MVSIRILMSI VGUYAQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGRRLRAQM QPLVAGQNAQ QAIQPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVSS NGEYMKERM VTDPLTLN
751 SGIAPQPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*
```

a791/m791 99.9% identity in 805 aa overlap

10

20

30

40

50

60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAGNVVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE
	RAYGFASAAQIYFNKNVRDLTLAEAAMLAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFKVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQQVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
	RADHQQVATEALRKALRNFDRGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	VVLDDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	AVVQEPLLQGALVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
	KGMTASTVVNDAPISLPGKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	GVGYAQQYIRRFGRSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKAFAWVGFPDVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKGK
	TTNDNKAFAWVGFPDVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKGK
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVVSSNGEYYMKERMVTDPLGLTLNDSGIAPQPSRRAKEDDGGAAEGGRQAADDEV
	MKMPEGVVSSNGEYYMKERMVTDPLGLTLNDSGIAPQPSRRAKEDDGGAAEGGRQAADDEV

1272

	730	740	750	760	770	780
	790	800				
a791.pep	RQDMQETPVLPSNTGSKQQQLDSLFX					
m791	RQDMQETPVLPSNTGSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1   ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GGAAGAGGCG GGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAACCAATC GAATGGCACT ACGGCgtTTT
501 CGGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAAACCG GCcgcagACC
551 TGACcAAACA GCAGgcggcg aaactgacgg tactcgtccc cgcgccgttt
601 tactactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcattgggtt cggcaaatTA ccccaagcg aaacggactg
701 attgttcag atatggaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1   MFRIVKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKPP AADLTkQQA KLTVLVPAPF
201 YYSDHPSKR LRNKTNIIVLR RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1   ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51  CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAAAACGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCgTTTCG
251 CCGGGCAGCG CGGCTTCGAT TGGGGCGGCA TTCAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTAC CGACAAAGAC
451 AGGATTTTTC AACTGTATTT AAACCAATC GAATGGCACT ACGGCgTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAATACCC GCCGCCAAGC
551 TGACCAAACA GCAGGCGGCA AAACGACGG CGCGCGTCCC CGCCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1   MFRIIKWLIA LPVGIFIFFN AYVYGNIIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTkQQA KLTARVPAPL
201 YYADHPSKR LRNKTNIIVLK RMGSAELPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

	10	20	30	40	50	60
g792.pep	MFRIVKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQ	EGRDVALDYR				
	10	20	30	40	50	60
	70	80	90	100	110	120
g792.pep	WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRRNNSGEVKAGGSTISQQLAK					

[illegible]

```
a792.seq
1      ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51     CTTTTTCAAT GCGTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101    CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151    GAAGGTCGCG ATGTCGCATC GGATTAACCG TGGATGCCCT ACAAAACGAT
201    TTCCACCAAC TCGAAAAAAG CCGTGAATTG TTCCGAAGAT CGCGGTTTCG
251    CGGCGCACGG CGGCTTCGAT TGGGGCGGCA TTCAAAAAGC CATCAGGCGC
301    AACCGGAAAC GCGGCAAAAT GAAGCGGGCG GGCTCGACCA TCAGCCAGCA
351    GCTTGCCAAA AGCCTGTTTT TAAAGCAAGG CCGCAGCTAT ATCCGCAAG
401    GCGAAGAAGC GCGGATTACC GCGATGATGG AAGCCGTATC CGACAAGAC
451    AGGATTTTTG AACTGTATTT AAACCTCAAT GAATGGCATC ACGGCGTTTT
501    CGGCGCGGAA GCGCGTCTCC GGTATTTTTA TCAAAATACC GCCGCCAAGC
551    TGACCAAAAC CCAGCGGGCA CGCATGACGG CGCGCGTCCC CGCCCGCGTC
601    TACTAGCCCG ACCATCCGAA AAGCAAACGG CTCGCAACA AAACCAATAT
651    CGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701    GA
```

```
a792.pep
1  MFRIIKWLIA LPVGIFIFFN AYYVYNIITY RAVAPHRTAF MSMRMKQFEQ
51  EGRDVALDYR WMPYKRISTN LKKALIASED ARFAGHGGFD WGGIQNAIFR
101 NRNSGKVKAG GSTISQQLAK NLFNLNRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYGFQIP AAKLTKQQA KLTARVPAPL
201 YYADHPKSKR LRKNTNVLVR RMGSALPEL DTD*
```

a792.pep	10	20	30	40	50	60
	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRD	VALDYR			
m792	MFRIIKWLIALPVGIFIFFNAYVYGNII	TYRAVAPHRTAFMSMRMKQFEQEGRD	VALDYR			
	10	20	30	40	50	60
a792.pep	70	80	90	100	110	120
	WMPYKRISTNLKKALIASEDARFAGHGG	FDWGGIQNAIRNRNRNSGKVKAGGST	ISQQLAK			
m792	WMPYKRISTNLKKALIASEDARFAGHGG	FDWGGIQNAIRNRNRNSGKVKAGGST	ISQQLAK			
	70	80	90	100	110	120
a792.pep	130	140	150	160	170	180
	NLFLNESRSYIRKGEEAAITAMMEAVTD	KDRIFELYLNSIEWHYGVFGAEAA	SRFYQIP			
m792	NLFLNESRSYIRKGEEAAITAMMEAVTD	KDRIFELYLNSIEWHYGVFGAEAA	SRFYQIP			
	130	140	150	160	170	180
a792.pep	190	200	210	220	230	
	AAKLTQQAAKLTARVPAPLYADHPKSK	RLRNKTNIVLRRMGSAELPESD	TDX			
m792	AAKLTQQAAKLTARVPAPLYADHPKSK	RLRNKTNIVLRRMGSAELPESD	TDX			
	190	200	210	220	230	

q793.seq

1274

```

1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATGGCCGGT CTTGTTTGCC TGCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCGAGCT
351 TGTGCGATGT CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AAACTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGAAC TTTCGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTTGTTTTG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCAGCA AACCGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTGGCCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCTGGTTTC GCAATCAAAC CGTTCGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAGGTT TGTGAGAAA TTGGCGCAGG TGGCGGCCCA TCGAACAGGC
1251 GACGATGTCT TTCGGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTGCGCC GCAAGGCAAA CGCATATTCA AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGCGGGA
1451 CCGGTACGGC GGGTGCGGTG GACGGTTTCG ATGTCGGCGC TAAACCGGC
1501 ACGGCGCGCA AGTTCGTCAA CGGGCGTTAT GCCGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCAAAAAA CCCCCTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCACGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCTT TCAAAAAAAT TATGGGCGGC AGCCTGAACA TCTTGGGCAT
1701 TTCCCCGACC AAGCCACTGA CCGCCGACG CGTCAAAACA CCGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

g793.pep

```

1  MLIKSEYKPR MLPKEEQVKK PMTSNGRISF VLMAMAVLFA CLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYD MGNLFAHVIG FTDIDGKQGE GLELSLEDLSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPD RADSEQRRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSARFGAEEM YDFYHELGIK VRMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSL QLARAYTALT HDGVLLPLSF
451 EKQAVAPQ GK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGARTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYYGGVVA
551 GPPFKKIMGG SLNILGISPT KPLTAAAVKT PS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

m793.seq

```

1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAACAA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCGAGCT
351 TGTGCGATGT CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AAACTTTGTA TTTGAAAAAG AATTAAAACG
501 CCATTACCCG ATGGGCAACC TGTTTGCACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTG CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACCGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGAA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTGGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCGCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1275

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1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGC GCGATAC CCATGTTTAC
1051 CCTCTTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CAAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

m793.pep

```

1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RRGAVLALSA PTESLFAVEK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIVIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYPMGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEEVLRDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPGRADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRWR RPIEQATMSF GYGLQLSLLO LARAYTALTH DGVLLPVSE
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVAVG
551 PPFKKIMGGS LNLIGISPTK PLTAAAVKPT S*

```

g793/m793 98.5% identity in 582 aa overlap

	10	20	30	40	50	60
g793.pep	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKEEQVKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
g793.pep	GDNRIVRTQALPATRGTVSDRNGAVLALSAPTESLFAVPKDMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
	130	140	150	160	170	180
g793.pep	PVDVLRNKLEQKGKSFIVIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLEQKGKSFIVIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
	190	200	210	220	230	240
g793.pep	FTDIDGKGQEGLELSLEDSLYGEDGAEEVLRDRQGNIVDSLDSPRNKAPQNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEDGAEEVLRDRQGNIVDSLDSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
	250	260	270	280	290	300
g793.pep	QRIQTLAYEELNKAVEYHQAAGTVVVLDA RTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAAGTVVVLDA RTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
	310	320	330	340	350	360
g793.pep	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIM					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIM					
	310	320	330	340	350	
	370	380	390	400	410	420
g793.pep	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRWRPIEQATMS					
m793	QKSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRWRPIEQATMS					
	360	370	380	390	400	410

1276

```

          430      440      450      460      470      480
g793.pep  FGYGLQLSLLQLARAYTALTHDGVLLPLSF EKQAVAPQ GKRI FKESTAREVRNLMVSVTE
          |||||
m793      FGYGLQLSLLQLARAYTALTHDGVLLPLSF EKQAVAPQ GKRI FKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep  PGGTGTAGAVDGFVDVGA KTGTARKFVN GR YADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          |||||
m793      PGGTGTAGAVDGFVDVGA KTGTARKFVN GR YADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep  AHGYGGVVAGPPFKKIMGGS LNILGISPTKPLTAAAVKTPSX
          |||||
m793      AHGYGGVVAGPPFKKIMGGS LNILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACTTTTT GAAAGAACAG GGCACACACC GGATTGTGCG
201 GACTCAAACA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTGGC GTTGAGTGCG CCGACGGAGT CCCTGTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGCGATGTG CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGGA AAACCTTGTA TTTGAAAAAG AATTAACG
501 CCATTACCCG ATGGGCAACC TGTTTGACA CGTCATCGGA TTACCGATA
551 TTGACGGCAA AGGTCAGGAA GGTTTGGAAC TTTCGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCGGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 GATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 AAACAGCGCG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCAACCG
1451 CTACGCGCGG TCGGTTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 CTTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGGCGT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 CCCGACCAAG CCACTGACCG CGGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYP MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIIISLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPG RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRWR RPSEQATMSF GYGLQLSLLQ LARAYTALTH DGVLLPLVSFE
451 KQAVAPQGRK IFKESTAREV RNLMSVSTEP GGTGTAGAVD GFDVGA KTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLKLEQKGKFSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
m793	PVDVLRNKLKLEQKGKFSFIWIKRQLDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVIG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVLDARTGEILALANTPAYDPNRPGRADSEQRRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVLDARTGEILALANTPAYDPNRPGRADSEQRRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGPSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
m793	GYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGTGTAGAVDGFVDGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGTGTAGAVDGFVDGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYYGGVVAGPPFFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
m793	HGYYGGVVAGPPFFKKIMGGSNLILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

1	gtgcgtttca	ATCATTTTCAT	AATGGTAACG	ATTATTATAT	ATGTGATTTTC
51	CCCTGCAAAC	AAGCCGGTCC	GCCGCCCCCGG	CGTTCCCACT	TATCCGGCTT
101	TGCCTTATAA	TTGCTTTTTT	TATGTAACAG	ATTACCTAT	GAATTTCCCC
151	AAAACAGCGG	CCTCCCTGCT	GCTGCTTCTC	GCCTCCCTCG	CCGCACACGC
201	GCTCGATACC	GGCCGCATTC	CGCAAAACGA	AATCGCTGTA	TATGTCCAAG
251	AGCTTGACAG	CGGAAAAGTC	ATCATTGACC	ACCGTGCCGG	CATACCCGTC
301	AATCCC CGCT	CCACGATGAA	GCTCGTTACC	GCGTTTGCCG	CCTTCAAAAC
351	CTTCGGCAGC	AATTACCGCT	GGGCGACCGA	GTTTAAAAGC	AACGGTACGG
401	TAAACGACGG	CACGCTTGAC	GGAACCTGT	ATTGGGCGGG	CAGCGGCGAC
451	CCCGTTTTCA	ATCAGGAAAA	CCTGCTTGCC	GTCCAACGCC	AGTTGCGCGA
501	CAAAGGCATC	CGCAATATCA	CGGGCGCCT	GATGCTCGAC	CACAGCCTGT

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTTCGCCG
601 TTTATGACGC CCCCAAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTCCGTCAA AAAACTGATG CGCGCATCTT TTTCCGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTTCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGTTCCTGCT TCCTCAAAC TCCGCGCGGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGCGGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CCGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCGAAATG TTGAAACCGG CTTATTTTACG
1251 CCGGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCAGCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGCG
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1 VRFNHFIMVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNEP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRAGIPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRLMLD HSLWGEVSPG DHFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAOTLAVAH SKPMKEILT MNKRSNLI
351 RSVFLKLGDD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMAQOM LETAYFSPFA QDFIDTLPIA GTDGLRNRK KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVAKNIISGG
501 DGWLDKLMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1 GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51 CCCTGCAAAAC AAGCCGGGCC GCGGCCACAG CGTTCCCACT TATCCGGCTT
101 TGCCCTTATAA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTG CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGGTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGGCG CCTTCAAAAC
351 CTTCGGCAGC AATTACCGCT GGGCGACCGA GTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAG CACAGCCTGT
551 GGGGCGAAGT CGGACGCCCC GACGATTTCG AAGCCGACAG CGGTTTCGCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGTA TCGGCATAGC
951 CGACACGCCG GAAGGCGCGC AGACACTTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAAC TCCGCGCGGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGCGCGCA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CCGGCCCTGT CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAAATG TTGGAACGGC CTTATTTTACG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCAGCG TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1 VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNEP
51 KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV

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1279

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101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLD AQQLREQGI LNITGHLMLD HSLWGEVGSP DDFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILD MNKRSDNLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMQOM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
501 DGWLDKLMC KERRA*

```

g794/m794 95.5% identity in 515 aa overlap

```

              10      20      30      40      50      60
g794.pep      VRFNHFIMVTIIIIYVISPAKPVRRPGVPTYPALPYNCFFYVTDSPMNFPKTAASLLLLL
              ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          VRLNHFIMIAIIYVISPAKPARRHVSPTYPALPYNCFFYVTDLPMNFPKTAASLLLLL
              10      20      30      40      50      60

              70      80      90      100     110     120
g794.pep      ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFAAFKTFGS
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          ASLAAHALDTGRIPQNEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
              70      80      90      100     110     120

              130     140     150     160     170     180
g794.pep      NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLRDKGIRNITGRLMLD
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          NYRWATEFKSNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQQLREQGILNITGHLMLD
              130     140     150     160     170     180

              190     200     210     220     230     240
g794.pep      HSLWGEVGSPDHFADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          HSLWGEVGSPDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
              190     200     210     220     230     240

              250     260     270     280     290     300
g794.pep      QNNLKITASQAACPSVKKLMRASFSGNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT
              250     260     270     280     290     300

              310     320     330     340     350     360
g794.pep      NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSDNLIARSVFLKLGGD
              310     320     330     340     350     360

              370     380     390     400     410     420
g794.pep      GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
              370     380     390     400     410     420

              430     440     450     460     470     480
g794.pep      QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKLTGTLNNVRALAGYWLGDKPM AVVVIINSGR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          QDFIDTLPIAGTDGTLNRNRFKQSGGLRLKLTGTLNNVRALAGYWLGDKPM AVVVIINSGR
              430     440     450     460     470     480

              490     500     510
g794.pep      AVSLLPDLDNFVAKNIIISGGDGWLDKLMCKERRAX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m794          AVSLLPDLDNFVANNIIISGGDGWLDKLMCKERRAX
              490     500     510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

```

a794.seq
1  GTGCGTCTCA ATCATTTTCAT AATGATAGCG ATTATTATAT ATGTGATTC
51 CCCTGCAAC AAGCCGGCCC GCCGCCACAG CGTCCCCTACT TATCCGGCTT
101 TGCCCTTATA TGTCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACA GGTGCGATTC CGCAAAACGA AATCGCCGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCCGTC

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1280

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301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTTTCGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTTC AAGCCGACAG CGGTTTCGCCG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATTAC CGCCTCCCAA
751 GCTGCTGCC CTTGATCAA AAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTTCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CCGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTGCACAC TCAAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAAC CGGCGCGGAC GGCAAACTGC CCGCCGTTT
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGT CAGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCGCAAATG TTGGAACGG CTTATTTTCA
1251 CCCGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGACTTTAGC CAACCGCTTC AAACAAAGCG GCGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGCGCA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGTGCCCCGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

```

a794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLG GNLWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVGSF DFEADSGSP
201 FMTPPNPMTL SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILTD MNKRSNLI
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVTARMMQOM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLK
451 TGTLNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLDN FVANNIISGG
501 DGWLDAKLMC KERRA*

```

a794/m794 98.6% identity in 515 aa overlap

```

a794.pep      10      20      30      40      50      60
VRLNHFIMIAIIIYVISPANPARRHSVPTYPALPYNCFFYVTDLPMNFPKTAASLLLLL
|||||
m794          10      20      30      40      50      60
VRLNHFIMIAIIIYVISPANPARRHSVPTYPALPYNCFFYVTDLPMNFPKTAASLLLLL
|||||

a794.pep      70      80      90      100     110     120
ASLAHALDTGRIPONEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
|||||
m794          70      80      90      100     110     120
ASLAHALDTGRIPONEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFAAFKTFGS
|||||

a794.pep      130     140     150     160     170     180
NYRWATEFKSNGTVNDGTLGDNLYWAGSGDPVFNQENLLAVQRQLREQGIRNITGHLMLD
|||||
m794          130     140     150     160     170     180
NYRWATEFKSNGTVNDGTLGDNLYWAGSGDPVFNQENLLDAQQLREQGILNITGHLMLD
|||||

a794.pep      190     200     210     220     230     240
HSLWGEVGSPPDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAADSTDILTDPPLPHIFA
|||||
m794          190     200     210     220     230     240
HSLWGEVGSPPDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA
|||||

a794.pep      250     260     270     280     290     300
QNNLKITASQAACPSIKKLMRASFSNTLKLRGNIPESCLGKPVGVRMFADELIRQSFT
|||||
m794          250     260     270     280     290     300
QNNLKITASQAACPSIKKLMRASFSNTLKLRGNIPESCLGKPVGVRMFADELIRQSFT
|||||

a794.pep      310     320     330     340     350     360
NHWLLGGGRISDGIISDTPEGAQTLAVAHSKPMKEILTD MNKRSNLIARSVFLKLGGD

```

g900.seq

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:

q900.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

m900.seq

1 ATGCCGTCTG AAACGCGGCA GCGGAGGTT CGGACGGCAT CGGGTTCATT
51 TCAACGGGCG GATGcCGACC GCATCgG.TA CTTTGTCCAA TAATTCGCGT
101 GCTTCTTTAC GCGCTTTCGC CGCGCCTGCC TGCAAAATCT CTTCGATTG

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151 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
201 CCGCGTTGAT TTTCGCCGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
251 CCGTCGGCAA GCATTTTCGT AAATTCCACC GTTTCAGACG GCGTGGAGAA
301 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TTCGGCTCGC
351 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TTTGGTTTTT
401 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
451 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
501 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGGCGATG
551 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
601 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
651 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCTGCCC GTTTTCTGCA
701 TTTGCTGCA CCGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCCTT
751 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGGAGTGT
801 CGCTTTGGCG GTAGAAGGTG GTGCGCTCGG GGTGAGTCC GCAGGCAAGC
851 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
901 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTTCGGTAT
951 CGAGGTTTTG CGCCGCGCGG ACGGCGGGGC GGATGGCGCC GACGTAGTTG
1001 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
1051 GCTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
1101 TGTGCCGATT ATACCCGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
1151 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

```

m900.pep
  1 MPSETRQAEV RTASGSFQRA DADRIXVFQV *FACFFTRFR RACLQNLFDL
 51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVPKR NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVEHQNIGS HQNRITEQTH FHTEIRVFLP VFCICLHGGF VGMGAVHQTL
251 GSDAGQNPVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHLRLV
301 AFDDTVVIGE EEEFGFIEVL RRADGGADGA DVVAQMRDAG GGYAGQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFFPY*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

```

m900/g900

      10      20      30      40      50
m900.pep      MPSETRQAEVRTASGSFQRADADRIXVFQVXFACFFTRFRRAACLQNLFDLRRVGGQ
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGO
      10      20      30      40      50      60

      60      70      80      90      100     110
m900.pep      LVVAFARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRFRRRGEGFVDFKQWAFVGLFRL
      ||||| :| :||| ||||| :|| :||| ||||| :||| :||| ||||| :||| ||||| |||||
g900      CVVAFQAQFCQFGVDFRRRKFFRLAPSQAVGKHLRKFRFRRRRGEGFIDFKQRAVGLFRL
      70      80      90      100     110     120

      120     130     140     150     160     170
m900.pep      ARLFHIGDDFVDRFLGFFVVPKRNGVAVGFGHFASVQTDQEFVDFIDFHFGQGEFPEA
      ||||| :| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      ARLFHVGNDFVDRFLGFFVVPKRNGIAGVFGHFASVQTDQEFVDFVDFHFGQGEFLET
      130     140     150     160     170     180

      180     190     200     210     220     230
m900.pep      VVEAAGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTEIRVFLPVFCICL
      | |||| :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g900      VGEAAGNVARHFDVLDLVAPDGDGDFVGVEHQNVGSHQNRITEQTHFHTEIGVFLPVFRIGL
      190     200     210     220     230     240

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	240	250	260	270	280	290
m900 . pep	HGGFVGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	: : : : : :					
g900	NGGFVGVGAVHQTLGGDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH					
	250	260	270	280	290	300

	300	310	320	330	340	350
m900 . pep	LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL					
	: : : : : :					
g900	LLLVAFD DAVVIGEEEEFGFIEVLRRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL					
	310	320	330	340	350	360

	360	370	380
m900 . pep	AASMPSEREKDVPIIPDLPTSSRQQTFPYX		
	: : : :		
g900	TAAMPSEREKDAPIIPDLPTSSRQQTFPYX		
	370	380	390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2703>:

a900 . seq (partial)

```

1   GAGGTTCCGA   CGGCATTGGG   TTTATTTCAG   CGGGCGGATA   CCGACCGCAT
51  CACGTACTTT   GCCCAATAAT   TCGCGTGCTT   CTTTACGCGC   TTTTGTGCGG
101 CCTGCCTGCA   AAATCTCTTC   GATTTCGCGA   GGGTCGGCGG   TCAGCTCGTT
151 GTAGCGTTTC   CGCGGTTTCG   CGAGTTCGGC   GTTGATTTTC   GCCGCCAAAA
201 GTTTTTTTGC   CTCGCCCCAA   GCCAAGCCGT   CGGCAAGCAT   TTTTCGTAAAT
251 TCTGCCGTTT   CAGACGGCGT   GGAGAAAGCT   TTGTAGATTT   CAAACAGAGG
301 GCTTTCGTCG   GGCTTCTTCG   GCTCGCCCGG   CTCTTTCATA   TTGGTGATGA
351 TTTTGTGAC   CGATTTTGG   GTTTTTTGT   CGTTTCCCA   AAGCGGAATG
401 GTGTTGCCGT   AGGATTTGGA   CATTTTGCGT   CCGTCCAAAC   CAACCAAGAG
451 TTCGACGTTT   TCGTCGATTT   TCACTTCGGG   CAGTGTGAAG   AGTTCCCGGA
501 AGCGGTGGTT   GAAGCGGCCG   GCAATATCGC   GTGCCATTTC   AACGTGTTGG
551 ATTTGGTCGC   GACCGACTGG   AACTTCATGG   GCATTGAACA   TGAGAATGTC
601 GGCAGTCATG   AGGATAGGGT   AGCTGTACAA   ACCCATTTCC   ACGCCGAAAT
651 CGGGGTCTTC   CTGCCCGTTT   TCCGCATTTC   CCTGCACGGC   GGCTTTGTAG
701 GCGTGGGCGC   GGTTCATCAA   ACCCTTGGCG   GTGATGCAGG   TCAGAAATCCA
751 GTTCAATTCC   ATCACTTCGG   GAATGTCGCT   TTGACGGTAG   AAGGTGGTGC
801 GCTCGGGGTC   GAGTCCGCAG   GCAAGCCAAG   TGGCGGCAAC   GGCTTGGGTG
851 GATTGGTGAA   TCATCTCCGG   CTCGTGGCAT   TTGATGATAC   CGTGGTAATC
901 GGCGAGGAAG   AGGAAGGATT   CGGTATCAGG   GTTTTGCGCC   GCGCGGACGG
951 CGGGGCGGAT   AGCACCGACG   TAGTTGCCCA   GATGCGGGAT   GCCGGTGGTG
1001 GTTACGCCGG   TCAGAACTCG   TTTTTTGCTC   ATAAAAATGT   CCTTGGCGCA
1051 TCAATGCCGT   CTGAAAGGGA   AAAAGATGCG   CCGATTATAC   CCGATTTGCC
1101 ACCTACATCC   AGCCGACAAC   AGACTTTTCC   ATATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2704; ORF 900.a>:

a900 . pep (partial)

```

1   EVRTALGLFQ   RADTDRITYF   AQ*FACFFTR   FLRACLQNLF   DLRRVGGQLV
51  VAFARFGEFG   VDFRRQKFFC   LAPSQAVGKH   FRKFCRFRRR   GESFVDFKQR
101 AFVGLLRLLAR   LFHIGDDFVD   RFLGFFVVP   KRNGVAVGFG   HFASVQTNQE
151 FDFVDFHFG   QCEEFPEAVV   EAAGNIACHF   NVLDLVATDW   NFMGIEHENV
201 GSHEDRVAVQ   THFHAIEGVF   LPVFRICLHG   GFVGVGAVHQ   TLGGDAGQNP
251 VQFHHFGNVA   LTVEGGALGV   ESAGKPSGGN   GLGGLVNHRL   LVAFDDTVVI
301 GEEEEFGFIR   VLRRADGGAD   STDVVAQMRD   AGGGYAGQNS   FFAHKNVLA
351 SMPSEREKDA   PIIPDLPTS   SRQQTFPY*

```

m900/a900 88.4% identity in 378 aa overlap

	10	20	30	40	50	60
m900 . pep	MPSETRQAEVRTASGSFQRADADRIXVFQXFACFFTRFRRAACLQNLFDLRRVGGQLVVA					
	: : : : :					
a900	EVRTALGLFQRADTDRITYFAQXFACFFTRFLRACLQNLFDLRRVGGQLVVA					
	10	20	30	40	50	
	70	80	90	100	110	120

1284

```

m900.pep  FARFGEFGVDFRRQKFFGFTPRQAVGKHFRKFHRRRRGEGFVDFKQWAFVGLFRLARLF
a900      FARFGEFGVDFRRQKFFCLAPSQAVGKHFRKFCRFRRRGESFVDFKQRAFVGLLRRLARLF
           60      70      80      90      100     110

           130     140     150     160     170     180
m900.pep  HIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTDQEFDFVDFIDFHFGQGEFPEAVVEA
a900      HIGDDFVDRFLGFFVVFPRKNGVAVGFGHFASVQTNQEFDFVDFIDFHFGQCEEFPEAVVEA
           120     130     140     150     160     170

           190     200     210     220     230     240
m900.pep  AGDVARHFDVLDLVAPDGHFVGVEHQNIGSHQNRITEQTHFHTAIRVFLPVFCICLHGGF
a900      AGNIACHFNVLDLVATDWNFMGIEHENVGSHEDRVAVQTHFAEIGVFLPVFRICLHGGF
           180     190     200     210     220     230

           250     260     270     280     290     300
m900.pep  VGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSSGGNGLGGLVNHRLRV
a900      VGVGAVHQTLGGDAGQNPVQFHHFGNVALTVEGGALGVESAGKPSSGGNGLGGLVNHRLRV
           240     250     260     270     280     290

           310     320     330     340     350     360
m900.pep  AFDDTVVIGEEEEFGFIEVLRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVLAASM
a900      AFDDTVVIGEEEEFGFIRVLRADGGADSTDVVAQMRDAGGGYAGQNSFFAHKNVLAASM
           300     310     320     330     340     350

           370     380
m900.pep  PSEREKDVPIIPDLPTSSRQQTFFPYX
a900      PSEREKDAPIIPDLPTSSRQQTFFPYX
           360     370

```

g901.seq not found yet

g901.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```

m901.seq
1  ATGCCCGATT TTTGATGTC CAATTTGGCC GTTGCCTTT CCATCACATT
51  GGCTGCCGGT TTGTTACCG TATTAKyAG TGGCTTGGTG ATGTTTTCCA
101 AAACGCCCAA TCCGCGTGTG TTGTCGTTG GTTTGGCGTT TGCCGGCGGT
151 GCGATGGTAT ATGTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTGGC CGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAACTTTAGA CGCGCAAGAC CCGTCGTTT AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGCGCGTTT GCGATTACTG
401 CGCACAATTT CCCCGAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAATAA
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTGGGGG
601 GCGGCTTTGG GCTATTTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGT TTGGCGTTGG
701 ACGAGCTGnt GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
751 TACGGCCTGA CAACGGGTAT GCGGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```

m901.pep
1  MPDFSMSNLA VAFSITLAAG LFTVLXSGLV MFSKTPNPRV LSFGLAFAGG
51  AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAG MG GIALIDRLVP

```

1285

```

101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELXPAA KRYSDGHETV
251 YGLTTGMAVI AVSLVLFHF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq

```

1 ATGCCCCGATT TTTTCGATGTC CAATTTGGCC GTTGCCCTTTT CCATTACGTT
51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTTCCA
101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGCGCGT
151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC
201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTGCGGCG GCGACCATGG
251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG
301 AACCCGCATG AAAC TTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA
351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GGCGGCGTTT GCGATTACTG
401 CGCACAAATTT CCCC GAAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAAT
451 CCAGCAGTCG GGATGCCTTT GGCCTTGGCG ATTGCCATCC ATAATATTCC
501 GGAGGGCATT TCCATCGCCG CGCCGGTTTA TTTTGGCACC CGCAGCCGTA
551 AGAAAACGGT GTGGGCGTGT CTGTATCCG GCTTGGCCGA GCCGTTGGGG
601 GCGGCTTTGG GCTATTGGT TTTGCAGCCG TTTTGTGCGC CTGCCGTGTT
651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGT TTGGCGTTGG
701 ACGAGCTGCT GCCGGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT
751 TACGGCCTGA CAATGGGCAT GGCGGTGATT GCCGTCAGCC TGGTATTGTT
801 CCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep

```

1 MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG
51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP
101 NPHE TLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN
151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWVAC LLSGLAEPLG
201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV
251 YGLTMGMAVI AVSLVLFHF*

```

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
a901	10	20	30	40	50	60
m901.pep	70	80	90	100	110	120
a901	70	80	90	100	110	120
m901.pep	130	140	150	160	170	180
a901	130	140	150	160	170	180
m901.pep	190	200	210	220	230	240
a901	190	200	210	220	230	240
m901.pep	250	260	270			
a901	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

```
g902.seq
1  ATGCCGTCCG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCGTATTG CGCCGCCGCA TTGTCCAAGC GGTGATTTC
151 ACGCCGCGCC TGTTGCGCGT CCGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GGCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GGCGGCGGTT
401 TGTTTGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCCGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCCTCGCC TTTGTACATT TGCGTGcgcg CGcgcccgtg aacggcaaGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgctcgtcg tgccaacca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTGac caccgcctcc aAAatggcGg caaccagcgg CTCGTCCTGC
701 ATCagcGCGC TACCGGCTTG GACGTTGCAC ACTTTCttgg cgggGCAGCC
751 CATAAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTTg taacgcgccg
801 catCCGCCAT CtgttcggGG TCGTGCCGG CAATCTGCAC GGCAACGATG
851 CCGccttcac cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTCTT
901 GAGCGTCGGA TCGCTGGCCA GCATTTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGGC
1001 GCAAGTGCGA TGGGGTTGTC GATAAAATAA CCGCCGATGT GCATAATGGG
1051 CCCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

```
g902.pep
1  MPSEPERRHG NTALPFPIAA RPTVGFSGKP FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQON GGS AFCQTQG
101 RR*NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNA AIF GDFDGGQVL
201 IVVPTQTGF EGNFYARRLD HRLQNGGNQR LVLHQRATGL DVAHFLGGAA
251 HIDVDLRPE SDVVTRIRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKITADVHNG
351 PAFQKSAPLY IF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

```
m902.seq
1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTT GGGCGGTAGG
51  CGCACGCCCC ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGTTGA TTTCACGACG
151 TgTCTgTTCG CCGTcGGGCA TTTCTGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG TATGGCGCGG
251 ATGTGGTTCA AAATAGCGGC GGCGCATTCT GCCAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTTCGGCAT AATGTTTCAA ATCGCGGAAG AACCACGGCC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCGGCGGC GGTTTGTTTG
401 AGGACGGCTT GGGCTTTTTG CGGCGAAGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGTTTTTCGC GATGAGTTCT TAACGCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTGCCTC CGTGACGGC AAGGGCGGCG
551 ATGCCGCAAT CTTCCGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTGATA AGCTGCGCCC CAAGGCTGAC GTTGTAACGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCCT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTGCGTAA TGCCCGCCAT CGGcGCaAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

1287

m902.pep

```

1  LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQCQTQRR
101 QNTVFGIMFQ IAEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD
151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYACRTDDG FQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

m902.pep	10	20	30	40	50
	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLLRR RTVQAVDFTT CLFAVGHF				
g902	10	20	30	40	50
	MPSEPERRHGNTALPFPPIAARPTVGFSKPKITGKC VVLLRRRIVQAVDFTPRLFAVGHF				
m902.pep	60	70	80	90	100
	VDVPAYVFACDAHTGGVAVKRVY GADVQNSG GAFQCQTQRR QNTVFGIMFQ IAEPRPA				
g902	60	70	80	90	100
	ADVPAYVFACDAHTDGLTIKRVH GADVQNGGSAFCQTQRRXNAVFGIMLQIAEKPRPA				
m902.pep	120	130	140	150	160
	LRAAPYHNAVGGGLFEDGLGFLRRSNVAVD PDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
g902	120	130	140	150	160
	LRAAPYHDAVGGGLFEDGGGFLRRSDVAVD PGRDVQTAFGLGDEFVTRLAFVHLRARAPV				
m902.pep	180	190	200	210	220
	DGKGGDAAI FGDGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGL				
g902	180	190	200	210	220
	NGKGGNAAI FGDGDDGQVLI VVVPTQTGFEGNGYARRLDHRLQNGGNQRLVLHQRATGL				
m902.pep	240	250	260	270	280
	DIADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAA VQGFSSIS				
g902	240	250	260	270	280
	DVAHFLGGAHIDVDDL RPESDVVTRRI RHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
m902.pep	300	310	320	330	340
	ERRVAGQHFAHR PTCAKISAKS AERFVGNARHRRKDCGVVDKIAADVHNGSAFQKSTPLY				
g902	300	310	320	330	340
	ERRIAGQHFAHR PTCAKRPTEA AEGFVGNARHRRKDCGVVDKITADVHNGPAFQKSAPLY				
m902.pep	360				
	IFX				
g902	360				
	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

```

1  TTGCACTTTC AAAGGATAAT CAAGTGTTCA GAAGGCATTG GGC CGGTAGG
51 CGCACGCCCA ACTGTCGGTT TTTTCGGCAA GTCTTTCAAG ATAACCTGCA

```


1288

```

101 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
151 TGTCTGTTTC CCGTCGGGCA TTTCGTCGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGGCG GTGTCGCCGT AAAACGCGTG CATGGCTCGG
251 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAAACTCA AGGCAGGCGG
301 TAAAACACCG TGTTTCGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
351 TGCCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTGTTGTTT
401 AGGACGGCTT GGGCTTTTTC CGGCGAGGTA ATGTCGCCGT TGACCCAGAC
451 CGGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
501 CGCCTTTGTA CATTTCGCTG CGCGTGCCTC CGTGGACGGC AAGGGCGGCA
551 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
651 TGACCACCGC CTCCAAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAACG GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCTT
851 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTCGC CCAAAATCTC
951 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCCCAT CCGCGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCGCCG ATGTGCATAA TGGATCCGCG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

a902.pep

```

1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLRR RTVQAVDEFTT
51 CLFAVGHEVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
101 *NTVFGVMFQ IAEEPRALR AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
151 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGGNAIFGD FGDDGQVLMV
201 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
301 RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCGDGVVDK IAADVHNGSA
351 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLRR RTVQAVDEFTT CLFAVGHEVD					
a902	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVLRR RTVQAVDEFTT CLFAVGHEVD					
	10	20	30	40	50	60
m902.pep	VPAYVFACDA HTGGVAVKRVY GADVQNSGGAFCQTQGRRQNTVFGIMFQIAEEPRPALR					
a902	VPAYVFACDA HTGGVAVKRVHGS DVVQNSGGTFCQTQGRRXNTVFGVMFQIAEEPRALR					
	70	80	90	100	110	120
m902.pep	VPAYVFACDA HTGGVAVKRVY GADVQNSGGAFCQTQGRRQNTVFGIMFQIAEEPRPALR					
a902	VPAYVFACDA HTGGVAVKRVHGS DVVQNSGGTFCQTQGRRXNTVFGVMFQIAEEPRALR					
	70	80	90	100	110	120
m902.pep	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRARASVDG					
	130	140	150	160	170	180
m902.pep	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAFVHLRARASVDG					
	130	140	150	160	170	180
m902.pep	KGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGGNAIFGDFGDDGQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
m902.pep	KGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGGNAIFGDFGDDGQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
m902.pep	ADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
m902.pep	ADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHV DVDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
m902.pep	RVAGQHFAHR PTCAKISAKS AERFVGNAHR RRCGDGVVDK IAADVHNGSA FQKSTPLYIF					
	310	320	330	340	350	360

1289

```

a902      |||||
          RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep   X
           |
a902       X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcG gatgaggCAA GCCCCTGCTT
51 TCCTATTTCT GAGGTGGAaT TGGTGGGTGA aGaaacggct aAATTCGgt
101 tTGCGCTcaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGgcaagtgt
151 CTGcATGcgg gcgacattAA TCAAAtcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAAccctga tgccggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTT CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtaGAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGCGA TTATCGGAAG TCTATGACTA TAATGGAAA AGTTACAACA
851 CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAACCC
901 TATCTCAGTG TAAAACTGTG GACGAGGGAA AAAAAAGTT ACATTGATGA
951 TGCCGAAC TGCTGTACAAC GCGGTAAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTGCGAGTA CGGCAGATTT TAAGTTGAAA
1051 TATAAACACG GCACCGGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCGCTA ACATCGCAAG ACAAACGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTGAGCTG GCAATTTAAA
1351 CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGCA GATAAGCTT GCGGGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGAAAAAGCC cgaatatatt cAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLO LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAEQ NKFPTRNDL LNLRLDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPP
251 GKWTWAFNHN GYRYHQAQVS LSEVYDYNK SYNTDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKSYYDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYLGLAD VGHVSGQSAK WLSGQTLAAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWTGTFQ VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTAACTG ATGCAAATGT
51 CCGTTTTGAG CAACCATTTG AGAAGAACAA TTATGTCTG AGTGAAGATG
101 AAACACCGTG TACTCGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

```

m903 . pep

m903/g903

	10	20	30	40	50	60
m903.pep	MQRQQHIDAELLTDANVRFEQPLEKNYYVLSEDETPCTRVNYISLDDKTVRKFSFLPSVL					
				:::	: :	: : :
g903			MATQVGGANSDEASPCFP	ISEVELVGEETAKFRFALNHA		
			10	20	30	
	70	80	90	100	110	120
m903.pep	MKETAFKTMCLGSNNLSRLQKAAQILIVRGYLTSAIIQPQNMSGILKLRVSAGEIG					
	: : :	: : : : : : :	:	: : :	: : :	: : : :
g903	LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKQLQTLMPGYLR					
	40	50	60	70	80	90

1291

	130	140	150	160	170	180
m903 . pep	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRDVEQGLNLRRLPSVKTDIQIIPSE					
g903	SIRIDRSNDQTHAGRIAAAFQNKFPTRSDLLNLRDLEQGLNLRKCLPTAEADLQIVPVE					
	100	110	120	130	140	150
	190	200	210	220	230	
m903 . pep	EE-GKSDLQIKWQONK-PIRFSIGIDDAGGKTTGKYQGNVALSFDNPLGLSDLFYVSYGR					
g903	REPNSQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQGNITFSADNPFGLSDMFYVNYGR					
	160	170	180	190	200	210
	240	250	260	270	280	290
m903 . pep	GLAHKTDLTDATGTETESGSRYSVHYSVPVKKWLFNFHNGHRYHEATEGYSVNYDYNG					
g903	SIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAFNHNGYRYHQAVSGLSEVYDYNG					
	220	230	240	250	260	270
	300	310	320	330	340	350
m903 . pep	KQYQSSSLAAERMLWRNRLHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAY					
g903	KSYNTDFGFNRLLYRDAKRKTYLSVKLWTRTKSYIDDAELTVQRRKTTGWLAELSHKGY					
	280	290	300	310	320	330
	360	370	380	390	400	410
m903 . pep	LNRWQLDGKLSYKRGTMQRSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFF					
g903	IGRSTADFKLYKHGTGMKDALARPEEAFGE--GTSRMKIWTASADVNTPFQIGKQLFA					
	340	350	360	370	380	390
	420	430	440	450	460	470
m903 . pep	YATAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFY					
g903	YDTSVHAQWNKTPLTSQDKLAIGGHHTVIRGFDGEMSLPAERGWYWRNDLSWQFKPGHQLY					
	400	410	420	430	440	450
	480	490	500	510	520	530
m903 . pep	LGADYGRVSGESAQYVSGKQLMGAVVGFRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTV					
g903	LGADVGHVSGQSAKWLSGQTLAIGIRGQIKLGGNLHYDIFTGRALKKPEYFQTKKWV					
	460	470	480	490	500	510
	540					
m903 . pep	YGFNLNYSFX					
g903	TGFQVGYSFX					
	520					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2719>:

a903 . seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAATTTT	CTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	AACTGGGATG	TGTTTAGGTT	CCAATAATTT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGGCTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTG	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGGCAGTAT	TAGTGCATTC	AATAACAAAT	TTCCCTTATA	TAGGAACAAA
451	ATTCTCAATC	TCGCGATGT	AGAGCAGGGC	TTGGAAGAAC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAAGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTTCAGT

a903.pcp

1	MQRQQHIDAE	LLTDANVRFE	QPLEKNNYVL	SEDETPCTRV	NYISLDDKTA
51	RKFSFLPSVL	MKETAFKTGM	CLGSNNLSRL	QKAAQQILIV	RGYLTSQLII
101	QPQNMDSGIL	KLRVSAGEIG	DIRYEKRDG	KSAGSISAF	NNKFPLYRNK
151	ILNLRDVEQG	LENLRSLPSV	KTDIQIIPSE	EEGKSDLQIK	WQONKPIRFS
201	IGIDDAAGKT	TGKYQGNVAL	SFDNPLGLSD	LFFYVSGRGL	VHKTDLTDAT
251	GTETESGSR	YSVHYSVPVK	KWLFSEFNHG	HRHYEATEGY	SVNYDYGKQ
301	YQSSSLAERM	LWRNRFHKTS	VGMKLWTRQT	YKYIDDAEIE	VQRRRSAGWE
351	AELRHRYALN	RWQLDGKLSY	KRGTMGRQSM	PAPEENGSGT	IPGTSRMKII
401	TAGLDAAPFL	MLGKQFFFYA	TAIQAQWNKT	PLVAQDKLSI	GSRYTVXGFD
451	GEQSLFGERG	FYQWNTLTWY	FHPNHQFYLG	ADYGRVSGES	AQYVSGKQLM
501	GAVVGFRGGH	KVGGMFAYDL	FAGKLPHKPK	GFQTTNTVYG	FNLNYSF*

	10	20	30	40	50	60
m903.pep	MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDET	PCTRVNYISLDDKTVRKFSFLPSVL				
a903	MQRQQHIDAELLTDANVRFEQPLEKNNYVLSEDET	PCTRVNYISLDDKTVRKFSFLPSVL				
	10	20	30	40	50	60
m903.pep	70	80	90	100	110	120
	MKETAFKTGMCLGSNNLSRLQKAAQQILIVRGYLT	SQAI IQPQNMDSGILKLRVSAGEIG				
a903	MKETAFKTGMCLGSNNLSRLQKAAQQILIVRGYLT	SQAI IQPQNMDSGILKLRVSAGEIG				
	70	80	90	100	110	120
m903.pep	130	140	150	160	170	180
	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRD	VEQGLENLRLPSVKTDIQIIPSE				
a903	DIRYEEKRDGKSAEGSISAFNNKFPLYRNKILNLRD	VEQGLENLRLPSVKTDIQIIPSE				
	130	140	150	160	170	180
m903.pep	190	200	210	220	230	240
	EEGKSDLQIKWQQNKPIRFSIGIDDAGGKTTGKYQ	GNVALSFDNPLGLSDLFVVSYGRGL				
a903	EEGKSDLQIKWQQNKPIRFSIGIDDAGGKTTGKYQ	GNVALSFDNPLGLSDLFVVSYGRGL				
	190	200	210	220	230	240
m903.pep	250	260	270	280	290	300
	AHKTDLTLDATGTETESGSRYSVHYSVPVKKWL	FSFNHNGHRYHEATEGYSVNYDYNKGKQ				
a903	AHKTDLTLDATGTETESGSRYSVHYSVPVKKWL	FSFNHNGHRYHEATEGYSVNYDYNKGKQ				

1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSSLAERMLWRNRLHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
a903	YQSSSLAERMLWRNRFHKTSVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHAYLN					
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTGMRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQFFYA					
a903	RWQLDGKLSYKRGTGMRQSMPEENGDDIPGTSRMKIITAGLDAAAPFMLGKQFFYA					
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

```

g904.seq
1  ATGATGCAGC ACAATCGTTT CTTGCGGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGC CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAAGC GCAGCGGCGC GCGCGGCCGG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACAAAT CGGTCGGGAA
451 CGGGCCCCGA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGCCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TTTGTTTCAA CACGCggaac acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTACAG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGTCGT
901 GCGGATTTTG CCTTTGCCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCCAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGGTTT TTTGCCGCCG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGGAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatata A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

```

g904.pep
1  MMQHNRFPAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADSRFAP

```

1294

```

51 AGHGFVNRF A GFHRI RTARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
101 HTGNAV DLDG AFQGGGIKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
201 QRTLRAF KQQ FFAVFVFFVQ HAGHVG NHRR NARRDFFDNR HHVFRFNRS G
251 VMQVLELDV V IGKDG IQFFT QFFRMQ QIGG ANGAACHFV F VGRADAAAGR
301 ADFAF AARCF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
401 AGFFRQPVND FTFTLVAPLC ADYINIFSHS HITYRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

```

m904.seq
1 ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51 CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTC AAATA TGCTTTGGCG
101 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTTCCACC GCATCGGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCGT CGGGCAATTC ATAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
301 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG CCGCGGCAT
351 CAAACCAGCC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAATT CCGTCGGGAA
451 CGGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCCGCGC CTGCCGAAGC TGCGCCCGCC
551 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGC GCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
651 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTAA CCGGCTCGGC
751 ATTGTGCAGA TGTTGCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTTCAG CAGTTTtTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CCGCGTGCCA CTTTGTCCTT GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTGCCGCG GCG .AtcTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAAACTTT
1101 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTT TTTGCCGCCG
1151 ACAACCAAGG TATGCCCCGC ATTGTGCGCG CTTTGAAGC GCACCaCGCC
1201 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCCACTGTGC GCCGATTAsT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

```

m904.pep
1 MMQHNRRFFSV GAGGDDGDRR AADFFNPFQI CFGVFGQCAV VLHAESGFAP
51 AGHGFVNRLA GFHRIGHTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAV DLDG AFQGGGIKPA AAACASGYRT EFVSAFCQTY AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAF KQQ FFAVFVFLVQ HAGHVG NHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDG IQFFT QFXRMQ QIGG ANGAACHFV F VGRADAAAGR
301 ADFAF AAXIF AGLVERDVVR QDQRAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMAR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITYRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

```

m904/g904
10 20 30 40 50 60
m904.pep MMQHNRRFFSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g904 MMQHNRRFFAVGAGGDDGDRRAADFFNPFQICFGIGRQCVAFHADSRFAPAGHGFVNRF
10 20 30 40 50 60
70 80 90 100 110 120

```

1295

m904 . pep	GFHRIGTARQDVGFAAVQGFIADADIDGFNAVHYIEFSNTHTGNVAVDLGAFQGGGIKPA
g904	GFHRIRRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNVAVDLGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	AAACASGYRTEFVSAFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCAVFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	CARQTVGRGNEGISA VVDVQORTLRAFQKQFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
g904	RAGETVGRGNEGVS VVDVQORTLRAFQKQFFAVFVFFVQHAGHVGNHRRNARRDFFDNR
	190 200 210 220 230 240
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDGIIQFFTFQFXRMQIGGANGAACHFVFGVGRADAAAGR
g904	HHVFRFNRSQVLELDVIVIGKDGIIQFFTFQFRMQIGGANGAACHFVFGVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	ADFAFAARIFAGLVERDVVRQDQRRDQFQAFDVFHACRVQLVDFQAQGGFGGDDNART
g904	ADFAFAARCFAGLVERDVVRQDQRRDQFQAFDVFHACRVQLVDFQAQGGFGGNDNART
	310 320 330 340 350 360
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAALAHHAAGFFRQPVNDFTFTLVAPLC
g904	DEAIQSFSVQDARNQAQNGFFAADDQGMARIVAALAHDAAGFFRQPVNDFTFTLVAPLC
	370 380 390 400 410 420
m904 . pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

1	ATGATGCAGC	ACAATCGTTT	CTTCGCGGTC	GGGGCCGGTG	GAGACGATGG
51	CGACCGGCGC	ACCGCAGACT	TCTTCAATCC	GTTTCAAATA	TGCTTTGGCA
101	TTGGCAGGTA	ATGCGTCGTA	GCTTTTCACG	CCGAAAGTGG	ATTGCTCCCA
151	ACCGGCGCATG	GTTTCGTAAA	TCGGCTTGCA	GGCTTCTACC	GCATCAGAGC
201	CGCAAGGCAG	GATGTCGGTT	TTGCCGCCGT	CGGGCAATTC	GTAGCCGACG
251	CAGATATTGA	TGGTTTCAAC	GCCGTCCATT	ACATCGAGTT	TGGTAATACA
301	CATACCGGAA	ATGCCGTTGA	TTTGATGGA	GCGTTTCAGG	GCGGCGGCAT
351	CAAACGAGCC	GCAGCGGCGT	GCGCGTCCGG	TTACCGAACC	GAATTCGTGT
401	CCGCGTTCTG	CCAAACCTGC	TCCGACTTCG	TCGAACAATT	CGGTCGGGAA
451	CGGGCCCGAA	CCGACGCGCG	TGGTATAGGC	TTTGACGATG	CCCAAAACAT
501	AATCCAGCAT	TTGAGGGCCT	ACGCCGCGC	CTGCCGAAGC	CGCGCCGGCG
551	AGGCAGTTGG	ACGAAGTAAC	GAAGGGGTAA	GTGCCGTAGT	CGATGTCCAA
601	CAACGCACCT	TGCGCGCCTT	CAACAGCAG	TTTTTCGCCG	TTTTTGTTTT
651	TTTCGTTCAA	CACGCGGGAC	ACGTCGGTAA	TCATCGGCGT	AATGCGCGGC
701	GCGACTTTTT	CGATAACCGC	CATCACGTCT	TCCGCTTTCA	CCGACTCGGC
751	ATTGTGCAGA	TGTTGCAGTT	GGACGTTGTA	ATAAGCAAAG	ACGGCATCCA
801	GTTTTTCACG	CAGTTTTTCA	GGATGCAGCA	AATCGGCGGC	GCGAATGGCG
851	CGGCGTGCCA	CTTTGTCTTC	GTAGGCAGGG	CCGATGCCGC	GGCCGGTCGT
901	GCCGATTTTG	CCTTTGCCGC	GCGATGCTTC	TCGGGCTTGG	TCGAGCGCGA

951	TGTGATAAGG	CAGGATCAGC	GGGCAGGTCG	GCGCGATTTT	CAGACGGCCT
1001	TCGACGTTTT	TCACGCCTCG	CGCGTTCAAC	TCGTCGATTT	CGCCCCAACAG
1051	GGCTTCGGGG	GAGACGACAA	CGCCCCAACC	GATGAAGCAG	TCCAGACTTT
1101	CATGCAGGAT	GCCGCTCGGA	ATCAGGCGCA	AAATGGTTTT	TTTGCCGCGC
1151	ACAACCAAGG	TATGACCCGC	ATTGTGGCCG	CCTTGGAAGC	GCACCACGCC
1201	TCCGGCTTCT	TCCGCCAGCC	AGTCAACGAT	TTTACCTTTA	CCCTCGTCGC
1251	CCCAGTGTGC	GCCGATTACT	ACAACATTTT	TAGCCATAGC	CATATAACCT
1301	.TCGATATTA	A			

a904.pwp

m904/a904 91.3% identity in 436 aa overlap

430

1297

```

m904.pep    ADXYNIFSHSHITYRYX
             || ||||| |||| |||
a904        ADYYNIFSHSHITXRYX
             430

```

g906.seq not found yet
g906.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

```

m906.seq
 1  ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
51  GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC
151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAACAAA
301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

```

m906.pep
 1  MKYIVSISLA MGLAACSFEG FKNPNWDAAS FWELKNYANP YPGSASAALD
51  QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPENK
101 KYEWPREEGK TK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

```

g907.seq (partial)
 1  ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT
51  GCTGTGTGCC GCCGCGCGCG TGTGTATCAG CCCGCTGGCG CACGCCGGCG
101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGGCA AGATTGCTCC
251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga
351 aagcgggtac cgagctcgaa tcatatca..

```

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

```

g907.pep (partial)
 1  MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAQREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESGY RARIIS...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

```

m907.seq
 1  ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT
51  GTTGTGTGCC GCCGGTGCGT TGTGTCTCAG TCCTCTGGCG CACGCCGGCG
101 CGCAACGTGA GGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT
151 TCTGTCGGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGGCA AGGTTGCTCC
251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCCG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTkTGG AAAAActACA TCGGCAAAAC GGCGCACAAC
451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA
551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

```

m907.pep
 1  MRKPTDTLPV NLQRRRLCA AGALLLSPLA HAGAQREETL ADDVASVMRS
51  SVGSVNPPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVA RGLMQVMPXW KNYIGKPAHN

```

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151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRL	LLCAAGALLISPLAHAGA	QREETLADDVASVMR	SSVGSVNP	PRL	
	:	:	:	:	:	:
m907	MRKPTDTLPVNLQRRRL	LLCAAGALLSPLAHAGA	QREETLADDVASVMR	SSVGSVNP	PRL	
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMS	ARLARFVPEDEGER	RRLLVNIQYESSR	AGLDTQIVLGLIE	ESGY	
m907	VFDNPKEGERWLSAMS	ARLARFVPEEEER	RRLLVNIQYESSR	AGLDTQIVLGLIE	ESAF	
	70	80	90	100	110	120
g907.pep	RARIIS					
m907	RQYAISGVGARGLMQ	VMPXWKNYIGKPA	HNLFDIRTNLRYG	CTILRHRYNLEK	GNIVRAL	
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

1 ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTGCAAC GCCGCCGCCT
51 ATTGTGTGCT GCCGGCGCGC TGTGTGCTCAG CCCGCTGGCA CAAGCCGGCG
101 CGCAACGTGA AGAAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGC
151 TCTGTGCGCA GCATAAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA
201 GGGCGAGCGT TGGCTGTCCG CGATGTCTGC TCGGTTGGCA AGGTTCGTCC
251 CCGATGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC
301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA
351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA
401 TGCAGGTTAT GCCGTTTTGG AAAAATAACA TCGGCAAAAC GGCGCACAAAC
451 CTGTTGCGCA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA
501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCACTC GCCCGTTTTA
551 ACGGTAGCCT CGCAGCAAT AAATATCCGA ACGCGGTTT GGGCGCGTGG
601 CGCAACCGCT GGCAGTGGCG TTGA

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

1 MKKPTDTLPV NLQRRRLCA AGALLSPLA QAGAQREETL ADDVASVMRS
51 SVGSINPPRL VFDNPKEGER WLSAMSARLA RFVPDEEERR RLLVNIQYES
101 SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPFW KNYIGKPAHN
151 LFDIRTNLRY GCTILRHRYN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW
201 RNRWQWR*

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRL	LLCAAGALLSPLAHAGA	QREETLADDVASVMR	SSVGSVNP	PRL	
	:	:	:	:	:	:
a907	MKKPTDTLPVNLQRRRL	LLCAAGALLSPLAQAGA	QREETLADDVASVMR	SSVGSINP	PRL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMS	ARLARFVPEEEER	RRLLVNIQYESSR	AGLDTQIVLGLIE	ESAF	
a907	VFDNPKEGERWLSAMS	ARLARFVPEEEER	RRLLVNIQYESSR	AGLDTQIVLGLIE	ESAF	

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	70	80	90	100	110	120
	130	140	150	160	170	180
m907.pep	RQYAI	SGVG	ARGLM	QVMP	XWK	NYIGK
a907	RQYAI	SGVG	ARGLM	QVMP	FWKN	YIGK
	130	140	150	160	170	180
	190	200				
m907.pep	ARFNG	SLGS	SNKY	PNAVL	GAWR	NRWQ
a907	ARFNG	SLGS	SNKY	PNAVL	GAWR	NRWQ
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

```

g908.seq
1   ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAGT CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTAT
151 CAAAACGGTC CGCATTTAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTCCTA TTATCCGTGA
351 acaagtgaac cctgacagta ttgtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa ttagccatT TTagcttcgc tgaaacttcg
451 ttttcgtatC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

```

g908.pep
1   MXKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMFD GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIVYTDCY RSYDVLDVSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

```

m908.seq
1   ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAGT CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTTGGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTCCTA TTATCCGTGA
351 ACAAGTGAAC CCTGACAGCA TTTTATATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

```

m908.pep
1   MRKSRLSRYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMFD GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPNTQTAT LFPIIREQVK PDSIFYTDCY RSYDVLDVRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

```

g908/m908
10      20      30      40      50      60
g908.pep  MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXLIYQNGPHLEMFD

```

m908	MRKSRLS QYKQXKLI ELFVTGVTARTAAELVGVNKNTAAYYFHLRLLLIYQNSPHLEMFD
	10 20 30 40 50 60
g908.pep	GEVEADESYFGGQRKGRKRGGAAGKVAVFGLLKRNGKVYTVTVPNQTATLFPPIIREQVK
	70 80 90 100 110 120
m908	GEVEADESYFGGQRKGRKRGGAAGKVAVFGLLKRNGKVYTVTVPNQTATLFPPIIREQVK
	70 80 90 100 110 120
g908.pep	PDSIVYTDCYRSYDVLVDVSEFSHFSAETSFSYQSQHTFCRTTKPYX
	130 140 150 160
m908	PDSIFYTDCYRSYDVLVDVREFSHFSAETSFSYQSQHTFCRTTKPYX
	130 140 150 160

```

a908.seq
1  ATGAGAAAAA  GTCGTCTAAG  CCAGTATAAA  CAAAATAAAC  TCATTGAGCT
51  ATTTGTCGCA  GGTGTAAC TG  CAAGAACGGC  AGCAGAGTTA  GTAGGCGTTA
101 ATAAAAATAC  CGCAGCCTAT  TATTTTCATC  GTTTACGATT  ACTTATTTAT
151 CAAAACAGTC  CGCATTTGGA  AATGTTTGAT  GCGGAAGTAG  AAGCAGATGA
201 AAGTTATTTT  GCGCGACAAC  GCAAAGGCCA  ACGCGGTTCG  GGTGCTGCCG
251 GTAAAGTCGC  CGTATTCGGT  CTTTTGAAGC  GAAATGGTAA  GGTTTATACG
301 GTTACAGTAC  CGAATACTCA  AACCGCTACT  TTATTTCTTA  TTATCCGTGA
351 ACAAGTGAAA  CCTGACAGCA  TTGTTTATAC  GGATTGTTAT  CGTAGCTATG
401 ATGTATTAGA  TGTGCGCGAA  TTTAGCCATT  TTAGCTTCGC  TGAAACTTCG
451 TTTTCGTATC  AATCACAGCA  CACATTTTGC  CGAACGACAA  AACCATATTA
501 A

```

a908.pep

1	MRKSRLSQYK	QNKLIELFVA	GVTARTAAEL	VGVNKNTAAY	YFHLRLLIY
51	QNSPHLEMF	GEVEADESYF	GGQRKGKGR	GAAGKVAVF	LLKRNQKVY
101	VTVPNTQT	LFPIIREQVK	PDSIVYTD	RSYDVL	FSHFSFAET
151	FSYQSQTFC	RTTKPY*			

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLI	ELFVTGVTARTAAEL	VGVNKNTAAYYFHRL	RLLLIYQNSPHLEM	FDF	
a908	MRKSRLSQYKQKLI	ELFVAGVTARTAAEL	VGVNKNTAAYYFHRL	RLLLIYQNSPHLEM	FDF	
	10	20	30	40	50	60
	70	80	90	100	110	120
m908.pep	GEVEADESYFGGQR	KGKRGRGAAGKVAV	FGLLRNGKVYTVTV	PNTQTATLFPIIRE	QVK	
a908	GEVEADESYFGGQR	KGKRGRGAAGKVAV	FGLLRNGKVYTVTV	PNTQTATLFPIIRE	QVK	
	70	80	90	100	110	120
	130	140	150	160		
m908.pep	PDSIFYTDCYRSYD	VDLVREFSHFSFAET	SFSYQSQHTFCRTT	KPYX		
a908	PDSIVYTDYRSYD	VDLVREFSHFSFAET	SFSYQSQHTFCRTT	KPYX		
	130	140	150	160		

```
g909.seq (partial)
      1  atgcgtaaaa ccgtaacttat cCTgaccatc tccgccgcc ttttgtcggg
     51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
    101  caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcggctcg
```

1301

```

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg
201 caaccaaag cggggaagc ccgcgacgag gagagccgca acgctgggga
251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa
301 acgggggagg ggaagcgatc ggcgagg..

```

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

```

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS
51 KKVDCDEYGG ERRAVLNqK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE
101 TGEgKRSAR..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

```

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTTGTcGGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AACCAAAGTT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

```

1 MRKTFILFLTA AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLNqT GNNADEEHRQ HWQKPKFQNR *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFILFLTA AAALLSGCAW ETYQDNGGKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
	: : : : : : :::					
g909	MRKTVLILTI SAALLSGCTW ETYQDGSgKTAVRAKSTGTPLCWQDGRGSKKVDCEYGG					
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLNqTGNNADEEHRQH WQKPKFQNR X					
	: :: :: : :					
g909	ERRAVLRNqKRGKPTRRAATLGKPSFRARDGGGRVNRAETGEGKRSAR					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

```

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTTGTcGGG
51 CTGCGCGTGG GAAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC
101 AAAAAATATCC CGCCGGCACG CCCGTTTATT ACCAAGACGG CAGCTACTCG
151 AAAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC
201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA
251 AGCCCAAATT TCAAAACCGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

```

1 MRKTFILILMT AAALLSGCAW ETYQDNGGKT AVRQKYPAGT PVYYQDGSYS
51 KNMNYNQYRP ERHAVLNqT GNNADEEHRQ HWQKPKFQNR *

```

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFILFLTA AAALLSGCAW ETYQDNGGKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
	: : : : : : : : : : :					
a909	MRKTFILILMTAAALLSGCAWETYQDNGGKTAVRQKYPAGTPVYYQDGSYSKNMNYNQYRP					
	10	20	30	40	50	60

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	70	80	90
m909.pep	ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQKPKFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```
g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```
g910.pep
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```
m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```
m910.pep
1  MKKLLLAADV SLSAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

```
g910/m910
10 20 30 40 50 60
g910.pep MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW
m910      MKKLLLAADVSLSAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW
10 20 30 40 50 60
70 80 90
g910.pep GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
m910      GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX
70 80 90
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```
a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAAT CATCAAAGAG CAGCTCGATC GCTGA
```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

```
a910.pep
```

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1 MKKLLLVAVV SLSAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ
 51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLA	AVVSLS	AAAAFAG	DSAERQI	YGD	PHFEQNRTKAVKMLEQRGYQVYD
	:	:	:	:	:	:
a910	MKKLLLV	AVVSLS	AATAFAG	DSAERQI	YGD	PYFEQNRTKAVKMLEQRGYQVHDVDADDDHW
	10	20	30	40	50	60

	70	80	90
m910.pep	GKPVLEVEAYK	DGREYDIVLSYPDLKIIKEQLDRX	
	:	:	:
a910	GKPVLEVEAYK	DGREYDIVLSYPDLKIIKEQLDRX	
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq

1 ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTCG TCTTGATCGG
 51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCGGGC GGCGGCGCGT
 101 TCGGCGGTTT GGACAAACT TACGCCGTTT ATGCCGATT CCGCGACATC
 151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
 201 GCGCGTCGGC GCTATCGGGC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
 251 GCCTTGATTT GGACGGCAAG TATCAGTTCA GCAGTGACGT TTCCGCGCAA
 301 ATCCTGACTT CGGGACTTTT GGGCGAACAG TACATCGGGC TGCAGCAGGG
 351 CGGCGATACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT
 401 CTGCAATGGT TCTGGAAAAC CTGATCGGTA AATTCATGAC CAGCTTCGCC
 451 GAGAAAAACG CTGAGGCGCG CAATGCGGAA AAAGCCGcag aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep

1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
 51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
 101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
 151 EKNAEGGNAE KAAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq

1 ATGAAGAAGA ACATATTGGA ATTTTGGGTC GGACTGTTTCG TCCTGATTGG
 51 CGCGGCGGCG GTTGCCCTTC TCGCTTTCCG CGTGGCGGGC GGTGCGGCGT
 101 TCGGCGGTTT GGACAAACT TACGCCGTTT ATGCCGATT CCGCGACATC
 151 GGCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
 201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
 251 GCCTCGATTT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
 301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
 351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAGTT
 401 CTGCAATGGT TCTGGAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGC
 451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep

1 MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAAFGGSDKT YAVYADFGDI
 51 GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRLDLGK YQFSSDVSAQ
 101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
 151 EKNADGGNAE KAAE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10 20 30 40 50 60

1304

```

g911.pep  MKKNILEFWVGLFVLIGAAAVAFVLAFLRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          |||
m911      MKKNILEFWVGLFVLIGAAAVAFVLAFLRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          |||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAX
          |||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1  ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGAAGTGTTC TCCTGATTGG
51  CGCGGCGGCG GTTGCTTTC TCGCTTTCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAACT TACGCCGTT ATGCCGATT CGGCGACATC
151 GCGGTTTGA AGGTCAATGC CCCCCTCAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGGCGA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGAAAAAC CTTATCGGCA AATTCATGAC GAGTTTGGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1  MKKNILEFWV GLFVLIGAAA VAFVLAFLRVAG GAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDDGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQQGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

m911.pep  MKKNILEFWVGLFVLIGAAAVAFVLAFLRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          |||
a911      MKKNILEFWVGLFVLIGAAAVAFVLAFLRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          |||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDDGKYQFSSDVSAQILTSGLLGEQYIGLQQGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAX
          |||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1  gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GTTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

g912.pap

m912.seq

m912.pcp

g912/m912

	10	20	30	40	50	60
g912.pep	VKSSSFISALGIGILSIGMAFASPADAVGQIRQNATQVLTILKSGDAASARPKAEAYAVP					
	: : : : : : : : : : :					
m912	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g912.pep	YFDFQRM TALAVGNPWRTASDAQQALAKEFQTLLIRTYSGTMLKFKNATVNVKDNPIVN					
	: : : : : : : : : :					
m912	YFDFQRM TALAVGNPWRTASDAQQALAKEFQTLLIRTYSGTMLKLNANVNVKDNPIVN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g912.pep	KGGKEIVVRAEVGIPGQKPVNMDFTTYQSGGKYRTYNVAIEGTSLVTVYRNQFGEI I KAK					
	: : : : : : : : : :					
m912	KGGKEIIVRAEVGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTVYRNQFGEI I KAK					
	130	140	150	160	170	180
	190					
g912.pep	GIDGLIAELKAKNGGKX					

1306

```

m912      |:|||||
          GVDGLIAELKAKNGGKX
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

```

a912.seq
1  ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTTGAGCAT
51  CCGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAACCAA ATCCGTCAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TGCGATTCCC TATTTGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAA AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGGCGGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GGCGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

```

a912.pep
1  MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNATQVLS ILKSGDANTA
51  RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTL LIRTY S
101 GTMLKLK NAN VNVKDNPIVN KGGKEIIVRA EVGVP GQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI IKAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

```

m912.pep      10      20      30      40      50      60
MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNATQVLSILKNGDANTARQKAEAYAIP
|||||:|||||:|||||:|||||:|||||:|||||
a912          10      20      30      40      50      60
MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNATQVLSILKSGDANTARQKAEAYAIP

m912.pep      70      80      90      100     110     120
YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTL LIRTYSGTMLKLKNANVNVKDNPIVN
|||||:|||||:|||||:|||||:|||||:|||||
a912          70      80      90      100     110     120
YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTL LIRTYSGTMLKLKNANVNVKDNPIVN

m912.pep     130     140     150     160     170     180
KGGKEIIVRAEVGVP GQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK
|||||:|||||:|||||:|||||:|||||:|||||
a912         130     140     150     160     170     180
KGGKEIIVRAEVGVP GQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK

m912.pep     190
GVDGLIAELKAKNGGKX
|||||:|||||
a912         190
GVDGLIAELKAKNGSKX
190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

```

g913.seq
1  atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCGGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCGCGCGCGG GCTACCGCAA AGTTACGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTAAACAACC TGCGCGACGT GGTCAGTTTC GGCAGCAATA
251 TCTTGCGTTT GGAcatCAAA cgcgcAAGcg aAGACCTcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGgcgGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgC CCGtcttagg cccgtccacc

```

1307

```

451 gtccgcgacg cgctcggcac gggcattacc tCTGTTTATC CGCccaagaa
501 tatcgttttc catacccttg ccggacgctg GGgcacgact gCCGCTGCCG
551 CCGTcagtac gcgcgaaggc ctccctcgatt tgaccgacag Tctggacgaa
601 gccgccatCG ACAAATACAG CTACACGCGc gacctctata tgAAAGTCCG
651 CGcacgGCag AccgGTGCAA CACCTGCCGA AGgtacggaa gataacatcg
701 acatcgacat cgACGAATTG GTCGAAAGTG CCGAAACCGG CGCGGCAGAG
751 CCCGCCGTTC ACGAAGATTG CGTATCCGAA ACACAGGCAG AAGCAGCAGG
801 GGAAGCCGAA ACGCAACCTG GAACACAACC CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2766; ORF 913.ng>:

```

g913.pep
  1 MKKTAYAILL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVTP KPVRAVSNF FNNLRDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGVP DNKNLGDTF ASGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYPPKNIVF HTPAGRWTG AAAAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDIDEL VESAETGAAE
251 PAVHEDSVSE TQAEAAGEAE TQPCTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

```

m913.seq
  1 ATGAAAAAAA CCGCCTATGC CTTCCTCCTG CTGATCGGGT TCGCTTCCGC
 51 CCCTGCATTT GCCGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGTACAT TTTCGCCCTT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 TGCCAATTTT TTTAACAACC TGTGCGACGT GGTGAGCTTC GGCAGCAATA
251 TCTTGCGCTT GGACATCAAA CGCGCAAGCG AAGACCTTGT CCGCGTCGGC
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTGGG CGACACGTTT GCCTCGTGGG
401 GATGAAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCAGGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTgCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCCATCG ACAAATACAG CTACACGCGC GACCTCTATA TGAAGTCCG
651 TCGCGGCGAG ACCGGTGCAA CACCTGCCGA AGgtACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

```

m913.pep
  1 MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVSKFN DQADRYIFAP
 51 AARGYRKVAP KPVRAVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNLGDTF ASGWKNSNY FVLPVLGPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWTG AVSAVSTREG LLDLTDSLDE
201 AAIDKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

```

g913/m913
      10      20      30      40      50      60
g913.pep  MKKTAYAILLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVTP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
m913      MKKTAYAFLLLIGFASAPAF AETRPADPYE GYNRAVSKFNDQADRYIFAPAARGYRKVAP
          10      20      30      40      50      60

      70      80      90     100     110     120
g913.pep  KPVRAVSNFFNNLRDVVSF GSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGVP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
m913      KPVRAVSNFFNNLCDVVSF GSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP
          70      80      90     100     110     120

```

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	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYPPKNIVFHTPAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

a913.seq

1	ATGAAAAAA	CCGCCTATGC	CTTCCTCCTG	CTGATCGGGT	TCGCTTCCGC
51	CCCTGCATTT	GCCGAAACCC	GCCCCGCCGA	CCCTTATGAA	GGCTACAACC
101	GCGCCGTTT	CAAATTCAAC	GACCAAGCCG	ACCGCTACAT	TTTCGCCCCCT
151	GCCGCGCGCG	GCTACCGCAA	AGTTGCGCCG	AAACCCGTCC	GCGCCGGCGT
201	GTCCAATTT	TTTAACAACC	TGTGCGACGT	GGTCAGCTTC	GGCAGCAATA
251	TCTTGCGCTT	AGACATCAA	CGCGCAAGCG	AAGACCTTGT	CCGCGTCGGT
301	ATCAACACCA	CTTTCGGTTT	GGGCGGGCTT	ATCGACATCG	CCGGCGCGGG
351	CGGCATTCCC	GACAATAAAA	ACACCTTGGG	CGACACGTTT	GCTTCGTGGG
401	GATGGAAAA	CAGCAATTAT	TTCGTGTGTC	CCGTCTTAGG	GCCGTCCACC
451	GTCCGCGACG	CGCTCGGCAC	GGGTATTACC	TCCGTTTATT	CGCCCAAGAA
501	TATCGTCTTC	CGCACCCCTG	TCGGACGCTG	GGGCACGACT	GCCGTATCCG
551	CCGTCACTAC	GCGCGAAGGC	CTGCTCGATT	TGACCGACAG	TCTGGACGAA
601	GCCGCCATCG	ACAAATACAG	CTACACGCGC	GACCTCTATA	TGAAAGTCCG
651	TGCGCGGCAG	ACCGGTGCAA	CACCTGCCGA	AGGTACGGAA	GATAACATCG
701	ACATCGACGA	ATTGGTCGAA	AGTGCCGAAA	CCGGCGCGGC	GGAAACTGCC
751	GTTCAAGAAG	ATTCGGTATC	CGAAACACAG	GCAGAAGCAG	CAGGGGAAGC
801	CGAAACGCAA	CCTGGAACAC	AACCTGGAAC	ACAACCTTAA	

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

a913.pep

1	MKKTAYAFLL	LIGFASAPAF	AETRPADPYE	GYNRAVFKFN	DQADRYIFAP
51	AARGYRKVAP	KPVVAGVSNF	FNNLCDVVSF	GSNILRLDIK	RASEDLVRVG
101	INTTFGLGGL	IDIAGAGGIP	DNKNTLGDTF	ASWGWKNSNY	FVLPVLPST
151	VRDALGTGIT	SVYSPKNIVF	RTPVGRWGTT	AVSAVSTREG	LLDLTDSLDE
201	AAIDKYSYTR	DLYMKVRARQ	TGATPAEGTE	DNIDIDELVE	SAETGAEETA
251	VQEDSVSETQ	AEAAGEAETQ	PGTQPGTQP*		

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVVAGVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
a913	KPVVAGVSNFFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTPVGRWGTT					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pep	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pep	SAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCTG
451 taggctTCGA CGATTTTTTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GGTGAAGGTA TGGAAATACA GTCCTGCCAC GCCGTGCAGT TTCTACGCTG
551 CGTCTTTCAA TCCCGATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCAATTTGT TCGGGCGTGg tgTtttGcgC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGag cgTCCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPADF RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCGDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMRVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGA GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGGCA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CGGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTTCGACGAT TTTTTCGACC AAAGGATGCC GGACAACGTC
501 TTCGCCGGTA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTTGGGCAG GTCGATTGAG
601 CTGTTGTCGC CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGTTCAG
651 GAACATTTTC ATTTGTTTCG GCGTGGTGTG TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAGCGTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPADF RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KVKYSPSTL CSFSRASFPN DLMFLGRSIW
 201 LVSPVMTAFA PKPMRVRNIF ICSGVVFCAS SRMMYAPLSV LPRI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914 . pep	MKKCILGILTACAAMPAFADRISDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFSGNSTMYVC					
	10	20	30	40	50	60
g914 . pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEDEAIRCRKFDXCIGWTDKETD					
	70	80	90	100	110	119
g914 . pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEDEAIRCRKFDXCIGWTDKETD					
	70	80	90	100	110	120
g914 . pep	120	130	140	150	160	170
	-ELGFRLCFSLPDPFCIGFQTALEQCSCSADSXASTIFCTRGCRRTTSSPVKVKYSPATP					
m914	TELGFRICFSLPDPFCIGFQTALEQCSCSADSXASTIFCTKGCRTTSSPVKVKYSPSTL					
	130	140	150	160	170	180
g914 . pep	180	190	200	210	220	230
	CSFSRASFPNDLMFLGRSIWLVSVMATAFAPKPMRVRNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPNDLMFLGRSIWLVSVMATAFAPKPMRVRNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
g914 . pep	240					
	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914 . seq

1	ATGAAAAAAT	GTATTTTGGG	CATTTTGACC	GCGTGTGCCG	CCATGCCTGC
51	ATTTGCCGAC	AGAATCGGCG	ATTTGGAAGC	ACGTCTGGCG	CAGTTGGAAC
101	ACCGTGTCGC	CGTATTGGAA	AGCGGCAGCA	ATACCGTCAA	AATCGACCTT
151	TTCGGTTCAA	ATTCCACCAT	GTATGTATGC	AGCGTTACGC	CTTTTCAGAA
201	GACGTTTGAG	GCAAGCGATC	GGAATGAAGG	CGTGGCGCGG	CAGAAAGTGC
251	GTCAGGCGTG	CAACCGCGAA	ACTTCGGCAA	TGTTTTGCGA	AGATGAGGCA
301	ATCCGATGCA	GAAAATTCGA	TTGATGTATC	GGTTGGACGG	ATAAAGAAAC
351	GGATACGGAG	CTTGGCTTCC	GTATCTGTTT	TTCTCTGCCC	GATTTTCCAT
401	GCATCGGGTT	TCAGACGGCA	TTGGAATGTC	AGTCGTGTTC	TGCCGATTCG
451	TAGGCTTCGA	CGATTTTTTG	CACCAAAGGA	TGCCGGACAA	CGTCTTCGCC
501	GGTAAAGGTG	TGGAAATACA	GCCCTTCCAC	GCCGTGCAGT	TTCTCACGCG
551	CATCTTTTAA	TCCCGATTG	ATGTTTTTGG	GCAGGTCGAT	TTGGCTGGTG
601	TCGCCGGTAA	TGACGGCTTT	CGCGCCGAAG	CCGATGCGGG	TCAGGAACAT
651	TTTCATTTGT	TCGGGCGTGG	TGTTTTGCGC	TTCGTCGAGG	ATGATGTATG
701	CGCCGTTGAG	CGTCTGCCC	CGCATATAG		

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914 . pep

1	MKKCILGILT	ACAAMPAFAD	RIGDLEARLA	QLEHRVAVLE	SGSNTVKIDL
51	FGSNSTMYVC	SVTPFQKTFE	ASDRNEGVAR	QKVRQACNRE	TSAMFCDEEA
101	IRCRKFD*CI	GWTDKETDTE	LGFRICFSLP	DFPCIGFQTA	LEQCSCSADS
151	*ASTIFCTKG	CRTTSSPVKV	WKYSPSTPCS	FSRASFPNDL	MFLGRSIWLV
201	SPVMTAFAPK	PMRVRNIFIC	SGVVFCASSR	MMYAPLSVLP	RI*

1311

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
a914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGSNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	70	80	90	100	110	
	130	140	150	160	170	180
m914.pep	TELGFRICFSLPDFPCIGFQTALEQCSCSADSXASTIFCTKGCRTTSSPVKWKYSPSTL					
a914	TELGFRICFSLPDFPCIGFQTALEQCSCSADSXASTIFCTKGCRTTSSPVKWKYSPSTP					
	120	130	140	150	160	170
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					
	240					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```

1  MKKTLLAIVA VFALSACRQA EEAPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACATATTGCG AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTG CAAAGGATAA AGGCGGTAAG

```


1312

451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

```

m915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

```

m915/g915

      10      20      30      40      50      60
m915.pep MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g915      MKKTLLAIVAVFALSACRQAEEAPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          10      20      30      40      50      60

      70      80      90     100     110     120
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g915      DQPVWFSTIVKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS
          70      80      90     100     110     120

      130     140     150     160
m915.pep GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDTYIFKX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g915      GFIGGMAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDAYIFKX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

```

a915.seq
  1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG
 51 CCGGCAGGCG GAAGAGGGAC CGCCGCCCTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG AACTATTGC AGTATGAACC TGACCGAACA CAACGCCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TCGGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

```

a915.pep
  1 MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
 51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*

```

m915/a915 99.4% identity in 164 aa overlap

```

      10      20      30      40      50      60
m915.pep MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a915      MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
          10      20      30      40      50      60

      70      80      90     100     110     120
m915.pep DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a915      DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS

```

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccacT cgcCGTCctg actgctTtgc tgcttgccagc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101 accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151 ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351 TCTCAACCTT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTGGTG TTCAACCCCG AATACACGTT CAAACTCAA CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACTAT
601 TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTG ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCTTAT CCGGCCGCG GCATTGAAGT TTATGGTGCG
1101 CCACTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNQ IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS MIPNYKHLNP EMMRLMDGVD PDHEYAVPFY WGTNTFAINT
151 ERVKALGTD KLPDNQWDLV FNPEYTFKLK QCGISYLDAS AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCTVTIGF
251 GGDLNIAKRR AEEAGGKEKI RVMPKKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNEFTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351 SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101 ACCAAAACGT ATTGAAAATT TACAACGGT CGGAATATGT CGATCCGGAA
151 ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251 GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT
501 GGATTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACTAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC

```

1314

```

751  GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801  GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851  ATTCTTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901  TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951  CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```

1  MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNG IKVTYDVYDS DETLESKVLT GKSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSKLG QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDLDNIARR AEEAGGKEKI RVMPKKEG VG IWVDSFVI PK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTGKSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPDHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLG					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLD SAAEIYPMVLN YLGKNPNSSNT EDIREATALL KKNRPNIKRFTSSGFIDDLA					
g917	QCGISYLD SAAEIYPMVLN YLGKNPNSSNT EDIREATALL KKNRPNIKRFTSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMMPKEGVGIWVDSFVI PKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMMPKEGVGIWVDSFVI PKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARDLMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

1315

```

m917.pep    ALKFMVRQWQDVKAGKX
            |||||
g917        ALKFMVRQWQDVKAGKX
            370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

```

a917.seq
1   ATGACCAAAC ATCTGCCCCCT GGCCGTCTCTG ACTGCTTTGC TGCTTGCAGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA
101 ACCGAAACGT ATTGAAAATT TACAACTGGT CGGAATACGT CGATCCGGA
151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT
201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAACTGT
251 GTTACGACAT TGTGCGGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG
301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGCCACG
401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451 GAACGCGTGA AAAAGGCTTT GGTACGGAC AAGTGCCGG ACAACCAAGT
501 GGATTTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAATAT
601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701 GCTTTATCGA TGATTTGGCG CGCGCGGATA CCTGCGTAAC AATCGGTTTC
751 GGCGGCGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATCTTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

```

a917.pep
1   MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE
51  TVADFEKKNG IKVTYDVYDS DETLESKVL T GSKGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLPDNQWDLV FDPEYTSK LK QCGISYLD SAEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKR F TSSGFIDDLA RGDTCVTIGF
251 GGD LNI AKRR AEEAGGKEKI RVMPK EGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFV TY APSSK PAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

m917/a917 99.7% identity in 376 aa overlap

```

              10      20      30      40      50      60
m917.pep    MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG
            |||||
a917        MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG
              10      20      30      40      50      60

              70      80      90      100     110     120
m917.pep    IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
            |||||
a917        IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m917.pep    EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSK LK
            |||||
a917        EMMRLMDGVDPGHEYAVPFYWGNTNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSK LK
              130     140     150     160     170     180

              190     200     210     220     230     240
m917.pep    QCGISYLD SAEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
            |||||

```

1316

```

a917      QCGISYLDAAEIYPMVLNLYLGKNPNSSNTEDIREATALLKKNRPNIKRFTSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      RGDTCVTIGFGGDLNIAKRRAEAEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVITYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPAELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           ||||||||||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

g919.seq

```

1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGCGCG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGCG cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGGA AAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCggcTT GACGGCAAag cccCCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAAACCCg tcgggcaaat acatCCGCAt cggatagcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctata TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TCGGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCAGCAAG CCGGCGAACT
1251 TGCCGGCAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCCAACG
1301 GCATGAAGCC CGAATACCG CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

g919.pep

```

1  MKKHLRLSAL YGIAAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR PEGSRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELPFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS QNEGFPVGALG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

```
m919.seq
1  ATGAAAAAAT  ACCTATTCCG  CGCCGCCCTG  TACGGCATCG  CCGCCGCCAT
51  CCTCGCCGCC  TGCCAAAGCA  AGAGCATCCA  AACCTTTCCG  CAACCCGACA
101 CATCCGTCAT  CAACGGCCCC  GACCGGCCGG  TCGGCATCCG  CGACCCCGCC
151 GGAACGACGG  TCGCGCGCGG  CGGGGCCGTC  TATACCGTTG  TACCCGACCT
201 GTCCCTGCCC  CACTGGGCGG  CGCAGGATTT  GCCTAAAAGC  TCGCAATCCT
251 TCCGCTCGG  CTGCGCCAAT  TTGAAAAACC  GCCAAGGCTG  GCAGGATGTG
301 TGCGCCCAAG  CCTTTCAAAC  CCCCCTCCAT  TCCTTTCAGG  CAAAACAGTT
351 TTTTGAACGC  TATTTACAGC  CGTGGCAGGT  TGCAGGCAAC  GGAAGCCTTG
401 CCGGTACGGT  TACCGGCTAT  TACGAACCGG  TGCTGAAGGG  CGACGACAGG
451 CGGACGGCAC  AAGCCCGCTT  CCCGATTTAC  GGTATTTCCG  ACGATTTTAT
501 CTCCTGCCCC  CTGCTGCGCG  GTTTGCGGAG  CGGAAAAGCC  CTGTGCGGCA
551 TCAGGCAGAC  GGGAAAAAAC  AGCGGCACAA  TCGCAATATC  CGCGGCACAA
601 CATACCGCCG  ACCTCTCCcG  ATTCCCCATC  ACCGCGCGCA  CAACAGCAAT
651 CAAAGGCAGG  TTTGAAGGAA  GCCGCTTCCT  CCCCTACCAC  ACGCGCAACC
701 AAATCAACGG  CGGCGCGCTT  GACGGCAAAG  CCCCATACT  CGGTTACGCC
751 GAAGACCTTG  TCGAACTTTT  TTTTATGCAC  ATCCAAGGCT  CGGGCCGTCT
801 GAAAACCCCG  TCCGGCAAA  ACATCCGCAT  CGGCTATGCC  GACAAAAACG
851 AACATCCyTA  CGTTTCCATC  GGACGCTATA  TGGCGGATAA  GGGCTACCTC
901 AAACCTCGAC  AAACCTCCAT  GCAGGCATT  AAGTCTTATA  TGGCGGCAAAA
951 TCCGCAACGC  CTCGCCGAAG  TTTTGGGTCA  AAACCCAGC  TATATCTTTT
1001 TCCGCGAGCT  TGCCGGAAGC  AGCAATGACG  GCCCTGTCGG  CGCACTGGGC
1051 ACGCCGCTGA  TGGGGGAATA  TGCCGGCGCA  GTCGACCGGC  ACTACATTAC
1101 CTTGGGTGCG  CCCTTATTTG  TCGCCACCGC  CCATCCGGTT  ACCGCAAAAG
1151 CCCTCAACCG  CCTGATTATG  GCGCAGGATA  CCGGCAGCGC  GATTAAAGGC
1201 GCGGTGCGCG  TGGATTATT  TTGGGGATAC  GGCAGCGAAG  CCGGCGAACT
1251 TGCCGGCAAA  CAGAAAACCA  CGGGATATGT  CTGGCAGCTC  CTACCCAACG
GTATGAAGCC CGAATACCGc CCGTAA
```

m919.pep

1	<u>MKKYLFRAAL</u>	<u>YGIAAAILAA</u>	CQSKSIQTFP	QPDTSVINGP	DRPVGIPDPA
51	<u>GTTVGGGGAV</u>	<u>YTVVPHLSLP</u>	HWAAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	<u>CAQAFQTPVH</u>	<u>SFQAKQFFER</u>	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGDDR
151	<u>RTAQARFPIY</u>	<u>GIPDDFISVP</u>	LPAGLRSGKA	LVRIRQTGKN	SGTIDNTGGT
201	<u>HTADLSRFPI</u>	<u>TARTTAIKGR</u>	FEGSRFLPYH	TRNQINGGAL	DGKAPILGYA
251	<u>EDPVLEFFMH</u>	<u>IQSGMRKQPT</u>	SGKYIRIGYA	DKNEHPYVSI	GRYMADKGYL
301	<u>KLQGTSMQGI</u>	<u>KSYSRNLNPPR</u>	LAEVLGQNPS	YIFRELAGS	SNDGPVGAIG
351	<u>TPLMGEGYAG</u>	<u>VDRHYITLGA</u>	PLFVATAHPV	TRKALNRLIM	AQDTGSAIKG
401	<u>APRVDFYFWGY</u>	<u>GDEAGELAGK</u>	QKTTGYVWQL	LPNGMKPEYR	P*

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N.gonorrhoeae*
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF
919.ng) from *N. gonorrhoeae*:
m919/g919

	10	20	30	40	50	60
m919.pep	MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
	: : : : :					
g919	MKKHLLRSALYGIAAAILAACQSRSIQTFPPQDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAFQTPVHSFQAKQFFER					
	: :					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120

1318

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRNPQRLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
g919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TGCGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT TCGCCAAAAGC CTGCAATCCT
251 TCCGCCCTCG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCGTTCCAG CAAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGCGAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG

```

1319

```

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGCGAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:

a919.pep

```

      1 MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
    51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
   101 CAQAFQTPVH SVQAKQFFER YFTPQVAGN GSLAGTVTGY YEPVLKGDDR
   151 RTAQAQRFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
   201 HTADLSQFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
   251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
   301 KLGQTSMQGI KAYMQQNQR LAEVLGQNPS YIFFRELTS SNDGPVGALG
   351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
   401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

m919/a919 98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
      10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
      70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep YFTPQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQAQRFPIYGIPDDFISVPLPAGLRSGKA
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      YFTPQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQAQRFPIYGIPDDFISVPLPAGLRSGKA
      130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep LVRIRQTGKNSGTIDNTGGTHTADLSRFITARTTAIKGRFEGRSFLPYHTRNQINGGAL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPIARTTAIKGRFEGRSFLPYHTRNQINGGAL
      190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      DGKAPILGYAEDPVELFFMHIIQGSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
      250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep KLGQTSMQGIKAYMQQNQR LAEVLGQNPSYIFFRELTS SNDGPVGALGTPLMGEYAGA
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      KLGQTSMQGIKAYMQQNQR LAEVLGQNPSYIFFRELTS SNDGPVGALGTPLMGEYAGA
      310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
      370     380     390     400     410     420

      430     440
m919.pep QKTTGYVWQLLPNGMKPEYRXP
||||||| ||||||| ||||||| ||||||| ||||||| |||||||
a919      QKTTGYVWQLLPNGMKPEYRXP
      430     440

```


Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCCGAATAT CAGCCTACTT TCCGGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTTCGGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCT GGAAATCGTC
301 CCGCTGGACA ATCccgcccga caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGcgccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAtttec
551 CCGATcaaAG CCTGTGccga AAACAggcgA ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTAa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAIEY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPADIHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCCTG TTCCGTGGCG
551 AACCCTGACC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKXK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
```

1321

201 SDRSKTHXXE AQAFSDSTDD KGEVDIIXLR QGFWKANVEH KTDFPDQSVK
 251 QKQANYSTLT FQIGHSHH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 920 shows 91.3% identity over a 207 aa overlap with a predicted ORF (ORF 920.ng) from *N. gonorrhoeae*:

g920/m920

				10	20	30
g920 . pep				PMQLVTEKGKENMIQRGT	NYQYRSNRPVK	
m920	GGEY	LKAD	LGYG	EFPE	LEPI	AKDRLHIFSKPMQLVTEKGKENMIQRGTNYQYRSNRPVK
	40	50	60	70	80	90
g920 . pep						
m920	DGSYL	VTA	EYQ	PTFR	SKNK	AGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIIT
	100	110	120	130	140	150
g920 . pep						
m920	KPV	GQNL	EIV	PLDN	PAN	IHVGERFKVRVLF
	160	170	180	190	200	210
g920 . pep						
m920	QAF	SDTT	DGEG	VDII	PLRQ	GFWKASVEYKADFPDQSLCRKQANYTTTLFQIAHSHHX
	220	230	240	250	260	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2799>:

a920 . seq

1	TGAAAGAAAA	CATTGACACT	GCTCGCCGTT	TCCGCCCTAT	TTGCCGCATC
51	CGCCACAGCC	CACCGCGTCT	GGGTCGAAAC	CGCCACACG	CACGGCGGCG
101	AATACCTTAA	AGCCGACTTG	GGCTACGGCG	AATTTCCCGA	ACTCGAACCC
151	ATCGCCAAAG	ACCGCCTGCA	CATCTTCAGC	AAACCGATGC	AGCTGGTTAC
201	CGAAAAAGGC	AAGGAAAACA	TGATTCAACG	CGGCACATAC	AACTACCAGT
251	ACCGAAGCAA	CCGTCCCGTT	AAGGACGGCA	GTTACCTCGT	CATCGCCGAA
301	TATCAGCCTA	CTTCTGGTGC	AAAAACAAA	GCAGGCTGGA	AACAGGCGGG
351	CATCAAACAA	ATGCCTGACG	CAAGCTATTG	CGAACAAACC	CGAATGTTCG
401	GCAAAAACAT	CGTCAACGTC	GGACACGAAA	GCGCGGACAC	CGCCATCATC
451	ACCAAACCGG	TCGGACAAAA	CTTGGAATC	GTCCCGCTGG	ACAATCCCGC
501	CAACATTCAC	GTAGGCGAAC	GCTTCAAAGT	CCGCGTCTG	TTCCGTGGCG
551	AACCGCTGCC	CAATGCCACC	GTTACCGCCA	CCTTTGACGG	CTTCGACACC
601	AGCGACCGCA	GCAAAACGCA	CAAAACCGAA	GCACAGGCTT	TCTCCGACAG
651	CACAGACGAC	AAAGGCGAAG	TGGACATCAT	CCCCTTGC	CAAGGCTTCT
701	GGAAAGCCAA	TGTGGAACAC	AAAGCCGACT	TCCCCGATCA	AAGCGTGTGC
751	CAAAAACAGG	CGAACTACTC	GACTTTAACC	TTCCAAATCG	GCCATTTCGCA
801	CCATTAA				

This corresponds to the amino acid sequence <SEQ ID 2800; ORF 920.a>:

a920 . pep

1	*KKTLLTLLAV	SALFAASAHA	HRVWVETAHT	HGGEY	LKADL	GYGEF	PELEP
51	IAKDR	LHIFS	KPMQLVTEKG	KENMI	QRGT	NYQYRSNRPV	KDGSYL
101	YQPTF	WSKNK	AGWKQAGIKQ	MPD	ASYCEQ	RMFGKNIVNV	GHESADTAII
151	TKPV	GQNL	EIVPLDN	PAN	IHVGERFKVRVLF	FRGEPLPNAT	VTATFDGFD
201	SDRSK	THKTE	AQAFSDSTDD	KGEVD	IILR	QGFWKANVEH	KADFPDQSVK
251	QKQAN	YSTLT	FQIGHSHH*				

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVS	ALFATS	SAHA	HRVW	VETAHT	HGGEY
	:	:	:	:	:	:
a920	XKKTLTLLAVS	ALFAAS	AHAHRV	WVETAHT	HGGEY	LKADL
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEK	GKENMI	QRGTYN	YQYRSN	RPVKDG	SYLVIA
	:	:	:	:	:	:
a920	KPMQLVTEK	GKENMI	QRGTYN	YQYRSN	RPVKDG	SYLVIA
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQ	TRMFGK	NIVNVG	HESADTA	IITKPV	GQNL
	:	:	:	:	:	:
a920	MPDASYCEQ	TRMFGK	NIVNVG	HESADTA	IITKPV	GQNL
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPN	ATVTAT	FDGFD	TSR	SKTHX	EAQAF
	:	:	:	:	:	:
a920	FRGEPLPN	ATVTAT	FDGFD	TSR	SKTHK	EAQAF
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFPDQ	SVCQKQ	ANYSTL	TFQIGH	SHHX	
	:	:	:	:	:	
a920	KADFPDQ	SVCQKQ	ANYSTL	TFQIGH	SHHX	
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCcggt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgcccCACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGccAAAG ACCgcccTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCCTG CAAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCCGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAACCC CGTATGTTTCG
401 TATAAAACAT TGTCACCGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTGGGAAATC GTCCCCTGCG ACAATCCCGC
501 CAACATTTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTTGACGG CTTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTTT
701 GGAAAGCGAG TGTCGAATAC AAAGCCGATT TCCCGATCA AAGCCTGTGC
751 CAAAAACAGG CGAACTACAC AACTTTAACC TTCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV SALFATS AHP HRVWVETAHT HGGEY LKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEK GKENMIQRTY NYQYRSNRPV KDGSYLVTA E
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAI I
151 TKPVGQNL EI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD T
201 SDRSKTHKTE AQAFSDT TDG KGEVDI IPLR QGFWKASVEY KADFPDQSLC
251 QKQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCCGCCC CACCgCGTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

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```

301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCCTGCG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTCTCG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNL EI VPLDNPANI H VGERFKVRVL FRGEPLPNAT VTATFDGFD T
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KTDFFPDQSV C
251 QKQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

	10	20	30	40	50	60
m920-1.pep	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
m920-1.pep	KPMQLVTEKGKENMIQRGTYNQYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTEKGKENMIQRGTYNQYQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE					
	70	80	90	100	110	120
m920-1.pep	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANI H VGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNL EIVPLDNPANI H VGERFKVRVL					
	130	140	150	160	170	180
m920-1.pep	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKASVEY					
	190	200	210	220	230	240
m920-1.pep	KTDFFPDQSV CQKQANYSTLT FQIGHSHH X					
g920-1	KADFFPDQSLCQKQANYTTLT FQIGHSHH X					
	250	260	269			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51 CGCCACGCGC CACCGCGTCT GGTCTGAAAC CGCCACACAG CACGCGGCGG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAACAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCCTGCG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTCTCG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCCGACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

a920.pep

```

1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKO MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVK
251 QKQANYSTLT FQIGHSHH*
```

m920-1/a920 98.9% identity in 267 aa overlap

```

              10      20      30      40      50      60
m920-1.pep  MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
              |||||
a920        XKKTLTLLAVSALFAASAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
              10      20      30      40      50      60

              70      80      90      100     110     120
m920-1.pep  KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE
              |||||
a920        KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ
              70      80      90      100     110     120

              130     140     150     160     170     180
m920-1.pep  MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
              |||||
a920        MPDASYCEQTRMFGKNIVNVGHESADTAIITKPVGQNLEIVPLDNPANIHVGERFKVRVL
              130     140     150     160     170     180

              190     200     210     220     230     240
m920-1.pep  FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
              |||||
a920        FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
              190     200     210     220     230     240

              250     260     269
m920-1.pep  KTDFFPDQSVKQKQANYSTLTFQIGHSHHX
              |||||
a920        KADFPDQSVKQKQANYSTLTFQIGHSHHX
              250     260
```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

g921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacgga aatccccgTg aatcccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCCTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGCTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggaA AAATATGGAT GCCAAACCCG ATAATCCCGC ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA
```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

g921.pep

```

1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPAFTN
151 FLMEVMMQMP LK*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

m921.seq

```

1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA
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251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	:					
g921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGEINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
	: :					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GTGGCAGTTC TTTCCGGCTG
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAAAG GTTTCGCCT TGCCTCTCG
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGGC CAATATCTGA
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
 301 TATGAAATCT ACCTGCGTTC GGCGATAGAC AGCCAGCGGG GCGCAATCAA
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNNFRKRL VGRNAVDDSM
 101 YEIYLRSAID SQRGAINTEQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN
 151 FLMEVMKMQP LK*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	:					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m921 . pep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921 . pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922 . seq

1	ATGGAAGA	GAAAAATACT	GCCGCTGGCA	ATTTGTTTGG	CGGCTTTGTC
51	TGCCTGTACG	GCGATGGAGG	CCCGCACACC	CCGGGCAAAT	GAAGCCCAAG
101	CCCCCGCGC	GGATGAAATG	AAAAAAGAAA	GCCGCCCGC	GTTTGACGCG
151	GCAGCCGTAC	CGGTATCCGA	CAGCGGTTT	GCCGCCAATG	CAAATGTCCG
201	CCGTTTTGTG	GACGATGAAG	TCGGGAAAGG	GGATTTTCC	CAGGCGGAAT
251	GGCAGGATTT	TTTGTACAAA	GCGGCTTACA	AGGCGGACAT	CGTCAAGATt
301	ATGCACCGAC	CCTCCACATC	GCGtCCGTGG	TATGtgttcc	gCacggGAaA
351	ttcGGgcagg	gcgaaAtttc	ACggcgCGCG	Caggttttat	GcggaaAacc
401	gcgcggttat	cgatgatgtg	gcgCAAAAat	acggcgtGCC	TGCCGAGCTT
451	ATCGTGGCGA	TTATCGGGAT	TGAAACGAAT	TACGGCAAAA	ATACGGGCAG
501	TTTCCGTGTG	GCGGACGCAT	TGGCGACTTT	AGGCTTTGAT	TATCCCCGCC
551	GCGCCGGGTT	TTTCCAAAAA	GAATTGGTCG	AGCTTTTAAA	GCTGGCAAAA
601	GAAGAAGGCG	GTGATGTTTT	CGCCTTTAAG	GGCagcTATG	CGGGTGCAAT
651	GGGTATGCCG	CAATTATATG	CTTCGAGCTA	CCGGAATGG	GCGGTGGATT
701	ATGAcgggga	cggacatCGG	GATATAtggg	GCAACGTcgg	tgatgtcgcg
751	gcatcggTTG	CCAATTAtat	gaagCAGCAC	GGTTGGCGCA	CgggcggtAA
801	AATGTTGGTG	TCGGCGAcgt	tggcgcggg	tgcggtATGT	CaggcAATCA
851	TTGGCGAAAA	AACCGCCCTG	ACGCGGACGG	TGGCGGATTT	GAaggCGTAc
901	ggcatcatcc	ccggggaaac	GCTCGCAGAT	GATGAAAAGg	cgGTTTTGTT
951	CAAACGGGAA	ACCGCACCCG	GCGTGTTTGA	ATATTATTG	GGCTTGAACA
1001	ATTTTATAC	GGTATGGCAG	TACAACCACA	GCCGGATGTA	TGTAACGgcg
1051	gtcaggGACA	TTGCCAATTC	GCTCGGCGGC	CCGGGATTGT	Aa

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922 . pep

1	MEKRKILPLA	ICLAALSACT	AMEARTPRAN	EAQAPRADEM	KKESRPAFDA
51	AAVPVSDSGF	AANANVRRFV	DDEVGKGDFS	QAEWQDFFDK	AAYKADIVKI
101	MHRPSTSRPW	YVFRGNSGR	AKPHGARRFY	AENRAVIDDV	AQKYGVPAEL
151	IVAIIGIETN	YGKNTGSFRV	ADALATLGF	YPRRAGFFQK	ELVELLKLAK
201	EEGDDVFAFK	GSYAGAMGMP	QFMPSSYRKW	AVDYDGDGHR	DIWGNVGDVA
251	ASVANVMKQH	GWRTGGKMLV	SATLAPGADV	QAIIGEKTAL	TRTVADLKAY
301	GIIPGETLAD	DEKAVLFKLE	TAPGVFEYYL	GLNNFYTVWQ	YNHSRMYVTA
351	VRDIANSLGG	PGL*			

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922 . seq

1	ATGAAAAAGA	GAAAAATACT	GCCGCTGGCA	ATTTGTTTGG	CGGCTTTGTC
51	TGCCTGTACG	GCGATGGAGG	CACGCCCACC	CCGGGCAAAT	GAAGCCCAAG
101	CCCCCGCGC	GGTTGAAATG	AAAAAAGAAA	GCCGCCCGC	GTTTGACGCG
151	GCAGCCGTAT	TTGACGCGGC	AGCCGTACCG	GTATCCGACA	GCGGGTTTGC
201	CGCCAATGCA	AATGTCCGCC	GTTTTGTGGA	CGATGAAGTC	GGGAAAGGGG
251	ATTTTCCCG	GGCGGAATGG	CAGGATTTTT	TTGACAAAGC	GGCTTACAAG
301	GCGGACATCG	TCAAGATTAT	GCACCGCCCC	TCCACATCGC	GTCCGTGGTA
351	TGTGTTCCGC	ACGGGAAATT	CGGGCAAGGC	GAAATTTTCGC	GGCGCGCGCC
401	GGTTTATATG	GGAAAACCGC	GCGCTTATCG	ATGATGTGGC	GCAAAAATAC
451	GGCGTGCCTG	CCGAACCTAT	CGTGGCGGTT	ATCGGGATTG	AAACGAATTA
501	CGGCAAAAAT	ACGGGCAGTT	TCCGTGTGGC	GGACGCATTG	GCGACCTTAG
551	GCTTTGATTA	CCCCCGCCGC	GCCGGGTTTT	TCAAAAAGA	ATTGGTCGAG

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601 CTTTAAAGC TGGCAAAAGA AGAAGGCGGC GATGTTTTTCG CCTTTAAAGC
651 CAGCTATGCG GGCACAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGGC ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TGCTGGTGTC TGCAACATG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCAGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACGG CATCATCCCC GCGGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACC GGCG GTGTTTGAAT
1001 ATTATTTGGG CTGAAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CGGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1 MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKERPAFDA
51 AAVFDAAAVP VSDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SSKRWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEEYLG LNNFYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
g922	MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKESRPAFDAA-----AVP					
	10	20	30	40	50	
	70	80	90	100	110	120
m922.pep	VSDSGFAANANVRRFVDDEVGKGDFSRAEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
g922	VSDSGFAANANVRRFVDDEVGKGDFSQAIEWQDFFDKAAYKADIVKIMHRPSTSRPWYVFR					
	60	70	80	90	100	110
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelIVAVIGIETNYGKNTGSFRVADAL					
g922	TGNSGRAKFHGAARRFYAENRAVIDDVAQKYGVPaelIVAIIGIETNYGKNTGSFRVADAL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m922.pep	ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
g922	ATLGFDYPRRAGFFQKELVELLKLAKKEEGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	180	190	200	210	220	230
	250	260	270	280	290	300
m922.pep	DGDGHRDIWGNVDVAASVANMKGHWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV					
g922	DGDGHRDIWGNVDVAASVANMKGHWRTGGKMLVSATLAPGADVQAIIGEKTALTRTV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m922.pep	ADLKAYGIIPGEELADDEKAVLFLKLETAPGVFEYLLGLNNFYTVWQYNHSRMYVTAVRDI					
g922	ADLKAYGIIPGETLADDEKAVLFLKLETAPGVFEYLLGLNNFYTVWQYNHSRMYVTAVRDI					

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	300	310	320	330	340	350
	370					
m922.pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```

a922.seq
1   ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGGAATGG CAGGATTTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGAAATTT CCGGCAAGGC GAAATTTCGC GGCGCGCGCC
401 GGTTTTATGC GGAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GGCGTGCCTG CCGAACTTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGGCAAAAAT ACGGCGAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCGC GCCGGGTTTT TCCAAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAAAGA AGAAGCGGC GATGTTTTCG CCTTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGGAAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CGGATGTTCA GGCAATCATT GGCGAAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTTGA AGGCGTACGG CATCATCCCC GGCGAAGAGC TTGCCGATGA
951 TGAAGAGGCG GTTTTGTTC AACTGGAAAC CGCACCGGCG GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CCGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```

a922.pep
1   MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KESRPAFDA
51  AAVFDAAAVP VDSGFAANA NVRRFVDDEV GKGDFSRAEW QDFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelivav IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEEG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHGWRT GGKILVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYYLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAFDAAAVFDAAAVP					
	:					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKKESRPAFDAAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922.pep	VDSGFAANANVRRFVDDEVGKGDFSRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
a922	VDSGFAANANVRRFVDDEVGKGDFSRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
a922	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelivavIGIETNYGKNTGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep  ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          |||
a922      ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRGKGMLVSATLAPGADVQAIIGEKALTRTV
          |||
a922      DGDGHRDIWGNVGDVAASVANYMKQHGWRGKGILVSATLAPGADVQAIIGEKALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIIPGEEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          |||
a922      ADLKAYGIIIPGEEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          |||
a922      ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCTGTC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCCG
201 CGGTTGGACG GGCGCATACT TGGGTAGTAG GATGTTTCAGG CATAAACCGG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTTC GTTCCGCCCG AACTTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKRQAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRRAVR
51  GKRRIPHEHL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRLLTVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCTGTC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GGCAGCTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGA TTAAATTTAA ACCAGTACGG
351 CGTTGCCTCG CCTTGCCGTA CTATTGTGAC TGTCTGCGGC TTCGTGCGCT
401 TGTCTGATT TTTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATTT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCRIR
51  GQRRIPHEHL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRLLTVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

1330

Homology with a predicted ORF from *N. gonorrhoeae*ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923.pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923.pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRLLTVSGNVLATCILID-----					
m923	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
					110	120
g923.pep	-----YFVPPELFFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

1	ATGAAGCGGC	AGGCTTTCTT	CAAACATGATG	GCGTGTGCGG	CATTTCTGTC
51	TGCCGTTTCG	CTGCGCCTCC	CCGTATTGGG	CGCGTGTAC	GCAATATTGT
101	CCCTCTATGC	GTTTGCACCT	TACGGCATCG	ACAAACGCGC	TGCCGTGCGG
151	GGAAAACGCC	GCATCCCCGA	ACACCGCCTG	CTGCTGCCTG	CCTTGTTCCG
201	CGGTTGGGCG	GGCGCATACT	TGGGCAGCAG	GATATTCAGG	CATAAAACGG
251	CGAAAAAGCG	TTTTGTTGTG	CTGTTCCGTC	TGACTGTTTC	GGGCAATGTC
301	CTGGCGACCC	TCATCCTGAT	TTATAGTGGA	TTAAATTAA	ACCAGTACGG
351	CGTTGCCTCG	CCTTA.GCTC	AAAGAGAACG	ATTCTCTAAG	GTGCTGAAGC
401	ACCAAGTGAA	TCGGTTCCTG	ACTATTGTA	CTGTCTGCGG	CTTCGTCGCC
451	TTGTCCTGAT	TTTTGTAAAT	CCACTAT.AT	TATTTTGTCC	CGCCTGAATT
501	TTTCGTAAAA	CTCGGCGAGA	ATACCTGA		

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

1	MKRQAFFKLM	ACAAFLSAVS	LRLPVLGACY	AILSLEYAFAL	YGIDKRRRAVR
51	GKRRIPEHRL	LLPALFGGWA	GAYLGSRIFR	HKTAKKRFV	LFRLTVSGNV
101	LATLILIIYS	GNLNQYGVAS	PXAQRERFSK	VLKHQVNRFR	TICTVCGFVA
151	LS*FLLIHYX	YFVPPEFFVK	LGQNT*		

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923.pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923.pep	LLPALLGGWVGAYFGSMTFKHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRLLTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
					130	159
m923.pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFRRTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

g925.seq

```

1   ATGAAACAAA TGCTTTTGGC cgtcggcgctg ggcGCGGTGT TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgagggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGC GG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

g925.pep

```

1   MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51  KINVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

m925.seq (partial)

```

1   ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTAATTCCTT

```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

m925.pep (partial)

```

1   MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGYFL..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGYFL				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGA LSINTGIGEIPIKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT				
	60	70	80	90	100
	110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

g925-1.seq

```

1   ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAAATCATC GCCCACCAGA AAAAGTGC GG
351 ACAAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51 KINVFTGKEE SLLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51 CGGCAAGGAT GCCGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
151 AATAAAATCC ACGTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51 NKIHVVTGKE ESLLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKE					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	
	70	80	90	100	110	120
m925-1.pep	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
g925-1	ESLLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110
	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLLX					
g925-1	AQAYLDARNALPSNQTYQQRQAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAAATCA ACGTGTTCAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51 AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CGGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVFTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51 KTDAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30
a925-1.pep		NKINVFTGKEESMLLSEKDGALSINTGIGE		
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKEESLLLSEKDGALSINTGIGE			
	30	40	50	60
	40	50	60	70
				80
				90

1333

```

a925-1.pep  IPIKLSDDGKELYVERROYVKTDAAMKDIIAHQKKCGQTAQAYLDARNALPSNQTYQQH
|||||
m925-1      IPIKLSDDGKELYVERROYVKTDAAMKDIIAHQKKCGQTAQAYRDARNALPSNQTYQQH
          90      100      110      120      130      140

          100      110      120
a925-1.pep  QAAIEQLKRRFEAEFDELEKEIKCNKGK-PTLLFX
|||||
m925-1      LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
          150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

g926.seq (partial)

```

1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGAcAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GGCGGGCGCG CCTtaccGCA
401 TCCGTTTACA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgcCGACAGT GGGGGGCaag tccgaacgtt gcaactGAa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

g926.pep (partial)

```

1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

m926.seq

```

1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51  GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GGCGGGCGCG CCTTACCGCA
401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAAC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTCA CCGAAATCGG TATGCCGTCT GAAACCGAAA
551 CCCCGGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

m926.pep

```

1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51  SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADSGGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

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g926/m926 91.6% identity in 155 aa overlap

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          10      20      30      40      50      60
g926.pep  MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
|||||
m926      MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
          10      20      30      40      50      60

          70      80      90      100     110     120
g926.pep  PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
|||||
m926      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAEEELSRQLVGFKLPIQYLHI
          70      80      90      100     110     120

          130     140     150     160
g926.pep  WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCRQWGASPNVATE

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|||||:|||||:|||||:|
 m926 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS
 130 140 150 160 170 180

a926.seq

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
 51 GCAATTACCT AAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC
 101 GCAGTTTCAC GCGGAAGGG CGGTTGGCAG TGAAAGCGGA AGGGAAAGGT
 151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCCGTGG AAACCATCAA
 201 TATCAACACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
 251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCGGAAAGT
 301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAATGTC CAATCCAATA
 351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GGCGGGCGCG CCTTACCGCA
 401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC
 451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
 501 GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA
 551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

a926.pep

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG
 51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
 101 AEELSRQLVG FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT
 151 ADSGGQVRTL QLNNGNLIR LVFTEIGMPS ETETQECCAA RIQ*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPS	EHTRSSFAEGR	RLAVKAEGKGS	SYANFDWTYQ		
a926	MKHTVSASVILLTACAQLPQNNENLWQPS	EHTRSSFAEGR	RLAVKAEGKGS	SYANFDWTYQ		
	10	20	30	40	50	60
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESAEELSRQLVG	FKLPIQYLHI			
a926	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESAEELSRQLVG	FKLPIQYLHI			
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESAEELSRQLVG	FKLPIQYLHI			
a926	PPVETININTPLGSTLGQLCQDRDGALAVD	GKGNVYQAESAEELSRQLVG	FKLPIQYLHI			
	70	80	90	100	110	120
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRT	ADSGGQVRTLQLNNGNLNIR	LVFTEIGMPS			
	130	140	150	160	170	180
m926.pep	ETETPERCAARTRX					
a926	ETETQECCAAARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

g927.seq

1 atgaaaacct acGCACAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG
 51 CAGCCCcgca GCcgatTcaa accaTCCGTC CCGAcAaAAT GCCCCGGCCA
 101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtagcat
 151 gtGACACGGT ATTTttacaa agaatacgac cacTtggttg tcggaaCATA
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG
 251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

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401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC
 501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA
 551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAaCTCGT CGCATCCATC
 601 CTCAAAAACA CACCCGTTTT TGAAAACGGC GGACGCGc.C CGCCGCCACC
 651 ACCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga
 701 agCcaactac gtCAGCAAAA AACTGA

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VTRYFYKEYD HLFVGTYSQSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV
 101 VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
 151 DWNDLAKDGV NIVIAKTSNG GRYAFLGAYG YGLKANNGNE QEAQKLVASI
 201 LKNTVPVFENG GRXPPPPPSH NATSATYSSL LKTKPTTSAK N*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

1 ATGAAACCTT ACGCACCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG
 51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA
 101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT
 151 GTGGCACGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCCACGGCG
 251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC
 301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA
 401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC
 501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG
 551 GTCTGAAAC CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA
 601 TCCATCCTCA AAAACACCCC CGTTTTTGAA AACGGCGGAC GcKcGCCACC
 651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTTGAAAA
 701 CGAAGCCAAC TACGTCAGCr AAAAaCTGA

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD
 51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV
 101 VTMNQSSDID LLEKXGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR
 151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA
 201 SILKNTPVFE NGGRXPPPPS HNATSATYSS LLKTKPTTSA KN*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
g927.pep	HLFVGTYSQSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
	:					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKXGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGNGRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNGRYAFLGA					
	130	140	150	160	170	180

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      180      190      200      210      220      230
g927.pep  YGYGLKANNGNEQEAQKLVASILKNTVPFENGGRXPPPPSHNATSATYSSLLKTKPTTS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m927      YGYGLKTTNGNEQEAQKLVASILKNTVPFENGGRXPPPP-SHNATSATYSSLLKTKPTTS
          190      200      210      220      230

      240
g927.pep  AKNX
          ||||
m927      AKNX
      240

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

```

a927.seq
1  ATGAAACCT  ACGCACCGGC  ACTCTATACC  GCAGCCCTGC  TCAGCGCCTG
51  CAGCCCCGCA  GCCGATTCAA  ACCATCCGTC  CGGACAAAAT  GCCCCGGCCA
101 ATACCGAATC  CGACGGAAAA  AACATTACCC  TGCTCAACGC  CTCATACGAT
151 GTGGCACGGG  ATTTTACAA  AGAATACAAC  CCCTTATTTA  TCAAAACATA
201 CCAATCCGAA  CACCCCGGCA  CATCCGTCAG  CATCCAACAG  TCCCACGGCG
251 GCTCCAGCAA  ACAGGCATTA  TCCGTAGCCA  ACGGCCTTCA  AGCCGATGTC
301 GTAACCATGA  ACCAATCCTC  CGACATCGAC  CTGCTCGAAA  AAAAAGGACT
351 GGTAGAAAAA  GGCTGGCAAC  AAGCCCTCCC  CGACCAGGCC  GCGCCCTACA
401 CCAGCACTAT  GGTTTTCTT  GTCCGAAAAA  ACAACCCCAA  ACAGATCCGC
451 GATTGGAACG  ACCTTGCCAA  AGACGGCGTT  AACATCGTCA  TCGCCAATCC
501 CAAAACCTCG  GGCAACGGAC  GCTACGCCTT  CCTCGGCGCA  TACGGTTACG
551 GTCTGAAAC  CACCAACGGC  AACGAACAGG  AAGCCCAAAA  ACTCGTCGCA
601 TCCATCCTCA  AAAACACCCC  CGTTTTTGAA  AACGGCGGAC  GCGCGCCACC
651 ACCACCTTCA  CACAACGCAA  CATCGGCGAC  GTACTCATCA  CTTTGTAAAA
701 CGAAGCCAAC  TACGTCAGCA  AAAAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

```

a927.pep
1  MKTYAPALYT  AALLSACSPA  ADSNHPSGQN  APANTESDGK  NITLLNASYD
51  VARDFYKEYN  PLFIKTYQSE  HPGTSVSIQQ  SHGGSSKQAL  SVANGLQADV
101 VTMNQSSDID  LLEKKGLVEK  GWQALPDHA  APYTSTMVFL  VRKNNPKQIR
151 DWNDLAKDGV  NIVIANPKTS  GNGRYAFLGA  YGYGLKTTNG  NEQEAQKLVA
201 SILKNTVPFE  NGGRAPPPPS  HNATSATYSS  LLKTKPTTSA  KN*

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m927/a927 99.2% identity in 242 aa overlap

```

      10      20      30      40      50      60
m927.pep  MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN
          10      20      30      40      50      60

      70      80      90      100     110     120
m927.pep  PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK
          70      80      90      100     110     120

      130     140     150     160     170     180
m927.pep  GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSGNGRYAFLGA
          130     140     150     160     170     180

      190     200     210     220     230     240
m927.pep  YGYGLKTTNGNEQEAQKLVASILKNTVPFENGGRXPPPPSHNATSATYSSLLKTKPTTSA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a927      YGYGLKTTNGNEQEAQKLVASILKNTVPFENGGRAPPPPSHNATSATYSSLLKTKPTTSA
          190     200     210     220     230     240

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m927.pep KNX
 |||
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq
 1 ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAacgctggG CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
 451 GGCGGCATTA TACATCcgAT TATGCagtcg attgCgggCA GttacggctC
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg
 551 tcaattaTCA TTCcaaTCCC atttcgctcg ctAtggctat taCTGcaact
 601 gCCCCcaaCC CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag
 651 tttccgtCTT TCttgggggg cgTGGGcgTg ggcaaTGGCT Gttcccggcg
 701 ttatcgccctt TttcgTTATG CCTTTGATT TATATTTTTT GTATCCGCCT
 751 GAAATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGTCTGAG
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
 901 CACGCTTTTA GTATCAacgc caccGCCACC GCATTTATCG GATTAAGCCT
 951 GCTTTTGCTT TCCGGTGTAT TGAATTGGGA CGATGTTTTG AAAGAAAAAA
 1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
 1051 TTTTAAATA AActcggact gattaaatGG TTCTCCGGAG TGTTGGCGGA
 1101 AagtgtcggC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
 1151 TGCTTGCTta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
 1201 ATTACCGCTA TGTTCCGCGC ATTTCTCGCT GCTGCCGTTT CACTGAATGC
 1251 CCCGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA
 1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG
 1351 GGCTACACCA CAATGGGAGA ATGGTGGAA GCGGGTTTTA TCATGAGCGT
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTGGG TGGAAAGTTC
 1451 TGGGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pep
 1 MKLGFKPIPL AIAAVLCALV LALFVPDGVK PQAWTLLAMF VGVIAAIIGK
 51 VMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
 101 SRGLLKTGLG MRIGLYFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
 151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMAITAT
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
 251 EIKETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASHTAH
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq
 1 ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA
 251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
 401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

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451 GGC GGC ATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCC GCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTTCGTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGTCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCC GGCG
701 TTATCGCCTT TTTTCGTTATG CCTTTGATTT TATATTTwyT GTATCCGCCT
751 GAAATTAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAAGCTT
951 GCTTTTGCTT TCCGTGTAT TGACTTGGGA CGATGTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGGCGGA
1101 AAGTGTCGGC GGTTTGGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGCGCATG CCGACCGCGC TGATGATGGC GgCCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTGG TGGAAAGTTC
1451 TGGGTATTG GTAA

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This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

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1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMKGK LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNVAV FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTMMGEWVK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929.pep	70	80	90	100	110	120
	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIYLFIAV					
m929	AVGLVAVTGV TADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIYLFIAV					
	70	80	90	100	110	120
g929.pep	130	140	150	160	170	180
	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMKGK					
m929	FGRKTLGIGYSLALSELLAPVTPSNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMKGK					
	130	140	150	160	170	180
g929.pep	190	200	210	220	230	240
	LALVNYHNSPISSAMAITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNSPISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM					

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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLSEMGKMSADEIIMAVIFGILLLLWADV PALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAHYMAHYMFASTTAHI TAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAHYMAHYMFASTTAHI TAMFGAFFAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

```

a929.seq
1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTGA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGCGGTA ACCGCCGACA AACCGGGTGC GGCGATGAGC GATGCGTTGA
251 TCGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TC GCGCGGTT TGCTCAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC
451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTGCTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGCTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTTGGCGGA
1101 AAGTGTGGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCCGGCG ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCGGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

1340

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```

a929.pep
1  MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTSPNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

```

              10      20      30      40      50      60
m929.pep      MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFVGVIAAIIGKAMPLGALSII
              |
a929           MKLGFKPIPLAIAAVLCALVLALPVPDGVK PQAWTLLAMFIGVIAAIIGKAMPLGALSII
              10      20      30      40      50      60

              70      80      90      100     110     120
m929.pep      AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV
              |
a929           AVGLVAVTGV TADKPGAAMS DALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV
              70      80      90      100     110     120

              130     140     150     160     170     180
m929.pep      FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
              |
a929           FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY
              130     140     150     160     170     180

              190     200     210     220     230     240
m929.pep      LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
              |
a929           LALVNYHNSP ISSAMFITATAPNPLIVNLI AENLGSSFRLSWGAWAWAMAVPGVIAFFVM
              190     200     210     220     230     240

              250     260     270     280     290     300
m929.pep      PLILYXLYPPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN
              |
a929           PLILYFLY PPEIKETPNAVQFAKDRLREMGKMSADEIIMAVIFGILLLLWADV PALITGN
              250     260     270     280     290     300

              310     320     330     340     350     360
m929.pep      HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW
              |
a929           HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFLNKLGLIKW
              310     320     330     340     350     360

              370     380     390     400     410     420
m929.pep      FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAVSLNAPAM
              |
a929           FSGVLAESVGGLGVSGTAAGVILVLAYMYAHYMFASSTAHITAMFGAFFAAVSLNAPAM
              370     380     390     400     410     420

              430     440     450     460     470     480
m929.pep      PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW
              |
a929           PTALMMAAASNIMMTLTHYATGTSPVIFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW
              430     440     450     460     470     480

m929.pep      WKVLGYWX
              |

```

1341

a929 WKVLGYWX

g930.seq not found yet
g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

```
m930.seq
  1  ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
 51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101  ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151  GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201  AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251  AACCGTGTTT TGCCATTAAC GAATGGGTGT TGGAAAGCGA ACACCATGCT
301  CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351  TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401  AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451  CCACAGGATT TGAATAgTGG aAGCTTCAAT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

```
m930.pep
  1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNP AEIRM QQDIQQRQRE
 51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLVEGEHHA
101  RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151  PQDLNSGSFN *
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

```
g930-1.seq (partial)
  1  GGCAAGTGTC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
 51  AAATGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101  CACAGGATTG GAATAGTGGC AAGCTTCAAT TAACCCGTAT GCCGGGTAT
151  CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAGG
201  ACGTATTGCA GCATTCCAAA ACAAAATTTCC CACCCGCTCG AACGATCTGT
251  TGAATCTGGC TGATTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301  ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351  AAGTGATGTC GTGGTGCAAT GCGGTAACG TCTGCTGCCC TACTGTGTGA
401  GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451  AATATCACTT TCTCTGCCGA CAATCCTTTT GGACTGAGTG ATATGTTCTA
501  TGTAATTATG GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551  ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601  GCCCCTTTTC GTAAATGGAC ATGGGCATTG AATCACAATG GCTACCGTTA
651  CCATCAGGCG GTTTCGGGAT TATCGGAAGT CTATGACTAT AATGGAAAAA
701  GTTACAACAC TGATTTCGGC TTCAACCGCC TGTGTATATC TGATGCCAAA
751  CGCAAAACCT ATCTCAGTGT AAAACTGTGG ACGAGGGAAA CAAAAAGTTA
801  CATTGATGAT GCCGAAGTGA CTGTACAACG GCGTAAAACC ACAGGTTGGT
851  TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901  AAGTTGAAAT ATAAACACGG CACCGCATG AAAGATGCTC TGCGCGCGCC
951  TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTTCAAATCG GTAAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGAAA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GGCGCAACGA TTTGAGCTTG
1201 CAATTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATCGGG CCAAACTCTA GCCGGCACAG
1301 CAATTGGGAT ACGCGGGCAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTTACCG GCCGTGCATT GAAAAAGCCC GAATATTTTC AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGGTTATTC GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

```
g930-1.pep (partial)
  1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPQDLNSG KLQLTLMPGY
 51  LRSIRIDRSN DDOTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKLCP
101  TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151  NITFSADNPF GLSDMFYVNY GRSIGGTPDE ENFDGHRKEG GSNYYAVHYS
201  APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251  RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301  KLKYKHGTGM KDALRAPEEA FEGGTSRMKI WTASADVNTF FOIGKQLFAY
351  DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401  QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGQ IKLGGNLHYD
```

1342

451 IFTGRALKKP EYFQTKKWVT GFQVGYSF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```

1   ATGAAACTTC CTTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTT TGCCATTAAC GAAGTGGTGT TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGTA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTTGGA ACAAGGACTG GAAAATCTCA AACGCTCTCC
651 GACTGCGGAA GCCGATCTCC AAATCGTTC CGTAGAGGGA GAACCAAACC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAAATTA TGGACGTCG ATTGGCGGTA CGCCCGATGA GGAAAGTTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GTTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCCG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAAACTGTG GATGAGGGAA ACAAAAAGTT
1151 ACATTGATGA TGCCGAAC TGCTGACAAC GCGGTAAAAC TCGGGGTTGG
1201 TTGGCAGAAC TTTCCACAA AGAATATATC GGTCGCAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTAC GTATGAAAAT TTGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACCTGG TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CCAGGCCATC AGCTTTATCT TGGGGCTGAT GTAGGACATG
1601 TTTCAGGACA ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GCGGCAACC TGCATTACGA
1701 TATATTTACC GCGCGCGCAT TGAAAAAGCC CGAATTTTTC CAATCAAGGA
1751 AATGGGCAAG CGGTTTTCAG GTAGGCTATA CGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2856; ORF 930-1>:

m930-1.pep

```

1   MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL
201 LNLRLDLEQL ENLKRLLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDSNGSE ATGKYQGNIT FSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHRKEGGSN NYAVHYSAPF GKWTWAFNHN GYRYHQA VSG LSEVYDYNK
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKS YIDDAEL TVQRRKTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWE WRNDLSWQFK PGHQLYLGAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*

```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEH	HARFQFALKRAL	RETGFQAGKCL	HAGNINQIMSLA	QNALIGRGYTT	TRI
g930-1.pep				:		
				GKCLHAGDINQIMSLA	QNALIGRGYTT	TRI
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKLQ	LTLLIPSYLRSIR	IDRSNDDQTHAGRI	AAFQNKFPTRSN	DLLNLRDLE	
g930-1.pep	:					
	LAAPQDLNSGKLQ	LTLLIPSYLRSIR	IDRSNDDQTHAGRI	AAFQNKFPTRSN	DLLNLRDLE	
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLENLKRLPTAE	ADLQIVPVEGEP	NPQSDVVVQWRQ	RLPYRVSVGMDS	SGSEATGKYQG	
	:					

1343

```

g930-1.pep  QGLENLKLCLPTAEADLQIVPVEREPNQSDVVVQWRXLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150

              270      280      290      300      310      320
m930-1.pep  NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210

              330      340      350      360      370      380
m930-1.pep  NHNGYRYHQAVSGLSEVYDYGKSYNTDFGFNRLLYRDAKRKTYLGVKLWMRETKSYIDD
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDYGKSYNTDFGFNRLLYRDAKRKTYLSVKLWTRETKSYIDD
              220      230      240      250      260      270

              390      400      410      420      430      440
m930-1.pep  AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTGMKDALRAPEEAFGEGETSRMKI
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  AELTVQRRKTGWLAELSHKGYIGRSTADFKLKYKHGTGMKDALRAPEEAFGEGETSRMKI
              280      290      300      310      320      330

              450      460      470      480      490      500
m930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390

              510      520      530      540      550      560
m930-1.pep  GWYWRNDLSWQFKPGHQLYLGAADVGHVSGQSAKWLSGQTLVGTAGIRGQIKLGGNLHYD
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  GWYWRNDLSWQFKPGHQLYLGAADVGHVSGQSAKWLSGQTLAGTAGIRGQIKLGGNLHYD
              400      410      420      430      440      450

              570      580      590
m930-1.pep  IFTGRALKKPEFFQSRKWASGFQVGYTF
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  IFTGRALKKPEYFQTKKWVTGFQVGYSEFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1  ATGAAACCCA AATTCAAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCC TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCCCGC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TACACGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT CGCCCGCGTC AAAACGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCAAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1  MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQGDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA QFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```


54	1	ATGAAACCCA	AATTCAAAAC	CGTTTTAACC	GCGTGCTTTT	TGGCGGTTTC
51		CCTGCCGTCT	ATGGCGGCAA	CCCATGTTTT	GATGAAACC	GATATGGGCA
101		ATATCCGTTT	GGTTTTTGAC	GAATCCAAAG	CCCCAAAAAC	CGTTGCTAAT
151		TTCGTGCGCT	ATGCCCCGAA	AGGCTTTTAC	GAGACACCG	TTTTTACCCG
201		CGTTATCGAC	GGTTTTGTTA	TCCAGGCGCG	TGGATTGAC	GAGGACTTGG
251		CACAAAAGGC	AAGCGATAAG	CGCGTTGCCA	ACGAATCCGG	CAACGGCTTG
301		AAAAACACCG	CCGGCACCAT	CGCCATGGCG	CGGACGACAG	CCCCCGATTG
351		CGCCACCAGC	CAATTCTTTA	TCAATCTGGC	GGACCA . kCT	TCGTTCGACT
401		ACAAAAACGG	ACAATACGGC	TATACCGTTT	TCGGCAGGGT	CGAAAGCGGC
451		ATGAACACCG	TTTCCAAAAT	CGCCCGCGTC	AAAACCGCCA	CGCGCGGCTT
501		TTATCAAAA	GTACCCGTAC	AGCCCGTCAA	AATCCGTGCG	GTTGTTGTGCG
551		GGCAGTAA				

m931.pap..

1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51 FVRYARKGFPY DDTVFHRRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYON VVPQPVKIRR VVVGQ*

Homology with a predicted ORF from *N.gonorrhoeae*

q931/m931

		10	20	30	40	50	60
g931.pep		MKPKFKTVLTALLAVSLPSMAATRVL	METDMGNIRLVL	DESKASKTVANFVRYARKGFY			
m931		MKPKFKTVLTALLAVSLPSMAATHVL	METDMGNIRLVL	DESKAPKTVANFVRYARKGFY			
		10	20	30	40	50	60
		70	80	90	100	110	120
g931.pep		DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
		: :					
m931		DDTVFHRVIDGFGVIOGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
		70	80	90	100	110	120
		130	140	150	160	170	180
g931.pep		QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPQPVKIRR					
m931		QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPQPVKIRR					
		130	140	150	160	170	180
g931.pep		VVVGQX					
m931		VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

1	ATGAAACCCA	AATTCAAAAC	CGTTTTAACC	GCGCTGCTTT	TGGCGGTTTC
51	CCTGCCGTCT	ATGGCGGCAA	CCATGTTTT	GATGGA AAC	GATATGGGCA
101	ATATCCGTCT	GGTTTTGGAC	GAATCCAAAG	CACCCAAAAC	CTTTGCCAAT
151	TTCTGTCGTT	ATGCCGGA AA	AGGCTTTTAC	GACAATACGA	TTTTTACCCG
201	CGTCATCGGC	GGCTTCGGTA	TCCAAGGCGG	CGGATTGACC	GAGGACTTGG
251	CACAAAAGGC	AAGCGATAAG	GCCGTTGCCA	ACGAATCCGG	CAACGGCTTG
301	AAAAACACTG	TCGGCACCAT	CGCCATGGCG	CGGACAGGCC	ATCCGGATTTC
351	CGCCACCAGC	CAATTCTTTA	TCAATCTGGT	GGACAATGGT	TCGCTCAACT
401	ACAAAAACGG	ACAATACGGC	TATACCGTTT	TCGCGAGGGT	CGAAAGCGGG

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451 ATGAACACCG TTTCCAAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
 501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL
 101 KNTVGTIAMA RTADPDSATS QFFINLVDND SLNYKNGQYG YTVFGRVESG
 151 MNTVSKIARV KTATRGFYQN VPQVPKIRR VVVGQ*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD	ESKAPKTVANFVRYARKGFY				
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD	ESKAPKTVANFVRYARKGFY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVQVPKIRR					
a931	QFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVQVPKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT
 101 TGAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCATTGAC
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA
 251 GGAAAAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAACAAA
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep
 1 MKYIVSISLA MGLAACSFGG FKPNPWAAS FWELKNYANP YPGSASAALD
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPENK
 101 KYEWPREEGK TK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCT CACTCACCGC

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```

51 CTGCCAAGAC GACACGCAGG CGCGGCTCGA ACGGCAGCAG AAACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCCAGG CGCAGGCAAA
201 CGGCAACAAC GGTACGCCC GGTACCGCAA .AGAcggGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGA TTGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCGG
351 GCAACCAAGA CAGCCCCGTC GCCCGTCGCG CGCGTGCTGC CTACCATCAG
401 TCCGCACGCC CCAATGCGCG CACCAGCAGG GATTGGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGT CAAttaccgc catcgcgcta tgcGCGGTTT CGgcagAagg
551 cggtaaaCCC GGCGCTCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
601 TTGTATTTGT TAGGGGCATT GTTATGTTGC CGTTTGATT TCAGACGGCA
651 TTTTGTTC AAGCGTTGA TGTcggGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2866; ORF 934.ng>:

g934.pep

```

1 MKKIIASALI ATFALTACQD DTQARLERQQ KQIEALQQQL AQQADDTVYQ
51 LTPEAVKDTI PAQAQANGNN GQPVTKRRA AVYLRPIDRK LAAAKPDWRG
101 GRRVYRQAG KQIHTGGQPR QPRRPSRACC LPSVRTPQCA HQQGFEHAQP
151 PCKTTGAGA ALPPDNAPAR QLPPSRYARF RQKAVNPARQ CRLKGFQTAF
201 LYLLGALLCC RLIFRRHFVS KRLMSGWQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2867>:

m934.seq (partial)

```

1 ..CGGCTCGAAC AGCAGCAGAA ACAGATTGAA GCCCTGCAAC AGCAGCTCGC
51 ACAGCAGGCA GACGATACGG TTTACCAACT GACTCCCGAA GCAGTCAAAG
101 ACACCATTCC TGCCGAAGCA CAGGCAAACG GCAACAACgG GCAACCCGTT
151 ACCGGTAA.A GACGGGCAGC AGTATATTTA CGACCAATCG ACAGGAAGCT
201 GGCTGCTGCA AAGCCTGGTC GGCGCGGCGG CAGGCGCGTT TATCGGCAAC
251 GCGCTGGCAA ACAAATTCAC ACGGGCAGGC AACCAAGACA GTCCCGTCGC
301 CCGGCGCGCG CGTGCAGCCT ACCATCAGTC CGCACGCCCC AATGCGCGCA
351 yCAGCAGGGA TTTGAACACG CGCAGCCTCC GTGCAAAACA ACAGGCGGCG
401 CAkGCGCAGC GTTACCGCCC GACAACGCGC CCGsCCGsCA ATTACCGCCG
451 CCCCCTATG CGCGTTTCG GCAGGAGGCG GTAAACCCCG CGCGCCAATG
501 CCGTCTGAAG AGCTTTCAGA CGGCATTtT GCATTTGTTA GGGACATTGT
551 TATGTTGCCG TTTGATTTTC AGACGGCATT TTGTTTCCAA GCGTTTGATG
601 TCGGGATGGC AATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2868; ORF 934>:

m934.pep (partial)

```

1 ..RLEQQQKQIE ALQQQLAQQ DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51 TGXRRRAVYL RPIDRKLAAA KPGRRGRRV YRQRAGKQIH TGRQPRQSRR
101 PARACSLPSV RTPQCAHQQ FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151 PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201 SGWQF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng)

from *N. gonorrhoeae*:

m934/g934

```

                                     10      20      30
m934.pep                          RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                     |||:|||||
g934                               MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                     10      20      30      40      50      60

                                     40      50      60      70      80      90
m934.pep                          PAEAQANGNNGQPVTKGXRRRAVYLRPIDRKLAAPKGRRGRRVYRQRAGKQIHTGRQPR
                                     ||:|||||
g934                               PAQAQANGNNGQPVTKGRRAVYLRPIDRKLAAPKPDWRGGRRVYRQRAGKQIHTGGQPR
                                     70      80      90      100     110     120

                                     100     110     120     130     140     150

```

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```

m934.pep  QSRRLPARACSLPSVRTPQCAHQQGFHEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g934       QPRRPSRACCLPSVRTPQCAHQQGFHEHAQPPCKTTGGAGAALPPDNAPARQLPPSRYARF
          130      140      150      160      170      180

          160      170      180      190      200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g934       RQKAVNPARQCRLKGFQTAFLLGALLCCRLIFRRHFVSKRLMSGWQFX
          190      200      210      220      230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2869>:

```

a934.seq
1  ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCG CACTCGCCGC
51 CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AACAGATTG
101 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CAGACGATAC GGTTTACCAA
151 CTGACTCCCG AAGCAGTCAA AGACACCATT CCTGCCGAAG CACAGGCAAA
201 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
251 TACGACCAAT CGACAGGAAG CTGGCTGCTG CAAAGCCTGG TCGGCGCGGC
301 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTC ACACGGGCAG
351 GCAACCAAGA CAGTCCCGTC GCCCGCGCGC CGCGTGCCGC CTACCATCAG
401 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTGAACA CGCGCAGCCT
451 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
501 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TCGCGGTTT CGGCAGAAGG
551 CGGTAAATCC GCGGTGCCAA TGCCGTCTGA AGGGCTTCA GACGCGATT
601 TTGTATTTGT TAGGGACATT GTTATGTTGC CGTTTGATT TTAGACGGCA
651 TTTTGTTC AAGAGTTGA TGTCGGGATG GCAATTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2870; ORF 934.a>:

```

a934.pep
1  MKKIIASALI ATFALAACQD DAQARLEQQQ KQIEALQQQL AQQADDTVYQ
51 LTPEAVKDTI PAEAQANGNN GQPVTX*RR AVYLRPIDRK LAAAKPGRRG
101 GRRVYRQAG KQIHTGRQPR QSRRLPARACR LPSVRTSQCA HQQGFHEHAQ
151 PCKTTGGAGA ALPPDNAPAR QLPPPRHARF RQKAVNPACQ CRLKGFQTAF
201 LYLLGTLCC RLIFRRHFVS KSLMSGWQF*

```

m934/a934 94.1% identity in 205 aa overlap

```

          10      20      30
m934.pep  RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a934       MKKIIASALIATFALAACQDDAQARLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
          10      20      30      40      50      60

          40      50      60      70      80      90
m934.pep  PAEAQANGNNGQPVTXRRRAVYLRPIDRKLAAPKGRRGRRVYRQAGKQIHTGRQPR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a934       PAEAQANGNNGQPVTXRRRAVYLRPIDRKLAAPKGRRGRRVYRQAGKQIHTGRQPR
          70      80      90      100     110     120

          100     110     120     130     140     150
m934.pep  QSRRLPARACSLPSVRTPQCAHQQGFHEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a934       QSRRLPARACRLPSVRTSQCAHQQGFHEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
          130     140     150     160     170     180

          160     170     180     190     200
m934.pep  RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a934       RQKAVNPACQRLKGFQTAFLLGTLCCRLIFRRHFVSKSLMSGWQFX
          190     200     210     220     230

```

g935.seq not found yet

1348

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  ATGTTGTATT TCAGATACGG CTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCAGATTGG
151 AAAGTTGAAA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGCGCTC AACGGCAATC
251 AGGCGGATTT AATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGCAAAATT
501 GGATTTGCCG GCACCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAA
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC
601 AATAGAAATG CCAATAATGC CGCGCCGCAA TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGGTTGAATT
701 ATGAAATCGA GCGGAAAAAG CTGACGCCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAT GACGGGTTCG GCAGGGCGTA TTTGGGTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAAACAAA CGGGTAAACA ACCGCCGCTT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGCTG TCCCATACTT
1001 ACCGCCCAAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GCAGGCAGGA
1101 CGGGTTTTAT GTTTCGTCTG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCAGCGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGTTG
1251 GGCAGCAGAG TGGCGGCAGT TGGCGGTTT GAACAGTCGG GTTCCGCTG
1301 CTTATGCCCG CCGCAACTAT AAGGGCATTG CGGCTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CGGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAAATG GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID.2872; ORF 935>:

m935.pep

```

1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVENDAPRVV DGDFLLAHPK MLEHSLRDAL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVERYREL HGENAADERI LLDLAAAEFD
151 DFRLKSAERH FAEAAKL DLP APVLENVGRF RKKTEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTPLADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGHVGVLQ SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNRQDGFY VSSAKRLGES ATVFQGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGIAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPYA KRRNSEVFVS
501 ADWRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  ATGTTGTATT TCAGATACGG TTTTTTGGTT GTTTGGTGTG CGGCAGGTGT
51  TTCTGCCGCC TATGGGGCGG ATGCGCCCGC GATTTTGGAT GACAAGGCAT
101 TGTTCAGAGT GCAGCGGTCG GTGTCGGATA AGTGGGCGGA ATCGGATTGG
151 AAAGTTGACA ATGATGCCCC GCGCGTGGTT GACGGGGATT TTTTGTGGC
201 GCATCCGAAA ATGTTGGAAC ATAGTTTGCG CGACGTGCTC AACGGCAATC
251 AGGCGGATTT GATCGCTTCG TTGGCGGATT TGTATGCCAA GCTGCCGGAT
301 TATGACGCGG TTTTGTACGG CAGGGCGCGG GCTTTGCTGG CGAAATTGGC
351 GGGAAGGCCG GCGGAGGCGG TGGCGCGGTA TCGGGAAGTG CACGGGGAAA
401 ATGCGGCAGA CGAGCGGATT TTGCTGGATT TGGCGGCGGC GGAGTTTGAC
451 GATTTCCGGC TGAAGTCGGC AGAAAGGCAT TTTGCGGAGG CGGAAAAAATT
501 GGATTTGCCG GCGCCGGTTT TGGAAAATGT GGGGCGTTTT CGGAAAAAAG
551 CGGAGGGGCT GACGGGCTGG CGTTTTTCGG GCGGCATCAG TCCGGCGGTC

```

1349

```

601 AATAGAAATG CCAATAATGC CGCGCCGCAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GGCGGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTTG
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTTCA GTAAAAAATC
801 AGCTTATGAC GACGGGTTTCG GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCTG
901 GGCAGCGACG GCTTTGATGC GAAAACAAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTTGTGC CGAAACGCGA AACGGTGGGC
1201 GGCGCGGTCA ATAATGCCGC CTACCGGCGC AACGGTGTTT ATGCCGGCTG
1251 GGCGCAGGAG TGGCGGCACT TGGGCGGTTT GAACAGTCGG GTTCCGCGT
1301 CTTATGCCCC CCGCAACTAT AAGGGCGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTTC GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTTGTGTCTG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

a935.pep

```

1 MLYFRYGFVLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51 KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFSGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVFYA KRRNSEVFVS
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGFVLVWVCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
a935	MLYFRYGFVLVWVCAAGVSAA YGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
m935.pep	RKKTEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFSGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

1350

	310	320	330	340	350	360
m935.pep	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDAKTKRVNNRRLPPYMLAHGVGVQLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVFKRETGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFVFKRETGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVASASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVASASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVPYAKRRNSEVFVSADWRFX					
a935	GRTESNVPYAKRRNSEVFVSADWRFX					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgcAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGT
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRQNNQ TKGYPQISV VGYNRHLLL QVATEGEKQ
101 FVGQIARSEQ AAEVYNYIT VASLPRTA...

```

Homology with a predicted ORF from *N.gonorrhoeae*

m936/q936

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAksAVDRRTTGAQTDDNVMALRIETT					
	::: : ::: :::					
g936	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAksVIDRRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT					
g936	ARSYLQNNTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVNYIT					
	70	80	90	100	110	120
	130					
m936.pep	VASLPRtAXXX					
g936	VASLPRtAGDIAgDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQaQIT					
	130	140	150	160	170	180

a936.seq

1	ATGAAACCCA	AACCGCACAC	CGTCCGCACC	CTGACTGCCG	CCGTCTCAG
51	CCTTGCCCTC	GGCGGTCTGC	TCAGCGCAGT	CGTGGCGCG	GCGGCGGTCTG
101	CGCGGAAATC	CGCCGTCGAT	CGCCGAACCA	CCGCGCGCA	AACCGACGAC
151	AACGTAATGG	CGCTGCGTAT	CGAAACCAACC	GCCGCTCTCT	ATCTGCGCCA
201	AAACAACCAA	ACCAAAGGCT	ACACGCCCCA	AATCTCCGTT	GTCGGCTACA
251	ACCGCCACCT	GCTGCTGCTC	GGACAAGTCG	CCACCGAAGG	CGAGAAACAG
301	TTCGTCCGTC	AGATTGCACG	TTCCGAACAG	GCCGCCGAAG	GCGTGTACAA
351	CTACATTACC	GTCCGCTCCC	TGCCCGGCAC	TGCCGGCGAC	ATCCGTCGCG
401	ACACTTTGGA	CACATCCAAA	GTCCGCGCCA	CGCTGTTGGG	CATCAGCCCC
451	GCCACACAGG	CGCGCGTCAA	AATCGTTACC	TACGGCAACG	TAACCTACGT
501	TATGGGCATC	CTCACCCTCG	AAGAACAGGC	GCAGATTACC	CAAAAAGTCA
551	GCACCACCTG	CGGCGTACAA	AAAGTCATCA	CCCTCTACCA	AAACTACGTC
601	CAACCTCTGA				

a936.pcp

1	MKPKPHTVRT	LTAAVLSLAL	GCGVSAVVGG	AAVGAKSAVD	RRTTGAQTDD
51	NVMALRIETT	ARSYLQNQ	TKGYTPQISV	VGYNRHLLL	GQVATEGEKQ
101	FVGQIARSEQ	AAEGVYNYIT	VASLRPTAGD	IAGDTWNTSK	VRATLLGISP
151	ATQARVKIVT	YGNVTYVMGI	LTPEEQAQIT	QKVSTTVGVQ	KVITLYQNYV
201	OR*				

	10	20	30	40	50	60
m936.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGA	SAVDRRTTGAQTDDNVMALRIETT				
		:: :	:			
a936	MKPKPHTVRTLTAAVLSLALGGCVSAVVGGA	SAVDRRTTGAQTDDNVMALRIETT				
	10	20	30	40	50	60
	70	80	90	100	110	120
m936.pep	ARSYLQNNQTKGYTPQISVVGYNRHL	LLLGQVATEGEKQFVGQIARSEQAAEGV	NYIT			
a936	ARSYLQNNQTKGYTPQISVVGYNRHL	LLLGQVATEGEKQFVGQIARSEQAAEGV	NYIT			
	70	80	90	100	110	120
m936.pep	VASLPRTA					

1352

|||||
 a936 VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
 130 140 150 160 170 180

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1 ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTGCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACGTCCAAA GTCGCGCca cgCTGTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAcggT CGGCGTACAA AAAGTCATTA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1 MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1 ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGCGCGGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTGCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACCTGGAA CACATCCAAA GTCGCGGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AAACCTACGTC
601 CAACGCTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1 MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*
  
```

m936-1/g936-1 95.5% identity in 202 aa overlap

	10	20	30	40	50	60
m936-1.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGA	SAVDRRTTGAQTDDNV	MALRIETT			
g936-1	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGA	KSVIDRRTTGAQTDDNV	MALRIETT			
	10	20	30	40	50	60
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHLLLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					
g936-1	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180

              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACC GCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCTG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGGCGCGCA AACC GACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCAA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTGCGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACAC TTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCGTC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACGTC CGCGGTACAA AAAGTCATCA CCCTCTACCA AAAC TACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTA AVL SLAL GGC VSA VVG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

a936-1/m936-1 97.0% identity in 202 aa overlap

```

              10      20      30      40      50      60
m936-1.pep  MKPKPHTVRTLTA AVLSLALSGCVSAVIGSAAVGAKSAVD RRTTGAQTDD NVMALRIETT
              |||||
a936-1      MKPKPHTVRTLTA AVLSLALSGCVSAVVGGA AVGAKSAVD RRTTGAQTDD NVMALRIETT
              10      20      30      40      50      60

              70      80      90      100     110     120
m936-1.pep  ARSYLRQNNQTKGYTPQISV VGYNRHLLL GQVATEGEKQ FVGQIARSEQ AAEGVYNYIT
              |||||
a936-1      ARSYLRQNNQTKGYTPQISV VGYNRHLLL GQVATEGEKQ FVGQIARSEQ AAEGVYNYIT
              70      80      90      100     110     120

              130     140     150     160     170     180
m936-1.pep  VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              |||||
a936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
              130     140     150     160     170     180

              190     200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
a936-1      QKVSTTVGVQKVITLYQNYVQRX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTAgT ATTTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctgA acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATT CAGACC GGCTCCGCTT CCTTTATCCC
201 CGTCCCAGAC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGAccg GCAataccgA CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAAC TCGacg GCAACGGCAA

```

1354

```

351 AACCCGCAAC AAACGGATGT CCGACATATC CGCCGGCATC AGCCACACCT
401 TCCTtaAAGA cgGCAAAAAT CCCGCACTCA TCGCTTTCCT CGAAAGCAGC
451 GTTTACGAAA AATCGCGCAA CAAAGCCTCG TCGGGAAAAT CGTGGCTCAT
501 CGGCGCCACC ACCTACAAAG CCATAGATCC GATTGTCCTT TCCCTCACCG
551 CCGCCTACCG CATCAACGGC AGCAAAACCC TTTCAGACGA CGTCAAATAC
601 AAAGCAGGCA ATTACTGGAT GCTGAATCCC AACATCTCAT TTGCCGCCAA
651 CGACAGAATC AGCCTGACCG GAGGCATCCA ATGGCTGGGC AAACAGCCCC
701 ACCGCATAGA CGGCAAAAAA GAATCCGCAA GAAACACATC CACCTACGCC
751 CATTTCCGCG CAGGTTTCGG TTTCACCAA ACCGCGGCTT TAAACGCATC
801 CGCAGTTTTT AACGTTTCAG GGCAAAGCAG TTCCGAACTG AAATTGGGCG
851 TACAGCATAC ATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2888; ORF 937.ng>:

g937.pep

```

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETSL TYLNSENSRA
51 ALASPVIYQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIYG
101 SSGSYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST
151 VYEKSRNKAS SGKSWLIGAT TYKAIDPIVL SLTAAYRING SKTSLDDVKY
201 KAGNYWMLNP NISFAANDRI SLTGGIQWLG KQPDRIKGGK ESARNTSTYA
251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVQHTF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2889>:

m937.seq

```

1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCAACATCT CATTGCTGTC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTCG GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2890; ORF 937>:

m937.pep..

```

1 MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTND DMLVGTGLRL YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 937 shows 86.9% identity over a 289 aa overlap with a predicted ORF (ORF 937.ng) from *N. gonorrhoeae*:

g937/m937

```

          10      20      30      40      50      59
g937.pep  MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETSLTYLNSENSRAALASPVIYQ
          || :| :: ::::| : :|||:|||||:|||||:|||||:| :| :|||
m937      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60
          60      70      80      90     100     110     119
g937.pep  TGSASFIPVPTTEIQENGSTNDMLAGTLGLRYGLTGNTDIYGSGSYLWHEERKLDGNGKTR

```

[illegible]

```
a937.seq
1 ATGAAGCGCA TCTTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC GTGCCCTTGA CGATTGAAGA CATATGACC GACAAGGGCA
101 AATGGAAACT CTGAAACTTC CTTACCTACC TGAACAGCGA AAACAACGCC
151 GCGGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGCATTTAC
301 GGCAGCGGCA GCTACTGTG GCACGAAGAA CCGAAACTCG ACGGCAACGG
351 CAAAACCCGA AGACAAACGA TGTCGACGCT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCGTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCGTTTCAAG CAACACAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTG CCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 CGGTACAGCA TACGTTTTAA
```

```
a937.pep
1 MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVL LSLTAAAYRIN GSKTLLSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGSSSE LKFGVQHTF*
```

	10	20	30	40	50	60
m937.pep	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
a937	MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m937.pep	TGATSFIPIPTEIQENGSNNDMLVGTGLGRYGLTGNTDIYSGSYLWHEERKLDGNSKTR					
a937	TGATSFIPIPTEIQENGSNNDMLVGTGLGRYGLTGNTDIYSGSYLWHEERKLDGNKTR					
	70	80	90	100	110	120

1356

	130	140	150	160	170	180
m937.pep	NKRMSDVSLSGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLSGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence <SEQ ID 2894; ORF 939>:

m939.pep (partial)

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCGATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATATCGG
201 CATCCGCGAC GGTAACGCAC CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGTATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT
501 TGTGTAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTGAA AGCGGTTCGCC
601 AACTTTATCC AAGGTTTGCG TTA
```

This corresponds to the amino acid sequence <SEQ ID 2896; ORF 939.a>:

a939.pep

```

1  MKRLTLLAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTGSAAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPKENPELGA KIYRGGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEDLDKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLLAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					
a939	MKRLTLLAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					

1357

```

              10      20      30      40      50      60
              70
m939.ppep    IYHQTIGIRDVNAP
              |||||
a939         IYHQTIGIRDGKRTHGSAAVMKPVVMNLSQDILNVSAFYAKQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGCCGCCGCG GCCTTTGCTG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.ppep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG
51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCG GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.ppep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.ppep    MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----
              |||||
g950         MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGCASKSAEGSCGASKSAEG
              10      20      30      40      50      60
              60      70      80      90      100
m950.ppep    ----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950         SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCCGCG GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

1358

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

```
a950/m950 100.0% identity in 102 aa overlap

          10      20      30      40      50      60
a950.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          |||||
m950      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG
          10      20      30      40      50      60

          70      80      90      100
a950.pep  EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||||
m950      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
          70      80      90      100
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCTACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCCG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTC ACCTGTGTTG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAATG GCCGTGTCGC TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TGCGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTGGAAG GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCAGGA TATTTTGCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GGTGGCTCAA AAAGCATCGA AAGCGGTTGC CCGTGC GCGC
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CCGTGTTCGG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTAATGAC GTTGCCTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAAC CTTTCGGCCG TCTGGCAGGA AATGGAAAT ATGAATCTGG
851 TTTCCCTGCG TAAGCCGGAT GATGCCTATG CGCGTTTGAA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CCTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGTGCGT CCGTTATCGA CGGCTACGCC GAAAAGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACGCGAG GGATTACGCC AAAGTCAGGC AGTGTTGAA
1101 AAAAGTGTCG GCGCCGGAAT ACCTGTTCGA CAAAGCGGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCCGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACTTTC GGCGGCGGGA
1351 AGCACGGAAC CTTTGGCGGA AGCATTGGCA CAGCGTTCCA TTATTTACGA
1401 ACAGTTCGGC AAACGGGGA AAATGATTGC CGACCTTGAA ACCGCGCTCA
1451 AACTTACGCC CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACGTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAATC AACCCGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCCAT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTTGACGTA TGGACGAGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGCGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GQAYAAGAAD VELPKEVGKV LRKHRRYSEE
```

1359

```

51  EIKNERARLA AVGERVNRVF TLLGGETALQ KGQAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHLDGLE EVLAQSDDDVQ KRRIFLLLVQ AAVQQGGVAQ KASKAVRRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL QRLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTQN LSAVWQEMEI MNLVSLRKPD DAYARLNVLL
301 EHNPNANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKVS APEYLFDKGV LAAAAAAELD GGRAALROIG
401 RVRKLPQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQTAYQI NPDDTAVNDS IGWAYYLLKG AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

```

m951.seq
1  ATGATTATGT TACCTAACCG TTTCAAAATG TTAAGTGTGT TGACGGCAAC
51  CTTGATTGCC GGACAGGTAT CTGCCGCCGG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTTC AAGAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAAACGA ACGCGCACGG CTTGCGGCAG TGGCGGAGCG
201 GGTAAATCAG ATATTTACGT TGCTGGGAGG GGAACCGGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGCTTGAA CAGGCGGAAA TGATTATCA GAAATGGCGG CAGATTGAGC
401 CTATACCGGG TAAGCGCGAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAGAGG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GGCAGGACGA GGACAGAACC GCAGGCTGTT TTTATTGTTG GCACAAGCCG
551 CCGTGCAACA GGACGGGTTG GCGCAAAAAG CATCGAAAGC GGTTCGCCGC
601 GCGGCGTTGA AATATGAACA TCTGCCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGGACGCG AAAAGGAAAA GGCAATCGGA GCTTTGCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCACCTTT AATGACGTTG
751 CGCTGACTG CACGCAATA TCCCGAAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAAACCTTT CGGCCGCTCT GCAGGAAATG GAAATTATGA
851 ATCTGGTTTC CCTGCACAGG CTGGATGATG CCTATGCGCG TTTGAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GGCGGCAAA CAAAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGACG GAGGAACAGC GGAGCAGGGC GGCGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCGGCGAGG TCGGGAACCT TCCCGAACAG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTG TCCAAAATAC AGATGCTCGC CTGTGCGAAG CTGCCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCTGCGC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGGTACAGC GGTCAGTTGT
1401 TTACGATCGG CTTGGCAAGC GAAAAAAT GATTTCAGAT CTGAAAGGG
1451 CGTTCAGGCT TGCACCCGAT AACGCTCAGA TTATGAATAA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATA CAAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GGCGACGCGG AAAGCGCGCT GCCGTATCTG
1651 CCGTATTCGT TTGAAACGA CCCCAGCCC GAAGTTGCCG CCCATTTGGG
1701 CGAAGTGTG TGGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCCGAAAA CTCGGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

```

m951.pep
1  MIMLPNRFKM LTVLTATLIA QVSAAGGGA GDMKQPEVG KVFRKQQRYS
51  EEEIKNERAR LAAVGERVNQ IFTLLGGETA LQKQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERNQHLDG LEEVLAQADE GQNRVFLLL AQAQVQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLRTARKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAILAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLAAAAAVE LDGGRAALRQ
401 IGRVRKLPQ QGRYFTADNL SKIQMLALS LKPKREALRG LDKIIEKPPA
451 GSNTLQAEA LVQRSVVYDR LGKRKKMISD LERAFRLAPD NAQIMNNGY
501 SLLTDSKRLD EGFALLQTAY QINPDDTAVN DSGWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:

1360

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

	10	20	30	40	50	60
m951.pep	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVEGKVFRKQORYSEEEIKNERAR					
g951	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGKVLKRRYSEEEIKNERAR					
	10	20	30	40	50	
	70	80	90	100	110	120
m951.pep	LAAVGERVNIQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
	60	70	80	90	100	110
	130	140	150	160	170	180
m951.pep	QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRRGNQHLDGLEEVLAQADEGQNRVFLLL					
g951	QAEMIQKWRQIEPIPGEAQKRAGWLRNVLREGGNQHLDGLEEVLAQSDDVQKRIFLLL					
	120	130	140	150	160	170
	190	200	210	220	230	240
m951.pep	AQAAVQQDGLAQKASKAVRRAALKYEHLPAAVADVVSQGREKEKAIGALQRLAKLDT					
g951	VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADAVFGVQGREKEKAIEALQRLAKLDT					
	180	190	200	210	220	230
	250	260	270	280	290	300
m951.pep	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLRKPDDAYARLNV					
	240	250	260	270	280	290
	310	320	330	340	350	360
m951.pep	LLERNPNADLYIQAAILAANRKEGASVIDGYAEKAYGRGTTEEQRSAALTAAMMYADRRD					
g951	LLEHNPNANLYIQAAILAANRKEGASVIDGYAEKAYGRGTGEQRGAAMTAAMIYADRRD					
	300	310	320	330	340	350
	370	380	390	400	410	420
m951.pep	YAKVRQWLKKVSAPEYLFDKGVLA AAAAELDGGRAALRQIGRVKRLPEQQGRYFTADNL					
g951	YAKVRQWLKKVSAPEYLFDKGVLA AAAAELDGGRAALRQIGRVKRLPEQQGRYFTADNL					
	360	370	380	390	400	410
	430	440	450	460	470	480
m951.pep	SKIQMLALSCLPKREALRGLDKIIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	SKIQMLALSCLPKREALIGLNNIIAKLSAAGSTEPLAEALAQRSIIEYQFGKRGKMIAD					
	420	430	440	450	460	470
	490	500	510	520	530	540
m951.pep	LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	LETALKLTPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
	480	490	500	510	520	530
	550	560	570	580	590	600
m951.pep	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
	540	550	560	570	580	590
	610					
m951.pep	KRHGIALPQPSRKPRK					
g951	KRYGIALPEPSRKPRKX					
	600	610				

1	ATGTTACCCG	CCCGTTTCAC	CATTTTATCT	GTGCTCGCGG	CAGCCCTGCT
51	TGCCGGGGAG	GCGTATGCCG	CCGGCGCGCG	GGATGCGAAG	CCCGCCGAAGG
101	AAGTCGGAAA	GGTTTTCAGA	AACGACGACG	GTTCACGGA	CGGAAGAACT
151	AAAAACGAAC	CGCGACCGCT	TGCGGCAGTG	GGCGAGCGGG	TTAATCAGAT
201	ATTTACGTTG	CTGGGAGGGG	AAACCGCCTT	GCAAAAGGGG	CAGGCGGGGAA
251	CGGCTCTGGC	AACCTATATG	CTGATGTGTG	AACGCACAAA	ATCCCCGAA
301	GTCCGCCAAC	CGCGCTTGGA	ATGAGCCGTG	TCGCTGAACG	CGTTTGAAAC
351	GGCGGAAATG	ATTTATCAGA	AATGCGCGCA	GATTGAGCCT	ATACCGGGTA
401	AGGCGCAAAA	ACGGGCGGGG	TGGCTGCGGA	ACGTGCTGAG	GGAAAGAGGA
451	AATCAGCATC	TAGACGGACT	GGAAGAAATG	TCGCTCAGG	CGGACGAAGG
501	ACAGAACCCG	AGGGTGTTTT	TATTGTTGGC	ACAAGCCGCC	GTGCAACAGG
551	ACGGGTTGGC	GCAAAAAGCA	TCCGAAGCGT	TTCCGCCGCG	GGCGTTGAGA
601	TATGAACATC	TGCCCGAAGC	GCGGCTTGCC	GATGTGGTGT	TACGCGTACA
651	GGGACGCGAA	AGGAAAAGG	CAATCGGAGC	TTTGCAGCGT	TTGGCGAAGC
701	TCGATACGGA	AATATTGCCC	CCCACTTTAA	TGACGTTGCG	TCTGACTGCA
751	CGCAAAATAT	CCGAAATACT	CGACGGCTTT	TTCCAGCAGA	CAGACACCCA
801	AAACCTTTTC	CGCGCTTGGC	AGGAAATGGA	AATTATGAAT	CTGTTTTCCT
851	TGCACAGGCT	GGATGATGCC	TATGCGCGTT	TGAACGTGGT	GTTGGAACGC
901	AATCCGAATG	GACCTCGTGA	TATTCAGGCA	CGCATATTGG	CGGCAAAACG
951	AAAAGAAAGT	GCTTCCGTTA	TCGACGGCTA	CGCCGAAAAG	CAGTACGGCA
1001	GGGGGACGGG	GGAACAGCGG	GGCAGGGCGG	CAATGACGGC	GGCGATGATA
1051	TATGCCGACC	GAAGGGATTA	CACCAAAGCT	AGGCAGTGCT	TGAAAAAAGT
1101	GTCCGCGCCG	GAATACCTGT	TCGACAAAGG	TGTGCTGGCG	GCTGGCGCGG
1151	CTGTGCGAGT	GGACGCGCGC	AGGGCGGCTT	TGCGGCAGAT	CGGCAGGGTG
1201	CGGAAACTTC	CCGAACAGCA	GGGGCGGTAT	TTTACGGCAG	ACAATTTGTC
1251	CAAAATACAG	ATGTTCCGCC	TGTCGAAGCT	GCCCGACAAA	CGGGAGGTTT
1301	TGAGGGGGTT	GGACAAGATT	ATCGAAAAAC	CGCCTGCCCG	CAGTAATACA
1351	GAGTTACAGG	CAGAGGCATT	GGTACAGCGG	TCAGTTGTTT	ACGATCGCCT
1401	TGGCAAGCGG	AAAAAAATGA	TTTCAGATCT	TGAAAGGGCG	TTCAGGCTTG
1451	CACCCGATAA	CGCTCAGATT	ATGAATTAAT	TGGGCTACAG	CTGCTTTTCC
1501	GATTCCAAAC	GTTTGGACGA	AGGCTTCGCC	CTGCTTCAGA	CGGCATACCA
1551	AATCAACCCG	GACGATACCG	CTGTCAACGA	CAGCATAGGC	TGGGCGTATT
1601	ACCTGAAAGG	CGACGCGGAA	AGCGCGCTGC	GCTATTGCGG	GTATTCTGTT
1651	GAAGACGACC	CCGAGCCCGA	AGTTGCCGCC	CATTTGGGCG	AAGTGTGTGT
1701	GGCATTGGGC	GAACGCGCAT	AGGCGGTTGA	CGTATGGACG	CAGGCGGCAC
1751	ACCTTACGGG	ACCAAGAAAT	ATATGCGCGG	AAACGCTCAA	ACGTACGGGC
1801	ATCGCATTTG	CCCAACCTTC	CGGAAACACT	CGGAAATAA	

1	MLPARFTILS	VLAALLAGO	AYAAGAADAK	PPKEVGKVFR	KQORYSEEEI
51	KNERARLAHV	GERVNIQITL	LGGETALQKG	QAGTALATYM	LMLERTKSPE
101	VAERALEMAV	SLNAFEQEM	IYQKWQIEP	IPGKAQKRAG	WLRNVLRERG
151	NQHLDGLEEV	LAQADEQGNR	RVFLLAQAA	VQDGLAQKA	SKAVRAALR
201	YEHLPEAAVA	DVVFESVQGR	KEKAIGALQR	LAKLDTEILP	PTLMTLRLTA
251	RKYPEILDGF	FEQTDQTNLS	AVWQEMEIMN	LVSHRLDDA	YARLNVILER
301	NPNAADLYTA	AILAANRRKE	ASVIDGYAEK	AYGRGTGEOR	GRAAMTAAMI
351	YADRDRYTKV	RQWLKKSVA	EYLFDKGVLA	AAAAVELDGG	RAALRQIGRV
401	RKLPEQQGRY	FTADNLSIK	MFALSKLPDK	REALRGLDKI	IEKPPAGSNT
451	ELQAEALVQR	SVVYDRLGKR	KKMISDLERA	FRLAPDNAQI	MNNLGYSLLS
501	DSKRLDEGFA	LLGTAYQINP	DDTAVNDSIG	WAYYLKGDAG	SALPYLRYSF
551	ENDPEPEVAA	HQEVLEWALG	ERDQAVDVWT	QAAHLTGDDK	IWRETLKRHG
600	IALPQPSRKP	RK*			

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

```

              10      20      30      40      50
a951.pep      MLPARFTILSVLAAALLAGQAYAAG--AADAKPPKEVGKVFRKQQRYSEEEIKNERAR
               ||| || :||:::||: ||| |::| |||||||||
m951          MIMLPNRFKMLTLVLTATLIAGQVSAAAGGGADMKPKEVGKVFRKQQRYSEEEIKNERAR
               10      20      30      40      50      60

              60      70      80      90     100     110
a951.pep      LAAVGERVNQIFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE

```

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```

|||||
m951      LAAVGERVNQIFTLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
              70          80          90          100         110         120

a951.pep   120          130          140          150          160          170
QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
|||||
m951      QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLDGLEEVLAQADEGQNRVFLLL
              130          140          150          160          170          180

a951.pep   180          190          200          210          220          230
AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
|||||
m951      AQAAVQQDGLAQKASKAVRRAALRYEHLPEAAVADVVSQGREKEKAIGALQRLAKLDT
              190          200          210          220          230          240

a951.pep   240          250          260          270          280          290
EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
|||||
m951      EILPPTLMTLRLTARKYPEILDGFFEQTDTQNLSAVWQEMEIMNLVSLHRLDDAYARLNV
              250          260          270          280          290          300

a951.pep   300          310          320          330          340          350
LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRGAAMTAAMIYADRRD
|||||
m951      LLERNPNADLYIQAAILAANKREGASVIDGYAEKAYGRGTGEQGRSRAALTAAMMYADRRD
              310          320          330          340          350          360

a951.pep   360          370          380          390          400          410
YTKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL
|:|||||
m951      YAKVRQWLKKVSAPEYLFDKGVLA AAAA VELDGGRAALRQIGRVRKLPEQQGRYFTADNL
              370          380          390          400          410          420

a951.pep   420          430          440          450          460          470
SKIQMFALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
|||||
m951      SKIQMLALSKLPDKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD
              430          440          450          460          470          480

a951.pep   480          490          500          510          520          530
LERAFRLAPDNAQIMNNLGYSLLSDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
|||||
m951      LERAFRLAPDNAQIMNNLGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK
              490          500          510          520          530          540

a951.pep   540          550          560          570          580          590
GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
|||||
m951      GDAESALPYLRYSFENDPEPEVA AHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL
              550          560          570          580          590          600

a951.pep   600          610
KRHGIALPQPSRKPRK
|||||
m951      KRHGIALPQPSRKPRK
              610

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2909>:

```

g952.seq (partial)
1  ..TTGCTCTATC GTTTGAATGC TGCACCGATG TTAAACGATA ATCCTGTTGT
51  TTACGGAAAA ATCAAATTGC AGAGTTGGAA AGCGCGGCGG GATTTCATA
101 TTGTAAAGCA GGATTTGGAT TTTCTCTGCG GGGCGGCTTC GGTGGCGACG
151 CTTTTGAACA ATTTTACGG GCAAAAGCTG ACGGAAGAAG AAGTGTTGGA
201 AAAACTGGGT AAGGAACAGA TCGCGCGCTC GTTTGAGGAT ATGCGGCGCA
251 TTATGCCCGA TTTGGGTTT GAGCGGAAAG GCTATGCCCT GTCTTTCGAA
301 CAGCTCGCGC AGTTGAAAT CCCCCTCATC GTGTATCTGA AATACCGCAA
351 AGACGACCAT TTTTCGGTAT TCGCGGAGT GGATGGCAAT ACGGTTTTGC
401 TTGCCGACCC GTCGCGGGT CATGTTTCGA TGAGCAGGGC GCAGTTTTTG
451 GAGGCTTGCG AAACCCGTGA GGGAAATTG GCAGGCAAAA TTTTGGCGGT
501 CGTGCCGAAA AAAGCGGAGG CGATTTCAAA TAAATTGTTT TTCACACATC
551 ATCCCAAGCG GCAGACGGAG TTTGCAGTCG GACAGGTAAA ATGGTGGCGT

```

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601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

```
g952.pep (partial)
  1  ..LSYRLNAAPM FNDNPVVYVK IKLQSWKARR DFNIVKQDLDFSCGAASVAT
  51  LLNNFYGQKL TEEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
 101  QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPS PG HVSMSRAQFL
 151  EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKRQTE FAVGQVKWWR
 201  AY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

```
m952.seq
  1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
 51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTGTGTT
 101  ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGGCGGGA TTTCAATATT
 151  GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
 201  TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
 251  AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
 301  ATGCCTGATT TGGGTTTTGA GGCGAAGGGC TATGCCCTGT CTTTCGAGCA
 351  GCTCGCGCAG TTGAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
 401  ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTGTCTT
 451  GCCGACCCGT CGCTGGGGCA TGTTTCAATG AGCAGGGCGC AGTTTGTGGA
 501  TGCTTGGCAA ACCCGTGAGG GAAATTGGC AGGTAAGATT TTGGCTGTCA
 551  TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
 601  CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
 651  AGAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

```
m952.pep
  1  MMKFYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
 51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRRI
 101  MPDLGF EAKGYALSFE QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPS PG
 151  ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTQH
 201  PKRQTEFTVG QIRQARAE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

		10	20	30	40		
g952.pep		LSYRLNAAPMFNDNPVVYVKIKLQSWKARRDFNIVKQDLDFSCG					
m952	MMKFYVFLACVVVLSYRLNAAPMFNDNPVVYVKIKVQSWKARRDFNIVKQDLDFSCG						
		10	20	30	40	50	60
		50	60	70	80	90	100
g952.pep	AASVATLLNNFYGQKLTEEEVLEKLGKEQMRASFEDMRRIMPD LGF EAKGYALSFEQLAQ						
m952	AASVATLLNNFYGQTLTEEEVLKKLDKEQMRASFEDMRRIMPD LGF EAKGYALSFEQLAQ						
		70	80	90	100	110	120
		110	120	130	140	150	160
g952.pep	LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPS PGHVSMSRAQFLEAWQTREGNLAGKI						
m952	LKIPVIVYLKVRKDDHFSVLRGIDGNTVLLADPSLGHVSMSRAQFLDAWQTREGNLAGKI						
		130	140	150	160	170	180
		170	180	190	200		
g952.pep	LAVVPKKAEAISNKLFFTHHPKRQTEFAVGQVKWWRAYX						
m952	LAVIPKKAETISNKLFFTQHPKRQTEFTVGQIRQARAE						
		190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

```
a952.seq
  1  ATGATGAAGT TCAAATATGT TTTTCTGTTG GCGTGTGTTG TCGTTTCTTT
```

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```

51 ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGCGGGA TTTCATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGCTTGCAA ACCCGTGAGG GAAATTGGC AGGTAAGATT TTGGCGGTCG
551 TGCCGAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCAGTGTC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1  MMKFYVFL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKKLDKEQM RASFEDMRRI
101 MPDLGFEEKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952    97.7% identity in 218 aa overlap

a952.pep      10      20      30      40      50      60
MMKFYVFLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG
|||||
m952          10      20      30      40      50      60
MMKFYVFLACVVVSLSYRLNAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG

a952.pep      70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRSASFEDMRRI MPDLGFEEKGYALSFEQLAQ
|||||
m952          70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKKLDKEQMRSASFEDMRRI MPDLGFEEKGYALSFEQLAQ

a952.pep      130     140     150     160     170     180
LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI
|||||
m952          130     140     150     160     170     180
LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI

a952.pep      190     200     210     219
LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE
|||:|||||:|||||
m952          190     200     210
LAVIPKKAETISNKLFFTOHPKRQTEFTVGQIRQARAE

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1  ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51  CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAACGTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGCTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCCGTC GCCAACCTGC AAAGCGGTTT GCAACCCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCGGGGCA AAACCGCCCC CGTCAAATC AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGCGGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACAAA TGGGCGGTGG ACTACCTCGT
501 TAACGCCGGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAAAATA A

```

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This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

```

g953.pep
  1  MKKIIFAALA  AAAVGTASAT  YKVDEYHANV  RFAIDHFNTS  TNVGGFYGLT
 51  GSVEFDQAKR  DGKIDITIPV  ANLQSGSQPF  TGHLSADIF  DAAQYPDIRF
101  VSTKFNFNKG  KLVSV DGNLT  MRGKTAPVKL  KAEKFNCYQS  PMAETEVC GG
151  DFSTTIDRTK  WGV DYL VNAG  MTKNVRIDIQ  IEAAKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

```

m953.seq
  1  ATGAAAAAAA  TCATCTTCGC  CGCACTCGCA  GCCGCCGCCA  TCAGTACTGC
 51  CTCCGCCGCC  ACCTACAAAG  TGGACGAATA  TCACGCCAAC  GCCCGTTTCG
101  CCATCGACCA  TTTCAACACC  AGCACCAACG  TCGGCGGTTT  TTACGGTCTG
151  ACCGGTTCGG  TCGAGTTCGA  CCAAGCAAAA  CGCGACGGTA  AAATCGACAT
201  CACCATCCCC  ATTGCCAACC  TGCAAAGCGG  TTCGCAACAC  TTTACCGACC
251  ACCTGAAATC  AGCCGACATC  TTCGATGCCG  CCCAATATCC  GGACATCCGC
301  TTTGTTTCCA  CCAAATTCAA  CTTCAACGGC  AAAAAACTGG  TTTCCGTTGA
351  CGGCAACCTG  ACCATGCACG  GCAAAACCGC  CCCCCTCAAA  CTCAAAGCCG
401  AAAAAATCAA  CTGCTACCAA  AGCCCGATGG  AGAAAACCGA  AGTTTGTGGC
451  GGCGACTTCA  GCACCACCAT  CGACCGCACC  AAATGGGGCA  TGGACTACCT
501  CGTTAACGTT  GGTATGACCA  AAAGCGTCCG  CATCGACATC  CAAATCGAGG
551  CAGCCAAACA  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

```

m953.pep
  1  MKKIIFAALA  AAAISTASAA  TYKVDEYHAN  ARFAIDHFNT  STNVGGFYGL
 51  TGSVEFDQAK  RDGKIDITIP  IANLQSGSQH  FTDHLKSADI  FDAAQYPDIR
101  FVSTKFNENG  KKLVSVDGNL  TMHGKTAPVK  LKAEKFNCYQ  SPMEKTEVCG
151  GDFSTTIDRT  KWGMDYLVNV  GMTKSVRIDI  QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

```

m953.pep      10      20      30      40      50      60
               MKKIIFAALAAAIASTASAAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
               |||||:::||||| |||||:::||||| |||||:::||||| |||||:::||||| |||||:::|||||
g953          10      20      30      40      50
               MKKIIFAALAAAAGVTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK
               |||||:::||||| |||||:::||||| |||||:::||||| |||||:::||||| |||||:::|||||

m953.pep      70      80      90      100     110     120
               RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNFNKKLVSV DGNL
               |||||:::||||| |||||:::||||| |||||:::||||| |||||:::||||| |||||:::|||||
g953          60      70      80      90      100     110
               RDGKIDITIPVANLQSGSQPF TGHLSADIFDAAQYPDIRFVSTKFNFNKKLVSV DGNL
               |||||:::||||| |||||:::||||| |||||:::||||| |||||:::||||| |||||:::|||||

m953.pep      130     140     150     160     170     180
               TMHGKTAPVKLKA EKFN CYQSPMEKTEVC GDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
               |||||:::||||| |||||:::||||| |||||:::||||| |||||:::||||| |||||:::|||||
g953          120     130     140     150     160     170
               TMRGKTAPVKLKA EKFN CYQSPMAETEVC GDFSTTIDRTKWGV DYL VNAGMTKNVRIDI
               |||||:::||||| |||||:::||||| |||||:::||||| |||||:::||||| |||||:::|||||

m953.pep      QIEAAKQX
               |||||
g953          QIEAAKQX
               |||||
               180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

```

a953.seq
  1  ATGAAAAAAA  TCATCATCGC  CGCGCTCGCA  GCAGCCGCCA  TCGGCACTGC
 51  CTCCGCCGCC  ACCTACAAAG  TGGACGAATA  TCACGCCAAC  GCCCGTTTCT
101  CTATCGACCA  TTTCAACACC  AGCACCAACG  TCGGCGGTTT  TTACGGTCTG
151  ACCGGTTCGG  TTGAGTTCGA  CCAAGCAAAA  CGCGACGGTA  AAATCGACAT
201  CACCATCCCC  GTTGCCAACC  TGCAAAGCGG  TTCGCAACAC  TTTACCGACC
251  ACCTGAAATC  AGCCGACATC  TTCGATGCCG  CCCAATATCC  GGACATCCGC
301  TTTGTTTCCA  CCAAATTCAA  CTTCAACGGC  AAAAAACTGG  TTTCCGTTGA

```

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```

351 CGGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAAA CTCAAAGCCG
401 AAAAATTCAA CTGCTACCAA AGCCCGATGT TGAAAACCGA AGTTTGCGGC
451 GGC GACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGTTAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
1  MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
51  TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYPDIR
101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAEKFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

a953/m953 97.3% identity in 187 aa overlap

	10	20	30	40	50	60
a953.pep	MKKIIIAALAAAIGTASAATYKVDEYHANARFSIDHFNTSTNVGGFYGLTGSVEFDQAK					
	: : : : : : : : : :					
m953	MKKIIFAALAAAISTASAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK					
	10	20	30	40	50	60
	70	80	90	100	110	120
a953.pep	RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL					
	: : : : : : : : :					
m953	RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAAQYPDIRFVSTKFNENGKKLVSDGNL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a953.pep	TMHGKTAPVKLKAEKFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	: : : : : : : : :					
m953	TMHGKTAPVKLKAEKFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI					
	130	140	150	160	170	180
a953.pep	QIEAAKQX					
m953	QIEAAKQX					

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
1  ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
51  GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AAACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGCG GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTACTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAAACAGGC TCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
1  MKKIFYVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KOAFYFERAA
51  RFRVLQQGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGTTDLTD KESYQNYRKS MQECRKTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

g957.seq (partial)

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGGAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATTCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAAT
751 ATGCGGGGAT TGATGCCCCG GGGGatgaaG gcgaacagtc ttgtggtcgg
801 ctatgatgcg gacggtCtgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaaaaaaacc ccaaagtgtc gaatattatt tgaaaaacgg aaatcctttt
901 attgcccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaac tatcatgccc aacaaacgtt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

g957.pep (partial)

```

1  MFKKFKPVLL SFFALVFAPW LGTGIAYEIN PRWFLSDTAT EVPENPNFAV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS VDNGKKPQSV EYYLKNGNLF
301 IAQSSTVTLK TDGVTADMQT YHAQQTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

m957.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCT TGCCGGAAT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CCGGGGAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATTCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAACCG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTTGGAT GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCTTGATTT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

m957.pep

```

1  MFKKFKPVLL SFFALVFAPW LGTGIAYEIN PRWFLSDTAT EVKPNPNFAV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
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1368

251 MRELMPRGMK ANSLVVGYDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
 301 IAQSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
 351 LENLEKEVRR YAEAAARRSG GRRDLSH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVVPENPNFAFVAKLARLFRNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVVPKPNFAFVAKLARLFRNA					
	10	20	30	40	50	60
g957.pep	70	80	90	100	110	120
	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
g957.pep	130	140	150	160	170	180
	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
g957.pep	190	200	210	220	230	240
	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
g957.pep	250	260	270	280	290	300
	DSRDYVFYQNMRELMPRGMKANSLLVVGADGLPQKVYWSVDNGKKPQSVEYYLKNGNLF					
m957	DSRSNVFYQNMRELMPRGMKANSLLVVGADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF					
	250	260	270	280	290	300
g957.pep	310	320	330			
	IAQSTVTLLKTDGVTADMOTYHAQQTLYLDG					
m957	IAQSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
m957	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTGTATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCCTCGGT	GTTATCAGAT	GGCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

1369

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951 CTATCATGCG CAACAGACGT GGTATTTAGA TGGCGGGCGG ATTGTCCGCG
1001 AAGAGAAACA GGGGGACAGA CTGCCTGATT TTCCTTTGAA CTTGGAAGAT
1051 TTGGAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGGCGA GACGTTCCGG
1101 CGGCAGGCGC GACCTTTCTC ACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

```

a957.pep
1  MFKKFKPVLL SFFALVFVAFW LGTGIAYEIN PRWFSLDTAT ENPNAFVAKL
51  ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDYL ALAVRLSRLK
101 EKAKWFHVTE QEHEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLYRN
151 DRPFSVNVYG GTVHGENYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH
201 CLGCMYMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE
251 LMPRGMKANS LVVGYDADGL PQKVYWSFDN GKKRQSFEYY LKNGNLFIAQ
301 SSTVALKADG VTADMQTYHA QQTWYLDGGR IVREEKQGDR LPDFPLNLED
351 LEKEVSRYAE AAARRSGGRR DLSH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10	20	30	40	50
m957	10	20	30	40	50
a957.pep	60	70	80	90	100
m957	60	70	80	90	100
a957.pep	110	120	130	140	150
m957	110	120	130	140	150
a957.pep	160	170	180	190	200
m957	160	170	180	190	200
a957.pep	210	220	230	240	250
m957	210	220	230	240	250
a957.pep	260	270	280	290	300
m957	260	270	280	290	300
a957.pep	310	320	330	340	350
m957	310	320	330	340	350
a957.pep	360	370			
m957	360	370			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

```

g958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCAGC CATTGCGCCG CCGATACCGT TCGGGCGGAA GAGGCGGACG

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1370

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101 GGCCTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAAGCT
151 TCCGATTTGA CCTCGGTTTC GACCTGCCTG TTTTGCAGTA ACGAAAGCGG
201 CAGCCCCGAG AGAACCAGAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
251 TCCCCGAAGA CTATACGCGC ATTGTGCGCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TCGCGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGTAGGCGA CCGGTTTCGCC CTCCAACAGG ACGGTACGCT GATTCCGGGC
451 GAAACCTTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACTG
501 CCGTATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAGC GTCAGCCGCA
551 CCGCCGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCAATTTC
601 AACACCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAAGCGGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
701 TGTTCCGGCG CGTTCCCTTT TCTATACGC CTTGGGCGGA CTTCCCGCTT
751 GACGGCAACC GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCCGGTTC
801 GGACGGCGTT TCCCTTTCCG TCCCCTATTA TTTCAACCTT GCCCCCAACT
851 TCGATGCCAC TTTCCGCCCC GGCATTATCG GCGAACGCGG CGCGACGTTT
901 GACGGACAAA TCCGTTACCT GCGTCCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCAGGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAAATGGCA GACCCGGCAC GACATTTCCG ACACGCTTCA GCGGGGTGTC
1051 GATTTCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAAGAAATC GCGCGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGGCGGCAG GCGCGCGGGA GCGAGCCTGA ATGCCGGCCT TTCGGTTCAG
1201 AAATACCAGA CGCTGGCAAA CCAAAGCGGC TACAAAGACG AACCTTACGC
1251 CATCATCCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAATCGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACGGCAGCC GACTGGTCGT GTATCCCGGT ATCAAATGGG ATTTACAGCA
1401 CAGCTGGGGC TACGTCCGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCTCGACAG TTTCGGCGGC AAAGCATCCC GCAGCGTCGG GCGCGTTTTG
1501 CCCGTTGTCA ATATCGACGG CGGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTCGGCGGC GGAGTCGTGC AAACCATCGA GCGCGCGCTG TTCTACAACT
1601 ATATTCTGTC CAAATCTCAA AACGACCTGC CCAATTTCTGA TTCGTCGGAA
1651 AGCAGCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGACCGCATC AACGCCGCCA ACAGCCTTTC CACCGCGGTG CAGAGCCGTA
1751 TTTTGGACGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTCAG
1801 AAATTCTATT TCAAGGATGA TGCGGTGATG CTTGACGGCA GCGTCGGCAA
1851 AAATCCGCGC AGCCGTTCCG ACTGGGTGGC ATTCGCTCC GCGCGCATAG
1901 GCGGGCGTTT CACCCTCGAC AGCAGCATCC ACTACAACCA AAACGACAAA
1951 CGCGCCGAAC ATTACGCGGT CGGCGCAGGC TACCGCCCGG CCCCCGAAA
2001 AGTGTGTAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGCGCGACGG TTCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCACAATGGC CGCTGACGCG CAACCTGTCT GCCGTCGTCC GCTACAACTA
2151 CGGTTTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGGT GCAGAATACA
2201 AAAGCAGTTG CGGCTGCTGG GCGCGGGGCG TGTACGCCCA ACGCTACGTT
2251 ACCGGCGAAA ACACCTACAA AAACGCCGTC TTTTTTTCAC TTCAGTTGAA
2301 AGACCTCAGC AGCGTCGGCA GAAACCCGCG AGGCAGGATG GATGTCGCCG
2351 TTCCCGGCTA CATCCCCGCC CACTCTCTTT CCGCCGACG CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

g958.pep

```

1  LARLFSLKPL VLALGFCEGT HCAADTVAAE EADGRVAEGG AQGASESAQA
51  SDLTLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMEGQS
101 KVKVRAEGSV IIERDGAVLN TDWADYDQSG DTVTVGDRFA LQQDGLTIRG
151 ETLTYNLDQQ TGEAHNVNRM TEQGGRRLLQ VSRTAEMLGE GRYKLTETQF
201 NTCSAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLPRD YSGQTDLTWL PHDKKSGRNN RYQAKWQHRH DISDTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLNRRV WLDYGGRAAG GSLNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSDHGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TYYSLDSFGG KASRSVGRVL
501 PVVNI DGGTT FERNTRLFGG GVVQTI EPRL FNYI PAKSQ NDLPNFDSSSE
551 SSFGYQLFR ENLYYGNDR NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGVS GKNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLOADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIEMLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLQLKDLS SVGRNPAGRM DVAVPGYIPA HSLSAGRNKR
801 P*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

m958.seq

```

1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51  CTTCCGACAG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGCCGA ACCCATAACG

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1371

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTGCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTGCTCG AACGCAACCG
351 GACGACCTC AATACCGATT GGGCGGATTA CGACCAAGTC GGCAGACCCG
401 TTACCGCAGG CGACCGGTTT GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGGCAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 GCCTCCGATG GAAATCGAAC AAGGCGGACG GCGGTGCAA AGCGTCAGCC
551 CGACCGCCGA AATGTTGGGC GAAGGCGATT ACAAACTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGTCGAAGCG GATCGGGAAG AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCGTGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCTTTT CCGTTCCTTA TTATTTC AAC CTGCCCCCA
851 ATCTCGATGC CAGGTTCCGG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CCTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCGGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCATCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCCGATTTGA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTAGGGCGG CAGGGCGGGC GGGCGCAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAACCGTA
1251 TGCCCTCATG CCGCGCCTTT CGGTGAGTGC GCGTAAAAAC ACCGGCAGGG
1301 CGCAATACGG CGTGTCGCCA CAATTTACCC GATTACAGCA CGACAGCCGC
1351 CAAGACGGCA GCCGCTGGT CGTCTATCCC GACATCAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAC TACTACCGCG GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCGCACT
1501 CTGCCCATTT TCAACATCGA CAGCGCGGCA ACTTTTGAGC GGAATACGG
1551 GATGTTCCGG GAGAAGTCC TGCAAACCT CGAGCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTGCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTCTTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGT
1801 CAGAAATTCT ATTTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGGCAGCA
1901 TCGGCGCCG CTTCATCCTC GACAGCAGCA TCCACTACAA CCAAACGAC
1951 AAACGCGCGC AGAATACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCGCT ACAAAATACG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCAAAA AACCAGATAG GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGGTACGCG CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTCG GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCGCGG CTATATCACC GCCCACTCTC TTTCCGCCG ACGCAACAAA
2401 CGACCTGA

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This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

```

m958.pep
1 LARLFLSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PLSLSLSTGSL LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQDQDTLIR
151 GETLTLYNLEQ QTGEAHNVLM EIEQGGRRLLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKIGIVAK HAAAFVGGVP IFYTPWADFP
251 LDGNNRKSGLL VPSLSAGSDG VLSVPPYYFN LAPNLDATFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLOAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLNAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRKN TGRAQIGVSA QFTRFSDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNI DSGA TFERNTRMFG GEVLQTLLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSVGKKP RNRSDWVAFA SGSGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GA EYKSSCGC WGAGVYAORY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

	10	20	30	40	50	60
m958.pep	LARLFSLKPLVLALGLCFGTHCAAA	DAVAEETDNPTAGESVRSVSEPIQPTSLSLG	STC			
g958	LARLFSLKPLVLALGFCFGTHCAA-DTVA	EEADGRVAEGGAQGASESAQASDLTLG	STC			
	10	20	30	40	50	
	70	80	90	100	110	120
m958.pep	LFCSNESGSPERTEAAVQGS	GEASIPEDYTRIVADRM	EGSQSQVQVRAEGNVVVERN	RTTL		
g958	LFCSNESGSPERTEAAVQGS	GEASVPEDYTRIVADRM	EGSQSKVKVRAEGSVIIERD	GAVL		
	60	70	80	90	100	110
	130	140	150	160	170	180
m958.pep	NTDWADYDQSGD	TVTAGDRFALQQD	GLIRGETLTYNLEQQT	GEAHNV	RMEIEQGGRR	LQ
g958	NTDWADYDQSGD	TVTVGDRFALQQD	GLIRGETLTYNLDQQT	GEAHNV	RMETEQGGRR	LQ
	120	130	140	150	160	170
	190	200	210	220	230	240
m958.pep	SVSRTAEMLGEGHYKLTETQ	FNTCSAGDAGWYVKAAS	VEADREKIGVAKHAA	FVFG	GV	
g958	SVSRTAEMLGEGRYKLTETQ	FNTCSAGDAGWYVKAAS	VEADRGKGIGVAKHAA	FVFG	GV	
	180	190	200	210	220	230
	250	260	270	280	290	300
m958.pep	IFYTPWADFPLDGNRKSGLL	VPSLSAGSDGVSLSVP	YFNLAPNLDATFAPSV	IGERG	AV	
g958	IFYTPWADFPLDGNRKSGLL	VPSVSAGSDGVSLSVP	YFNLAPNFDATFAPGI	IGERG	AT	
	240	250	260	270	280	290
	310	320	330	340	350	360
m958.pep	FDGQVRYLRPDYAGQSD	LTWLPD	DKKSGRNNRYQAKW	QHRH	DISDTLQAGV	DFNQVSDSG
g958	FDGQIRYLRPDYSGQD	LTWLPD	DKKSGRNNRYQAKW	QHRH	DISDTLQAGV	DFNQVSDSG
	300	310	320	330	340	350
	370	380	390	400	410	420
m958.pep	YYRDFYGNKEIAGNVN	LNRVWLDYGGRAAGGS	LNAGLSVLKYQTLAN	QSGYKDKPY	ALM	
g958	YYRDFYGGEEIAGNVN	LNRVWLDYGGRAAGGS	LNAGLSVQKYQTLAN	QSGYKDEPY	AIM	
	360	370	380	390	400	410
	430	440	450	460	470	480
m958.pep	PRLSVEWRKNTGRAQIG	VSAQFTRFSDSRQD	GSRLVVYPDIKWDFS	NSWGYVRPK	LGLH	
g958	PRLSADWHKNAGRAQIG	VSAQFTRFSDGRQD	GSRLVVYPGIKWDFS	NSWGYVRPK	LGLH	
	420	430	440	450	460	470
	490	500	510	520	530	540
m958.pep	ATYYSLNRFSGQEARRV	SRTLPIVNIDSGAT	FERNTRMFGGEVLQ	TLEPRLF	YNYIPAKS	
g958	ATYYSLDSFGGKASRS	VGRVLPVVNIDGGT	TFERNTRLFGGGV	QTIEPRLF	YNYIPAKS	
	480	490	500	510	520	530
	550	560	570	580	590	600
m958.pep	QNDLPNFDSESSFGYG	QLFRENLYYGNDRI	TANSLSAAVQSRIL	DGATGEER	FRAGIG	
g958	QNDLPNFDSESSFGYG	QLFRENLYYGNDRI	AANSLSAVQSRIL	DGATGEER	FRAGIG	
	540	550	560	570	580	590
	610	620	630	640	650	660
m958.pep	QKFYFKDDAVMLDGS	VGKPRNRS	DWVAFASGSIGSR	FILDSSI	HYNQNDKRA	ENYAVGA
g958	QKFYFKDDAVMLDGS	VGNPRNRS	DWVAFASGGIGR	FTLDSSI	HYNQNDKRA	EHYAVGA
	600	610	620	630	640	650
	670	680	690	700	710	720
m958.pep	SYRPAQGKVLNARYK	YGRNEKIY	LKSDGSYFYDKLS	QLDL	SAQWPLTRN	LSAVVRYNYGF
g958	SYRPAQKVLNARYK	YGRNEKIY	LQADGSYFYDKLS	QLDL	SAQWPLTRN	LSAVVRYNYGF
	660	670	680	690	700	710

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              730      740      750      760      770      780
m958.pep      EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g958           EAKKPIEMLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
              720      730      740      750      760      770

              790      800
m958.pep      MDVAVPGYITAHSLSAGRNRKP
              |||||:|||||:|||||:|||||:
g958           MDVAVPGYIPAHSLSAGRNRKRPX
              780      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTTCGGCACC CATTCGCGCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCATCCCCGA AGACTATACG CGCATTGTGT CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCCCTC AATGCCGATT GGGCGGATTA CGACCACTCG GGCGACACCG
401 TTACCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGCGAACCCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGTCCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCACCGCCGA AATGTTGGGC GAAGGGCATT ACAAACCTGAC GGAACCCCAA
601 TTCAACACCT GTTCCGCCGG CGATGCCGGC TGGTATGTCA AGGCCGCTTC
651 CGTCGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCGTGTTCGG CGCGTTTCCC ATTTTCTACA CCCCTTGGGC GGAATTCCCG
751 CTTGACGGCA ACCGCAAAAG CGGCCTGTCT GTTCCCTCAC TGTCCGCCGG
801 TTCGGACGGC GTTTCCTTTT CCGTTCCTTA TTTATTTCAA CTTGCCCCCA
851 ATCTCGATGC CACGTTTCGG CCCGGCGTGA TCGGCGAACG CGGCGCGGTC
901 TTTGACGGGC AGGTACGCTA CTGCGGCCG GATTATGCCG GCCAGTCCGA
951 CCTGACCTGG CTGCCGCACG ACAAGAAAAG CGGCAGGAAT AACCGCTATC
1001 AGGCGAAATG GCAGCACCGG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTCGATTTCA ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAACAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATTATGGCGC CAGGCGGGCG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTGAAATACC AGACGCTGGC AAACCAAAGC GGCTACAAAG ACAAAACGTA
1251 TGCCCTGATG CCGCGCCTTT CCGCCGATTG GCGCAAAAAC ACCGGCAGGG
1301 CGCAAATCGG CGTGTCGGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAAGACGGCA GCGCCCTCGT CGTCTATCCC GACATCAAAT GGGATTTCAG
1401 CAACAGCTGG GGTACGTCC GTCCAAACT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACGCG
1551 GATGTTTCGG GCGGAGTCC TGCAAACCCT CGAGCCGCGC CTGTTCTACA
1601 ACTATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTCG
1651 GAAAGCAGCT TCGGCTACGG GCAGCTTTT CTGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAAAGC
1751 GTATTTTGGG CCGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGG
1801 CAGAAATTCT ACTTCAAAAA CGACGCAGTC ATGCTTGACG GCAGTGTCGG
1851 CAAAAAACC CGCAGCCGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGACGCCG CTTATCCTC GACAGCAGCA TCCACTACAA CCAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCGGTGCA AGCTACCGTC CCGCACAGGG
2001 CAAAGTGCTG AACGCCCGCT ACAAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GGCCGCTGAC GCGCAACCTG TCGGCCGTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG CGGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTCT GCAGAAACCC CGCAGACAGG ATGGATGTCG
2351 CCGTTCCCGG CTATATCCCC GCCCACTCTC TTCCGCCCGG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1  LARLFSLKPL VLALGFCEFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PTSLSLSTGC LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMERGQ
101 SQVQVRAEEN VVERNRRTL NADWADYDQS GDTVTAGDRF ALQQDGTLLIR
151 GETLTYNLEQ QTGEAHNVRM ETEHGRRLO SVSRTEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP

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1374

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251 LDGNRKSGLL VPSLSAGSDG VSLSVPIYFN LAPNLDTFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRLVVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGKKP RSRSDWVAF SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQKVL NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVL GAEEKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

```

          10      20      30      40      50      60
a958.pep  LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC
          10      20      30      40      50      60
m958      LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC
          70      80      90      100     110     120
a958.pep  LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGSQVQVRAEGNVVVERNRTTL
          70      80      90      100     110     120
m958      LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGSQVQVRAEGNVVVERNRTTL
          130     140     150     160     170     180
a958.pep  NADWADYDQSGDVTAGDRFALQODGTLIRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ
          130     140     150     160     170     180
m958      NTDWADYDQSGDVTAGDRFALQODGTLIRGETLTYNLEQQTGEAHNVRMEIEQGGRRLQ
          190     200     210     220     230     240
a958.pep  SVSRTAEMLGEGHYKLTETQFNTCESAGDAGWYVKAASVEADREKGIGVAKHAAFFVGGVP
          190     200     210     220     230     240
m958      SVSRTAEMLGEGHYKLTETQFNTCESAGDAGWYVKAASVEADREKGIGVAKHAAFFVGGVP
          250     260     270     280     290     300
a958.pep  IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPIYFNLAAPNLDTFAPGVIGERGAV
          250     260     270     280     290     300
m958      IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSVPIYFNLAAPNLDTFAPSVIGERGAV
          310     320     330     340     350     360
a958.pep  FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG
          310     320     330     340     350     360
m958      FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG
          370     380     390     400     410     420
a958.pep  YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
          370     380     390     400     410     420
m958      YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM
          430     440     450     460     470     480
a958.pep  PRLSADWRKNTGTRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH
          430     440     450     460     470     480
m958      PRLSVEWRKNTGTRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH
          490     500     510     520     530     540
a958.pep  ATYYSLNRFSGQEARRVSRTLPIVNIDSGMTFERNTRMFGGGVLQTLERLFYNYIPAKS
          490     500     510     520     530     540
m958      ATYYSLNRFSGQEARRVSRTLPIVNIDSGMTFERNTRMFGGVLQTLERLFYNYIPAKS

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	490	500	510	520	530	540
	550	560	570	580	590	600
a958.pep	QNDLPNFDSSSESGYQGLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESGYQGLFRENLYYGNDRIANTANSLSAAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a958.pep	QKFYFKNDVMDGSGVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKNDVMDGSGVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
	670	680	690	700	710	720
a958.pep	SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
m958	SYRPAQGGKVLNARYKYGRNEKIYKSDGSYFYDKLSQLDLSAQWPLTRNLSAVVRYNYGF					
	670	680	690	700	710	720
	730	740	750	760	770	780
a958.pep	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
m958	EAKKPIEVLAGAIEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
	790	800				
a958.pep	MDVAVPGYIPAHSLSAGRNRKPX					
m958	MDVAVPGYITAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1 ATGAACATCA AACACCTTCT CTGACCGCC GCCGCAACCG CACTGTTGGG
51 CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1 MNIKHL L LTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51 AQAEKA AAWAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1 ATGAACATCA AACACCTTCT CTGACCTCC GCCGCAACCG CACTGCTGAG
51 CATTTCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACC GA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1 MNIKHL L LLS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51 AQAEKA AALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*

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m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MN	IK	HL	LL	TS	AA
g959	MN	IK	HL	LL	TS	AA

	70	80	90	100	109
m959.pep	VGG	KIT	DID	LE	HD
g959	VGG	KIT	DID	LE	HD

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

```

1  ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51  CATTTCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTC TCGATGCCCG TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

```

1  MNFKRLLLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MN	FK	RL	LL	LT	AA
m959	MN	IK	HL	LL	TS	AA

	70	80	90	100	109
a959.pep	VGG	KIT	DID	LE	HD
m959	VGG	KIT	DID	LE	HD

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

```

1  ATGCAAGTAA ATATTCAGAT TCCCTGTATG CTGTACAGAC GCGGGAGTGT
51  TAAGCCCCC TTGTTGAAG CTCCGCGGCT CCTGCCGAGC TTCACCGACC
101 CCGTTGTGCC CAAGCTCTCT GCTCCCGGCG GCTACATTGT CGACATCCCC
151 AAAGGCAATC TGAAAACCGA AATCGAAAAG CTGGCCAAAC AGCCCGAGTA
201 TGCCTATCTG AAACAGCTCC AAGTAGCGAA AAACGTCAAC TGGAAACCAGG
251 TGCAACTGGC TTACGATAAA TGGGACTATA AGCAGGAAGG CTTAACCAGA
301 GCCGCTGCAG CGATTATCGC GCTGGCTGTT ACCGTGGTTA CTGCGGGCGC
351 GGGAGTCGGA GCCGCACTAG GCTTAAACGG CGCAGCCGCA GCAGCGGCCG
401 ATGCCGCTT TGCCTCACTC GCTTCTCAGG CTTCCGTATC GCTCATCAAC
451 AATAAAGGCG ATGTCGGCAA AACCCTGAAG GAACTGGGCA GAAGCCGCAC
501 GGTAAAAAAT CTGGTTGTAG CGGCGGCAAC GGCAGGCGTA TCCAACAAC

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1377

```

551 TCGGTGCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTC AACGTTA ACCTGGCCAA TGCGGGCAGT GCCGCGCTGA TCAACACCGC
651 TGTTAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAAT ATCCTGGCGG
701 CATTTGGTAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GATCAGCACT ATGTCGCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGCTGCAGCG GCGAATAAGG GCAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTCGGG GAGGCTTTGG TTAAAATAC CGATTTTAGC
901 GATATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCTTA
951 TGCCAAACTT GCGGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATACTGCTGC ACAAACCGCA CAAAACGCGG TAGAAAATAA TGCGGTAAAA
1051 GCTGTTGTAA CTGCTGCAAA AGTGGTTTAT AAGGTAGCCA GAAAAGGATT
1101 AAAAAACGGG AAAATCAACG TTAGAGATTT AAAACAGACG TTGAAAGACG
1151 AAGGTTATAA TTTAGCCGAC AACCTGACCA CTTATTTCGA CGAAACATTG
1201 GATTGGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTCG GAACAGAGCT
1251 GAATCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTAG
1301 AAAAAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACATACATGA AAAATAATCC TTTTGGAAAA CAGCTGGCTC AAATTCAGA
1401 AAAGACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAAACCAAGG GTTATTAAAA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CATAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAACT TTAAGTTTGT
1551 TCTAAATATG GATGGTTCGC TTAACCAAT GAAACTGGG GCAGCAAAAG
1601 GTCGTAAATT AAACTTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

m960.pep

```

1 MQVNIQIPCM LYRRGSVKPP LFEAPRLPS FTDPVVPKLS APGGYIVDIP
51 KGNLKEIEK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDKQEGLTR
101 AGAAIALAV TVVTAGAGVG AALGLNGAAA AAADAAFASL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKN LVVAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GEAASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGKQDGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVVY KVARGLKNG KINVRDLKQT LKDEGYNLAD NLTTLFDETL
401 DWNDAKAVID IVVGTELNRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFGK QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDRFYLDGQ
501 HKNHLEVFDEK NGNFKEVLNM DGSLNQMKTG AAKGRKLNLK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

m961.seq

```

1 ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51 CACTTTCTGT AGCGGCGCAC TGCCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAAA GTCGTGACTA ACCTGACCAA AACCGTCAAT
301 GAAAACAACG AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTTGCTGA AGAGACTAAG ACAAAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAACA
651 AAACGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCGACAG CTGGACAAA AACGTAGCTA
851 ATCTGCGCAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTC AACTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGCGGGCTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCGCT
1001 TTACCGAAAA CTTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTCTTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

m961.pep

```

1 MSMKHFPKAV LTTAILATEFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

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```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FN DIADS LDETNTKADE
201 AVKTANEAKQ TAEETKQNV D AKV KAAETA A GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAVGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAYHVG V NYEW*

```

a961.seq not found yet
a961.pep not found yet

g972.seq not found yet
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCArTTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCTG GArGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTTTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTCTGTG GGAGCTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCCGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCCGGGATT TCCCAAAGGA TTAGAACC TG AAAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATTT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWISFTFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGXQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE D GSGKTFYVGR KKNRFRVRY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKRKF NMPVPERFDQ RKKKLNLTFE
301 HKLHYAKNAV GKLNVNFIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVVHQNV D YD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATCCG CAGCGAAGAG GTAAGCAAGA CGGGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGTTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTTTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAATGGG TAAGGTTCGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAG AAAATTTAAA AATATGCCCG
851 TTCCCGAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATTCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTGA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAAATGT
1251 AGATTATGAT TATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

```

a972.pep
  1 LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGK GK LLEIP QRRGKQDGVF
 51 VDWISFTFHE DTLLKVSGCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFGGQRNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNE D GSGKTFYVGR KKNRSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICRKFK NMPVPERFDQ RKKTLNLTFE
301 HKLHYAKNAV GKLNVNFIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVIHQNVVDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

```

              10      20      30      40      50      60
m972.pep      LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGK GK LLEIPQRRGKQDGVFVDWISFTFHE
              |||||
a972           LTNRGGAKLKTNSKSSERMSEVEYFSHFISDGK GK LLEIPQRRGKQDGVFVDWISFTFHE
              10      20      30      40      50      60

              70      80      90      100     110     120
m972.pep      DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE
              |||||
a972           DTLLKVSGCPLFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE
              70      80      90      100     110     120

              130     140     150     160     170     180
m972.pep      VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RT RITRIDLALDFFDGEYTPDQ
              |||||
a972           VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDDSI RT RITRIDLALDFFDGEYTPDQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m972.pep      ALLDHDNGFFDNSNQRPKSETIGTAWRNE D GSGKTFYVGRKKNRSRFVRVYEKGRQLGDKE
              |||||
a972           ALLDHDNGFFDNSNQRPKSETIGTAWRNE D GSGKTFYVGRKKNRSRFVRVYEKGRQLGDKE
              190     200     210     220     230     240

              250     260     270     280     290     300
m972.pep      SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQRKKTLNLTFE
              |||||
a972           SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFICRKFKNMPVPERFDQRKKTLNLTFE
              250     260     270     280     290     300

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	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGKLVNFMIEMGFDNSEIVESLKADSGFPKGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPTYDVEKERKYQEYLSKVYHQNVDDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPTYDVEKERKYQEYLSKVYHQNVDDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

```

g973.seq
1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCC
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCGG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATGCGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTTGCGC CCTGCCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCACC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGccgacg acatCCACTC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTCCGTACG GAatacggca gcaagaagc cgacaccatc ggcggctTGG
701 TCATTcAGGA ATTGGGACAC CTGCCCGTGC GCGCGAAAA AGTCCTTAtc
751 ggcgGTTTGC agttcaccgt CGCCCGCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgccgttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

```

g973.pep
1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLTRLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFFGT EYGSEEADTI GGLVIQELGH LPVRGEKVLII
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

```

m973.seq
1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCC
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCGG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTTCGGA TTTGGAAGTG CGGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTCGCGCT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCCTCGC CCCGCCGTCT
401 TCGTCCCGCA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCACC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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651 CTTCCGGCAGC GAATACAGCA KCGAAGAAGC CGACACCATT GGCGGCCTGG
 701 TCATTCAAGA GTTGGGACAT CTGCCCGTGC GCGGCGAAAA AGTCCTTATC
 751 GGCGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973.pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
 101 KDEVLGILHA KDLLKYMFPN EQFHLKSILR PAVFVPEGKS LTALLKEFRE
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIQELGH LPVRGEKVL
 251 GGLQFTVARA DNRRLHTLMA TRVK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLTRLEKVLDFAELEV					
	10	20	30	40	50	60
m973.pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFPN					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFPN					
	70	80	90	100	110	120
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFGTEYGSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973.seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG
 51 ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
 201 CAGCCGTATG AACGTTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG
 251 CCTACGTTAT CGATACCGCC CATTGCGGCT TCCCCGTCAT CCGTGAAGAC
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAAATATAT
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CTGCGCGTCT
 401 TCGTCCCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGGC GACATCGAAG
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTTCCGCC

1382

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCCGGCACG GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTACAGGA ATTGGGACAC CTGCCCCTGC GCGGCGAAAA AGTCCTTATC
751 GGCGGTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLV FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFPGT EYSSEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

m973/a973 97.8% identity in 274 aa overlap

```

              10      20      30      40      50      60
m973.pep      MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV
a973           MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV
              10      20      30      40      50      60

              70      80      90     100     110     120
m973.pep      RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP
a973           RDAMITSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP
              70      80      90     100     110     120

              130     140     150     160     170     180
m973.pep      EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
a973           EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG
              130     140     150     160     170     180

              190     200     210     220     230     240
m973.pep      EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH
a973           DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEADTIGGLVIQELGH
              190     200     210     220     230     240

              250     260     270
m973.pep      LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
a973           LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
 51 TGCCTGCGGC GGTACGGGCA AAGATGCCGC CGCGCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTTCTTCCGA AGATTTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601 AAAACAACAC CGGCCAAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAAATATT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

```

1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

```
g981.pep
  1  MKKWIAAALA CSALALSACG GQGKDAAPA ANPGKVYRVA SNAEFAPFES
 51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101  GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK KMNKVGVTG
151  HTGDFSUSKL LGNDNPFIAR FENVPLIIE LENGGLDSVV SDSAVIANVY
201  KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251  KIYAKYFAKE GGQAAK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

```
m981.seq
  1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC
 51  TGCCTGCGGC GGTCAGGGCA AAGATACCGC CGCGCCTGCC GCCAACCCCG
101  ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151  TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201  GATGGCGAAG GCGGGCAATT TAAAAATCGA ATCAAACAC CAGCCGTGGG
251  ACAGCCTTTT CCCCCTTTA AACAACGGCG ATGCGGACGT TGTGATGTCG
301  GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351  GTATTTTGAA ATCACCACAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401  CTTCTTCCGA AGATTTGAAA AACATGAACA AAGTCGCGCT GGTAACCGGC
451  TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA
501  AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551  GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTATCGC CAATTATGTG
601  AAAAAACAAT CCGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651  CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701  AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751  AAGATTTACG CCAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801  A
```

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

```
m981.pep
  1  MKKWIAAALA CSALALSACG GQGKDTAAPA ANPDKVYRVA SNAEFAPFES
 51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101  GVTITDDRKQ SMDFSDPYFE ITQVVLVPKG KKVSSSEDLK NMNKGVTG
151  YTGDFSUSKL LGNDNPFIAR FENVPLIIE LENGGLDSVV SDSAVIANVY
201  KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD
251  KIYAKYFAKE DGQAAK*
```

m981/g981 98.1% identity in 266 aa overlap

```

      10      20      30      40      50      60
981.pep  MKKWIAAALACSALALSACGGQGKDTAAPAANPDKVYRVASNAEFAPFESLDSKGNVEGF
          |||
g981      MKKWIAAALACSALALSACGGQGKDAAPAANPGKVYRVASNAEFAPFESLDSKGNVEGF
          |||

      70      80      90      100     110     120
981.pep  DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE
          |||
g981      DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRKQSMDFSDPYFE
          |||

      130     140     150     160     170     180
981.pep  ITQVVLVPKGKKVSSSEDLKMNKVGVTGTYTGDFSUSKLLGNDNPFIARFENVPLIIE
          |||
g981      ITQVVLVPKGKKVSSSEDLKMNKVGVTGHTGDFSUSKLLGNDNPFIARFENVPLIIE
          |||

      190     200     210     220     230     240
981.pep  LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
          |||
g981      LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL
          |||

      250     260
981.pep  EKVRESGEYDKIYAKYFAKEDGQAAKX
          |||
g981      EKVRESGEYDKIYAKYFAKEGGQAAKX
          |||
      250     260
```


1384

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1   ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAGGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCgcCTTG AACAAcGGCG ATGCGGACGT TGTGATGTCG
301 GGCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCcAAG TCGTCTCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTtGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TCCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAAAcAATC CGACCAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGcATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAAGAA GACGGACAGG CCGCAAAATA
801 A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1   MKKWIAAALA CSALALSACG GQGKDAAAPA ANPDKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRQK SMDfSDPYFE ITQVVLVPKG KkISSeDLK NMNKVGvVTG
151 YTGDFSVSKL LGNDNPkIAR FENVPLIIE LENGGLDSV SDSAVIANyV
201 KNNPTKGMDf VTLpDFTTEH YGIaVRKGDE ATvKMLNDAL KkVRESGEyD
251 KIYAKYfAKE DGQAaK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALACSALALSACGGQGKDTAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALACSALALSACGGQGKDAAPANPDKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
	70	80	90	100	110	120
m981.pep	ITQVVLVPKGKkVSSSEDkNMNKVGvVTGYTGDFSVSKLLGNDNPkIARFENVPLIIE					
a981	ITQVVLVPKGKkISSSEDkNMNKVGvVTGYTGDFSVSKLLGNDNPkIARFENVPLIIE					
	130	140	150	160	170	180
m981.pep	LENGGLDSVVSdSAVIANyVKNNPAKGMDfVTLpDFTTEHYGIaVRKGDEATvKMLNDAL					
a981	LENGGLDSVVSdSAVIANyVKNNPTKGMDfVTLpDFTTEHYGIaVRKGDEATvKMLNDAL					
	190	200	210	220	230	240
m981.pep	EKVRESGEyDKIYAKYfAKEDGQAaKX					
a981	KKVRESGEyDKIYAKYfAKEDGQAaKX					
	250	260				
m981.pep	EKVRESGEyDKIYAKYfAKEDGQAaKX					
a981	KKVRESGEyDKIYAKYfAKEDGQAaKX					
	250	260				

1385

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982.seq
1   atcgcacatcgc aaaacaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatatatttgc cggccgcCga ttgggtagcC ttgGGcgCgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CGCGTCCAAA ACCAACgaCg
251 tagCCGgcga cggtacgact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAAGgcA TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTtt ggttgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTG TTGCTGTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTG GGAACAAGTG GCGAAAGCCA GCCGCCGCTG GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 GCCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTTccGAAG Aagtccggcct GTCTTTGGAA AAAGcgactT TGgacgaCTT
951 Gggtcaaacc aaACGcatCG AAATCGGtga agaaaaact ACCGTCATcg
1001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTTCG CGAAATCCCG
1051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAAGTGGCAG GAGGCGTGGC AGTGATCAA GTCTGGCGCGG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCCTGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTAtC GCCGGTCTGA TGCTGACGAC
1551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1601 TGGGGGGAAT GGGCGGTATG GGCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982.pep
1   IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSI
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLLENLDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LFFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLO DIAILTGCVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVES
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN GSGEYDMIG MGVLDPKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGGM GGMM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982.seq
1   ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAAGAAGT TGCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAATATGTT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA

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1386

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651 TCCGTTTGTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCTGGC TTCGGCGACC
851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGCGGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA TGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2964; ORF 982>:

```

m982.seq
  1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
 51 AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TGCCTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGCACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGCGCGG ATTATCGCCG AAGCGATTGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA
651 TCCGTTTGTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCTGGC TTCGGCGACC
851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGCGGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCGAAGA CAAACCGGCT GTGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCATGA TGTAA

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

```

              10      20      30      40      50      60
m982.pep      MAAKDVFQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
              :|:::|:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

1387

g982	IASQNLRFDNRFLOKMNNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRG
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALENLHTGNADQAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEKGNYGYNA
	430 440 450 460 470 480
g982	RARAALENLHTGNADQAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEKGNYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQAAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQAAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM
	490 500 510 520 530 540
m982.pep	GGMMX
g982	GGMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq	1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAAATGGT
	51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
	101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCCC	GCACATCACC
	151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAACGTGAAAG	ACAAGTTTGA
	201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
	251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
	301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
	351	ACGCGGTATC	GACAAAGCCG	TCGCCGCTTT	GGTTGAAGAG	CTGAAAAACA

1388

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401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGCGAAAAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTA TTGCTGTTTCG AAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTCG CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTTGCC AAATGGCAG GCGCGTGGC AGTAATCAAA GTCGGTGCCG
1151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1301 CAGACCAAGA CGCAGGCGTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTGTTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1601 TGGGCGGCAT GGGTGGTATG GGCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS I
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLI I
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEVGLSLE KATLDDLQGA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALNLH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVNKKVL EGKGNYGYN A GSGEYGMIE MGVLDPKAVT
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*

m982/a982 99.3% identity in 544 aa overlap

10 20 30 40 50 60
m982.pep MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI
|||||
a982 MAAKDVQFGNEVRQKMVNGVNILANAVRVTLGPKGRNVVVVDRAFGGPHITKDGVTVAKEI
10 20 30 40 50 60

70 80 90 100 110 120
m982.pep ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAGMNPTDLKRG I
|||||
a982 ELKDKFENMGAQMVKEVASKTNDVAGDGT TATVLAQSIVAEGMKYVTAGMNPTDLKRG I
70 80 90 100 110 120

130 140 150 160 170 180
m982.pep DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
|||||
a982 DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
130 140 150 160 170 180

190 200 210 220 230 240
m982.pep KLENELDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
|||||
a982 KLENELDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
190 200 210 220 230 240

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m982.pep	250	260	270	280	290	300
	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
m982.pep	310	320	330	340	350	360
	ISEEVGLSLEKATLDDLGQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
a982	ISEEVGLSLEKATLDDLGQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY					
	310	320	330	340	350	360
m982.pep	370	380	390	400	410	420
	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
m982.pep	430	440	450	460	470	480
	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKGNYGNA					
a982	RARAALENLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPSVVVNKVLEGKGNYGNA					
	430	440	450	460	470	480
m982.pep	490	500	510	520	530	540
	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
a982	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
	490	500	510	520	530	540
m982.pep	GGMMX					
a982	GGMMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986.seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCGTTCTAC
301	GAATTTTCA	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCT	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAGc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTGCG	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCGAAGC	TGCCGGCCTG	CAGCGGGGCG	ACATCGTCCT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAATCAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAgcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

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1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccg tcaatgacga
1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGGTCatgcg ccgTGGCAAC ACGCTGTTCA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

```

g986.pep
1  VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
51  SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVAGMGS I
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVG I NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
401 SKTDEAPYTE QSGTFSVES AGITLQHTD SSGKHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

```

m986.seq
1  GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
51  GCTGGCAGGC TGCACAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCC CGCCCC GCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AAACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
301 GAATTTTTCA AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GCGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTACAT CCTGACCAAT ACCCAGCTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTC
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCGGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CATCGTCTGC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCTAGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTCCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

```

m986.pep.
1  VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
51  SMLLPDFAQL VQSEGPVVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNGYILT N THVVTGMGS I
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVG I NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QSGTFSVES AGITLQHTD SSGHLLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

Computer analysis of this amino acid sequence gave the following results:

1391

Homology with a predicted ORF from *N. gonorrhoeae*

m986/g986 97.0% identity in 499 aa overlap

	10	20	30	40	50	60
m986.pep	VFKKYQYLALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	: : : : : :					
g986	VFKKYQYFALAALCAALLAGCEKAGSFFGADKKEASFVERIEHTKDDGSVSMLLPDFAQL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m986.pep	VQSEGPVAVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
	: : : : : :					
g986	VQSEGPVAVNIQAAPAPRTQNGSGNAETDSDPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m986.pep	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	: : : : : :					
g986	GGLNFGSGFIISKNGYILTNTHVVAGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m986.pep	TEELPVVKIGNPKDLKPGEWVAAIGAPFGDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	: : : : : :					
g986	TEELPVVKIGNPKNLKPGEWVAAIGAPFGDNSVTAGIVSAKGRSLPNESYTPFIQTDVA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m986.pep	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	: : : : : :					
g986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m986.pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986.pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986.pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
g986	AGITLQTHTDSSGKHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
	490	500				
m986.pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2971>:

```

a986.seq
1  GTGTTCAAAA AATAACCAATA CCTCGCTTTG GCAGCACTGT GTGCCGCCCTC
51  GCTGGCAGGC TGCGACAAAG CCGGCAGCTT TTTCGGTGCG GACAAAAAAG
101 AAGCATCCTT TGTAAGACGC ATCAAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGTCCAACG GTTCAAAGCG AAGGCCCGGC
201 AGTCGTCAAT ATTCAGGCAG CCCC CGCCCC GCGCACCCAA AACGGCAGCA
251 GCAATGCCGA AACCGATTCC GACCCGCTTG CCGACAGCGA CCCGTTCTAC
301 GAATTTTTC AAGCGCTCGT CCCGAACATG CCCGAAATCC CCAAGAAGA
351 AGCAGATGAC GNGGATTGA ACTTCGGTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTATAT TCTGACCAAT ACGCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTGC CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAATCGGC AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGCGCGGCC CTTCGGCTTC GACAACAGCG TGACCGCCGG
651 CNTCGTGTCC GCCAAAGGCA GAAGCTGCC CAACGAAAGC TACACACCCT
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTGCG CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTCGGCAC AATCGTTCGG
951 TTTGGACAAA GCCGCGCGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CGGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCCCAT
1101 TACGCCGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GGCGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTCGAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCGG TCAATGACGA
1401 AGCCGTTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAA CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2972; ORF 986.a>:

```

a986.pep
1  VFKKYQYLAL AALCAASLAG CDKAGSFFGA DKKEASFVER IKHTKDDGSV
51  SMLLPDFVQL VQSEGPVAVN IQAAPAPRTQ NGSSNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKDGYYLTN THVVTGMGSI
151 KVLLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGXVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGO

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1393

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301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QSGTFSVES AGITLQHTD SSGGHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

m986/a986 98.2% identity in 499 aa overlap

      10      20      30      40      50      60
m986.pep VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMLLPDFAQL
a986      VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMLLPDFVQL
      10      20      30      40      50      60

      70      80      90     100     110     120
m986.pep VQSEGPVVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPNMPEIPQEEADD
a986      VQSEGPVVNIQAAPAPRTQNGSSNAETDSDPLADSDPFYEFFKRLVPNMPEIPQEEADD
      70      80      90     100     110     120

      130     140     150     160     170     180
m986.pep GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA
a986      GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m986.pep TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGIVSAKGRSLPNESYTPFIQTIVA
a986      TEELPVVKIGNPKDLKPGEWVAAIGAPFGFDNSVTAGXVSAKGRSLPNESYTPFIQTIVA
      190     200     210     220     230     240

      250     260     270     280     290     300
m986.pep INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ
a986      INPGNSGGPLENLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ
      250     260     270     280     290     300

      310     320     330     340     350     360
m986.pep LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL
a986      LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL
      310     320     330     340     350     360

      370     380     390     400     410     420
m986.pep PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES
a986      PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES
      370     380     390     400     410     420

      430     440     450     460     470     480
m986.pep AGITLQHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN
a986      AGITLQHTDSSGGHLVVVRVSDAAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN
      430     440     450     460     470     480

      490     500
m986.pep VPLLIMRRGNTLFIALNLQX
a986      VPLLIMRRGNTLFIALNLQX
      490     500

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

```

g987.seq
1  ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG

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1394

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51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCCACGA
201 AGCCTTTGCC GCGCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
351 ggacgacaAC AACAcgcgcg gcttggaacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCCTGTTCA ACCCCTtctg CCTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCGCGCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCTT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAAACTG GTGCAGGACG GCATAGACGT TACCGTCTCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAACCTC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCCG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLLCSSSW LPPLEERTES RHFNTSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERGV VRVRLLLDDN NTRGLDDLLL ALDSHPNI*V RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 LDDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHDPATRK TYPNEPEAKL WKRIAAILK
501 LLPIEGLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCCACGA
201 AGCCTTTGCC GCGCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCGCGCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GATTGGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTTCGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCTT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCCG
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGGT TCGTTCAACC TCGACCCCGG TTCCGCGCGT CTCAACACCG
1301 AAATGGGCGT TGTTCATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1  MKTRSLISLL CLLLCSSSW LPLEERTES RHFNTPSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS
501 LLPIEGLL*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m987/g987 97.8% identity in 508 aa overlap

          10      20      30      40      50      60
m987.pep  MKTRSLISLLCLLLCSSSWLPLEERTESRHFNTPSKPVRLDNILQIRHTPHTNGLSDIY
g987      MKTRSLISLLCLLLCSSSWLPLEERTESRHFNTPSKPVLLDNILQIRHTPHNGLSDIY
          10      20      30      40      50      60

          70      80      90     100     110     120
m987.pep  LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNVLVYLAERGVVRVRLLLDDN
g987      LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAERGVVRVRLLLDDN
          70      80      90     100     110     120

          130     140     150     160     170     180
m987.pep  NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
g987      NTRGLDDLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI
          130     140     150     160     170     180

          190     200     210     220     230     240
m987.pep  LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG
g987      LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG
          190     200     210     220     230     240

          250     260     270     280     290     300
m987.pep  KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR
g987      KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR
          250     260     270     280     290     300

          310     320     330     340     350     360
m987.pep  RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA

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1396

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g987      |||
          RKPP|AGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGD|VTVLTNSLQATDVA
          310      320      330      340      350      360

          370      380      390      400      410      420
m987.pép  AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKR|FIG
          |||
g987      AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKR|FIG
          370      380      390      400      410      420

          430      440      450      460      470      480
m987.pép  SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PAYAYRVTLDRHNRLQWHD|PATRK
          |||
g987      SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PEYAYRVTLDKHNRLQWHD|PATRK
          430      440      450      460      470      480

          490      500      509
m987.pép  TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          |||
g987      TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCCTCCTTC TCTGTTCATG
51  TTCTTCATGG TTGCCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCCG ACTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGTACCT GACCGACTTC CCGCGCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GCCCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGCG TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCGAGCG CAACATCGGC AAGGCTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCTCTAC CAAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCTTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCACAACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCGCGACGG CTCAATACTG
1301 AAATGGGCGT TGTTCATCGA AGCCCCAAAA TCGCAGACAA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987.pép
1  MKTRSLSILL CLLLCSCSSW LPPLEERTES RHFNTSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VVRRLLLDDN NTRGLDDLLL ALDSHPNIEV RLENPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|AGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGD|VTVLT

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPRSAR LNTEMGVVIE SPKIAEQMER
 451 TLADTSPEYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIA AKILS
 501 LLPIESLL*

m987/a987 98.8% identity in 508 aa overlap

m987.pep	10	20	30	40	50	60
	MKTRSLISLLCLLLSCSSWLPPLEERTESRHFNSTKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLSCSSWLPPLEERTESRHFNSTKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	130	140	150	160	170	180
	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
a987	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVTRTLISDDPAKGLDRDR					
a987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDDPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	310	320	330	340	350	360
	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNLQATDVA					
a987	RKPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLTNLQATDVA					
	310	320	330	340	350	360
m987.pep	370	380	390	400	410	420
	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
m987.pep	430	440	450	460	470	480
	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNR LQWHDPATRK					
a987	SFNLDPRSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNR LQWHDPATRK					
	430	440	450	460	470	480
m987.pep	490	500	509			
	TYPNEPEAKLWKRIA AKILSLLPIEGLLX					
a987	TYPNEPEAKLWKRIA AKILSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagtTTGCGc gGCGgacaag ctgGATTTGG TCAAATGccg Cgtcaggcg
301 catAAgGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCTGT TTATACGAAC GCCAgatgcg tggTgtcatG CAcggcgaca
401 ccgttACCGT CCGTCTGCG ggtatggaCC GCAGGGGccg ccgcGAAagg
451 acgtttctGG ATATTGTGCG ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTTGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAt cGAAATTGCC GTGCGCAAGC ATCATTGCC GCAccgaTTC
751 AGTGAagcgt gtGcCAATC CGcgaAAAA ATtcccgacc ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGTG CGACCTTCCT TTGTAACGA
851 TAGACGGCGA AACGGCGCGC GATTTGACG ACGGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 GCGTGTATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCGCGCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTCAG ACGGCATCGG GAATCCGCAC AAAGCCCAA TCGACACGCT
1251 TTACAAGCTG TTTAAATTT TGCAGAAAA ACCTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAA TTGTCCCGT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGCGC GCGGGATTTT CTGTTGAAAA
1451 ACAAACATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGCGGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGCAGGCC GGATGCGGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1751 CCGTCCACCG TGCCATCAA GCGGTATTGA ACCGAAAAAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTT GCGAACCCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAAAA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTCGGTGAA ATATTTGAAG GcaaaatCtc ccggggtgtg
1951 gcaaaTtttg gaATATTGT CACTTTGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGCGGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAAGGGAA ATCGAAAACC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GGAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGFAPV LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
201 SGQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNYRLVVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPNLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLYKL FKILQKKRLA RGAVEFESVE TQMI FDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQQLGL LGLQLGGGDN PSPKDYAALA EQFKGRPD AE LLQVMMRLSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKITYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYMRDKVGE IFEGKISRGV
651 ANFGIFVTL DDIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPAV AESGKKAKKP VPIKVKRKG KS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```
m988.seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51 CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TGCGAAAAAA ATTCCCGTCC ATGTACGCAA
351 AAGCGATTTG AAAGGCCGCG TCGATTTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACGCTCT GGTGCGTGGC ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATT TCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
751 TGGATTTTCA ACGGCATCGA CCATCCGTAC AAAGCCCAA TCGACACCCT
801 TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTTT CTGTTGAAAA
1001 ACAAGCATA GGCCTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1051 CTCGCCACCC TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1201 CAGCAGGCGG TTTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCCTA
1251 CGAAGCATA GCGCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1301 CCGTACACCG CGCCATCAA GCGGTGTTGA ATCAGCAAAC CTACACGCCA
1351 AAAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1401 TGCCGACGAC GCCAGCCGCG ACGTGGA AAA CTGGCTGAAA ACCTATTATA
1451 TGCGCGATAA GGTGCGCGAA GTATTCGAAG GTAAAATCTC CGGCATGACC
1501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTCCGC CCCGAAATCA
1601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
1651 GTTGCCGTCC GGGTCGCCCC TGCCGATTG GATGACGGAA AAATCGATT
1701 TGTCTGATT GCCGGGGGGA GCGGCAGGG GCGGAAAGTT AAATCATCCG
1751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAACCGGCC
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1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC
 1851 TGCCGCGCA GAATCGAGGA AAAAGGCAAA GAAACCGGTT CCGATTAAGG
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE
 51 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY AD SGMEIEIA VRKHHLP HQF
 101 SEACAKAAKK IPVHVRKSDL KGRVDLRDLP LVTIDGETAR DFDDAVFAEK
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQQTYP
 451 KKSQALGVH TSFCERRADD ASRDVENWLK TTYMRDKVGE VFEGKISGMT
 501 SFGIFVTLTG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRFNMGDR
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGDVTVTVRPAGMDRRGRREGTFLDIVERAQSKVVGRFYMDRGVAILEPED					
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLP HQFSEACAKAAKKIPVHVRKSDLKGRVDLRDLP LVTIDGETARDFDDAVFAEK				
g988		VRKHHLP HRFSEACAKSAKKIPDHVRKSDLKGRVDLCDLPLVTIDGETARDFDDAVFAEK				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRR VIPMLPENLSNGICSLNPDV				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMI PMLPENLSNGICSLNPDV				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMV VTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL				
g988		ERLCMVCDMV VTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIGNPHKAQIDTLYKL				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE				

1401

	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
g988	: : : : :					
	550	560	570	580	590	600
	460	470	480	490	500	509
m988.pep	KKSQWALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKIS-GMTSFGIFVTL					
g988	NKSQWALGVHTSFCERRADDAGRDVENWLKTYIMRDKVGEVFEGKISRGVANFGIFVTL					
	610	620	630	640	650	660
	510	520	530	540	550	569
m988.pep	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVL					
	670	680	690	700	710	720
	570	580	590	600	610	629
m988.pep	IAGGSGRGRKVKSSASAKPAGTAGKPKTAAEKKTARGGKVRGRGASAAESRKKAKKP					
g988	IAGESGRRRKVKLSASAKPAGAAGKSKTTAEKKTARCGKVRGRGVPAAVESGKKAKKP					
	730	740	750	760	770	780
	630	640				
m988.pep	VPIKVKRRKGKXS					
g988	VPIKVKRRKGKXS					
	790					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2983>:

```

a988.seq
1  ATGAATAAAA ATATTAATC TTTAAATTTA CGGGAAAAAG ACCCGTTTTT
51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CGGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCGTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACGGTCAGGT TTTAATCAAC CGTCGGGGCG
251 CGGTTTGCGC GGCGGACAAA TTGGATTGCG TCAAATGCCG TGTCAAGGCG
301 CACAAAGACC GCTTCGGTTT CGCCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCCG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGCGCAGT GCAAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAAATTGCC GTGCGCAAGC ATCATTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATGCGGTGTT TGCCGAGAAA
901 ATCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCGCCCCC GATGACGCTA TCGACACGGA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTACG CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGAAAA
1201 TGGCTTTCAG GCGGCATCGA GCATCCGTT AAAACCCAAA TCGACACGCT
1251 TTACAAATC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCGT TGTCCGCAAC GATGCCACAA AGCTGATTGA
1401 AGAATGTATG TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATTGTTC CGCAACCATT TGGGGCCAC GCCCGAAAAA
1501 CTCGCCGCT TGCGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA

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a988.pcp

1	MNKNIKSLNL	REKDPFLSRE	KQRYEHPLPS	REWIIELLER	KGVPSKIEAL
51	VRELSIKEEE	YEFFERRLKA	MARDGQVLIN	RRGAVCAADK	LDLVKCRVKA
101	HKDRFGFAVP	LTPAKDGDVF	LYERQMGRIM	HGDIVTVRPA	MDGGRGRREG
151	TVLIDIVERAQ	SKVVGFRFXM	RGVAILEPED	KRLNQSIVLE	PDMGARFKPE
201	SGQVIVGEIE	VYPEQNRPAV	AKIIEVLGDY	ADSGMEIETA	VRKHHLPHQF
251	SEACAKAAKK	IPDHVRKSDL	KGRVDLRDLP	LVTIDGETAR	DFDDAVFAEK
301	IGRNYRLVVA	IADVSHYVRP	DDAIDTDAQE	RSTSVYFPRR	VIPMLPENLS
351	NGICSLNPHV	ERLCVVCMDM	ITYAGNIKEY	RFYPAVMRSH	ARLTYNQVWK
401	WLSGSGIEHP	KTQIDTLYKL	FKILQKKRFE	RGAVEFDSIE	TQMLFDDNKG
451	IEKIVPVVRN	DAHKLIEECM	LAANVCAADF	LLKNKHTALF	RNHLGPTPEK
501	LAALREQGLL	LGLQLGGGDN	PSPKDYAALA	GQFKGRPDAE	LLQVMMLRSM
551	QQAVYEPHCD	GHFGLAYEAY	AHFTSPIRRY	PDLTVHRAIK	AVLNQQTYTP
601	KKSQWALGVH	TSFCERRADD	ASRDVENWLK	TYYMRDKVGE	VFEGKISGMT
651	SFGIFVTLDG	IHIDGLVHIS	DLGEDYFNFR	PEIMAEIEGER	SGIRFNMGDR
701	VAVRVARADL	DDGKIDFVLI	AGGSGRGRKV	KISSASAKPAG	TAGKGPKPTA
751	AEKKTARGGK	VRGRGASAAA	ESRKAKKPV	PIKVKKRKGK	S*

m988/a988 97.0% identity in 641 aa overlap

[illegible]

1403

	370	380	390	400	410	420
	280	290	300	310	320	330
m988.pep	FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
a988	FKILQKKRFERGAVEFDSIETQMLFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF					
	430	440	450	460	470	480
	340	350	360	370	380	390
m988.pep	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE					
a988	LLKNKHTALFRNHLGPTPEKLAALREQLGLLGLQLGGGDNPSPKDYAALAGQFKGRPDAE					
	490	500	510	520	530	540
	400	410	420	430	440	450
m988.pep	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
a988	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP					
	550	560	570	580	590	600
	460	470	480	490	500	510
m988.pep	KKSQWALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
a988	KKSQWALGVHTSFCERRADDASRDVENWLKTYMRDKVGEVFEGKISGMTSFGIFVTLDG					
	610	620	630	640	650	660
	520	530	540	550	560	570
m988.pep	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI					
	670	680	690	700	710	720
	580	590	600	610	620	630
m988.pep	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKKAKKPV					
	730	740	750	760	770	780
	640					
m988.pep	PIKVKKRKGSX					
a988	PIKVKKRKGSX					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

```

g989.seq
1   ATGACCCCTT TCACACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG ACGCGTCGAC CATCTTCTAC
151 AATCCCGCCG GCCTGACCAA ACTCGACAGC AGCCAGATTT CCGTCAACGC
201 CAACATCGTG CTGCCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
251 TTACCGGGCT TCCCGTCCAA GGTTCATAAA ACGGCAAAAT CACCAAAACC
301 ACGGTGCGAC CCCACATTTA CGGCGCATAC AAAGTCAACG ACAATCTGAC
351 CGTGGGCTTG GGCGTGACG TCCCCTTCGG CTCTGCCACC GAATACGAAA
401 AAGATTCGCT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
451 GCCGTCGAAC CTGTCGCCGC GTGGAACTC AACGAACGCC ATTCCTTCGG
501 CGCAGGCATC ATCGCCCAAC ATAATTCCGC CGAACTGCGC AAATATGCCG
551 ACTGAGGAAT CCCAAAAAAA GCGCAAATGC TGCAAGCAAC ACCTTCTAAT
601 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAAAGG
651 CACGATTGG GGCGTCGGCT ACCAACTGGC GTGGATGTGG GACATCAACG
701 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTTC ACACACGCTC
751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACAACAGTG
801 GAATGACAAT ATGCTCACAC CGCTCGGTTA CACGGCGAAT GAAAAAGCCA
851 GTGTCAAAAT CGTAACGCCT GAGTCTTTGT CCGTACACGG CATGTACAAA

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1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCGCGAAC GCCGACTacC
1151 GCATGAACAG CCTGCCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TGCGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989.pep
1  MTPFTLKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51  NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNNDLTVGL GVYVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPPK AQMLQATPSN
201 PTAAAIKAD GHADVKGSDW GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAKQQWNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMKY
301 VSDKADLFGD VTWTRHSRFN KAELEFEKEK NIANGKKS DR TTITPNWRNT
351 YKVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989.seq
1  ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
251 ATTCCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTG GAAAAGCGGC
301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTCAAGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAAC TAC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGCGGAA TGAAAAAGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCCGCCG
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCCTCGTC AAAGGCAAAAT CCGACCGCAC CACCATCACC
1051 CCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCC
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTCTCTCG CCGGTATGAA ATACCATATC GGTAAAAACC ACGTCGTCGA
1251 TGCCGCCTAC ACCACATCC ACATCAACGA CACCAGCTAC CGCACGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCACG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

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This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989.pep
1  MTPSALKKT V LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEK D SVLRHNINKL
151 GLTSIAVEPV AAWKLND RHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNGVA EAAKIQADGH ADVKGS DWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWAADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMKYKSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQLRAGIAFD KSPVRNADYR MNSLPDGNRI
 401 WFSAGMKYHI GKNHVVDAA YTHIHINDTSY RTAKASGNDV DSKGASSARF
 451 KNHADIIGLQ YTYKFK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989.pep	MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989.pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989.pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989.pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989.pep	NDRARVGVNYSKVSHTLKGDAEWAADGAAAKQQWNDNMLTPLGYTANEKASVKIVTPES				
m989	NDRARVGVNYSKVSHTLKGDAEWAADGAAAKAMWS-TMLAANGYTANEKARVKIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989.pep	LSVHGMVKVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKSDRTTITPNWRNTYK				
m989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989.pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA				
m989	VGFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA				
	360	370	380	390	400
	420	430	440	450	460
g989.pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989.seq
 1 ATGACCCCTT CCGCACTGAA AAAAACCCTC CTACTGCTCG GCACTGCCTT
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG
 101 TCAACGCGCA AAGCACGGCA AATGCCGCCG CCGCAGAAGC CGCCGACGCA
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
 201 GATTTCCGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG
 251 ATTCGCCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTC GAAAAGCGGC

1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAAC TA CCGTTCACAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GGCGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCCTATC AAATCAGCGA
1101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1151 ACGCCGACTA CCGCATGAAC AGCCTGCCCC ACGGCAACCG CATCTGGTTC
1201 TCCGCCGGCA TGAATACCA TATCGGCAAA AACCACGTCG TCGATCGCCG
1251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCACG GCGAAGGCAA
1301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTTCCGCACG TTTCAAAAC
1351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
  1 MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
 51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVNDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGS DWFGYQ LAWMWDINDR ARVGVNYRSK
251 VSHTLKGD AE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLFGDVTWTR HSRFDKAE LV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAAYTH IHINDTSYRT AKASGNDVDS KGASSAREFKN
451 HADIIGLQYT YKFK*

m989/a989 93.1% identity in 467 aa overlap

          10          20          30          40          50          60
m989.pep  MTPSALKKTVLLLGTAF AAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      MTPSALKKTVLLLGTAF AAASQAQSGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
          10          20          30          40          50          60

          70          80          90          100         110         120
m989.pep  TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN
          70          80          90          100         110         120

          130         140         150         160         170         180
m989.pep  LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSGAGIIAQHT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSGAGIIAQHT
          130         140         150         160         170         180

          190         200         210         220         230         240
m989.pep  SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFGYQLAWMWDI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      SAELRKYADWGIMEKAKALKETPPNPT---KAAQIKADGHADVKGSDWGFGYQLAWMWDI
          190         200         210         220         230

          250         260         270         280         290         299
m989.pep  NDRARVGVNYRSKVSHTLKGD AEWAADGAAAKAMW-STMLAANGYTANEKARVKIVTPES
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a989      NDRARVGVNYRSKVSHTLKGD AEWAADAMAKQLWDANKLALLGYTPSEKARVKIVTPES

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1407

	240	250	260	270	280	290
m989.pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTIVVKGKSDRTTITPNWRNTYKV					
a989	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAELVFEKEKTIVVKGKSDRTTITPNWRNTYKV					
m989.pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
m989.pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

```

m990.seq
1  ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51  CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CCGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATTACAAT AGCGGCATCC TCGCCGTCGA
201 TAATATGCCC GTTGTCAAAA AATATATTAC AGAGAAGTAT GGGGCTGATT
251 TAAAGCAGGC GGTAAAAAGT CAATTACAGG ATTTATACAA AACAGACCG
301 GAAGCTTGGG CAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGCACA
351 GTTTGGAACA AAATTTAGTA CGCTCAAACA GACGATGCCG GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCCAC GTCGCCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TACGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAACTGAC
651 CGTCCATAAG GATTATGCGG GCGGCGCGGA TTTCTGTTT GGTACGACG
701 TGCGGGAGTC GGACGAACCC GCCCTGACCT TTGAAGACAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTTGGA ACGCCGGCCG GAAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CAAAACGGC GGATTCCGGT TCGTTTGCCT
851 TTAAACAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTTGGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTGTT GGCTGCGCTT CATCGGCGGC CGGTCCGCATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GGTGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GACTGGCAAT CGGCTGATG
1201 GGCGGCAGGG CCGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTGAT TTGTATGGTT ATGGCGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GTGCGGTATT TGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTCGAAGG CGGCTACAAC GCGCTTGTGG
1451 CGGAAGGCAT TGTCGAAAAA GGCAATAATG TGCGGTTTTA CCTACAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GGCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGCAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCA
1651 CCTTTGCGC CTTTAAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCA CTCGAAGGGC
1751 GGTTCGGTAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TATGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990.pep

1408

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFVRQN EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGTA VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

a990.seq

```

1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAATAACAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGGACT GAGGAGGCGT ATATAGACA
351 GCTTGGACCA AAATTTAGTA TACTCAAACA GAAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTC AAATCGAAAA
501 CAAATCCAC GTGCGCGGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGTTTTGGA ACGCCGGCCG GAAAACTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTGCGCT
851 TTAAACAAAA TTACCGGCAG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGGCGGAT TTTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAAATACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGGC GACGACGTGT ATGCCGCCGA TCCGTCCCGT
1051 CAAAATTTGT GGCTGCGCTT CATCGGCGGC CGGTGCGATC AAAATAATAC
1101 GGGCGGCGCG GCTGCGGACG GCGGCGCAA AGGCGTGCAA ATCGGCGGCG
1151 AGGTGTTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CCGCGTGATG
1201 GCGGCGAGG CTGGCCAGCA CGCATCAGTC AACGGCAAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGGT ATGGCGGGG TGTATTGCT GCGTGGCATC
1301 AGTTGCGCGA TAAACAAACG GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAGAGGT TGGACGGCTT CTGTCGAAGG CCGCTACAAC GCGCTGTGG
1451 CGGAAGGCGT TGTCGAAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGGAAC AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCGT TTTGCTTTGC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTTAATGT TTTGCACAGG TCAAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCGGCAT TGAAGCCGGT TGGAAAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGGACGG CGACAAAGAA GCCGCATTGT CGCTCAATG
1851 GCTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

a990.pep

```

1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITDLY GDNLDKDAVK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEDKVSQ
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFVRQN EGSRLAIGVM

```

1409

401 GGRAGQHASV NGKGGAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY
 451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP
 501 QAQFTYLGVN GGFTDSEGT VLLGSGQWQ SRAGIRAKTR FALRNGVNLQ
 551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
 601 YGKRTDGKE AALSLKWLF*

m990/a990 96.0% identity in 619 aa overlap

	10	20	30	40	50	60
m990.pep	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
a990	MFRAQLGSNTRSTKIGDDADFSFSDKPKPGTSHYFSSGKTDQNSSEYGYDEINIQGKNYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m990.pep	SGILAVDNMPVVKKYITEKYGADLKQAVKSQLQDLYKTRPEAWAENKKRTEEAYIAQFGT					
a990	SGILAVDNMPVVKKYITDTYGDNLKDAVKKQLQDLYKTRPEAWAENKKRTEEAYIEQLGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m990.pep	KFSTLKQTMPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
a990	KFSILKQKNPDLINKLVEDSVLTPHSNTSQTSLNNIFNKKLHVKIENKSHVAGQVLELTK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m990.pep	MTLKDSLWEPRRHSDIHTLETSDNARIRLNTKDEKLTVHKDYAGGADFLFGYDVRESDEP					
a990	MTLKDSLWEPRRHSDIHMLETSDNARIRLNTKDEKLTVHKAYQGGADFLFGYDVRESDKP					
	190	200	210	220	230	240
	250	260	270	280	290	300
m990.pep	ALTFEDKVSGQSGVVLERRPENLKTLDGRKLIAAKTADSGSFAFKQNYRQGLYELLKQC					
a990	ALTFEKVSGQSGVVLERRPENLKTLDGRKLIAEKADSNSFAFKQNYRQGLYELLKQC					
	250	260	270	280	290	300
	310	320	330	340	350	360
m990.pep	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
a990	EGGFCLGVQRLAIPAEAVLYAQQAANTLFLGLRAADRGDDVYAADPSRQKLWLRFIGG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m990.pep	RSHQNIRGGAAADGWRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSD					
a990	RSHQNIRGGAAADGRRKGVQIGGEVFRQNEGSRLAIGVMGGRAGQHASVNGKGAAGSY					
	370	380	390	400	410	420
	430	440	450	460	470	480
m990.pep	LYGYGGGVYA AWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
a990	LHGYGGGVYA AWHQLRDKQTGAYLDGWLQYQRFKHRINDENRAERYKTKGWTASVEGGYN					
	430	440	450	460	470	480
	490	500	510	520	530	540
m990.pep	ALVAEGIVGKGNNVRFYLQPPAQFTYLGVNNGGFTDSEGTAVGLLGSQWQSRAGIRAKTR					
a990	ALVAEGVVGKNNVRFYLQPPAQFTYLGVNNGGFTDSEGTAVGLLGSQWQSRAGIRAKTR					
	490	500	510	520	530	540
	550	560	570	580	590	600
m990.pep	FALRNGVNLQPF AAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					
a990	FALRNGVNLQPF AAFNVLHRSKSGVEMDGEKQTLAGRTALEGRFGIEAGWKGHMSARIG					

1410

	550	560	570	580	590	600
	610	620				
m990.pep	YGKRTDGDKEAALSLKWLFX					
a990	YGKRTDGDKEAALSLKWLFX					
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

g992.seq

```

1 ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51 GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGCGCGTTG GGTATACGG
101 GATATGACAG TGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GGCACGTCAG GGGACGTGGG TTTCGACGCG CCCGTTTCGCC GACGGGCATC
201 GGCAGAAATCC GGCCACAGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGATACCCT TCACGTCATC GACGGCGACG GCGCGAAACA TAAATTCGG
301 ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTTT
351 GCGCGACAAC CTGCGCGCGG CGGCGGAGGG TAGGAAAGTC AGTGTACGTG
401 TGTTTGAAAC CGACCGCTAT CAGCGCGAAG TGCGCGAGGT ATCCGCCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATT
501 TAAAGATTAT GCTAAAGAAC AGCAGGATAA GGCGGATTTT GCCGACTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGAAAGCT
601 AAAAAATCCG AAGCGCCGTG GCGGTACCGC CGGGCAGGCA GGAGCGCGG
651 GGGCAATAAG GATTGGATGG ATTCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

g992.pep

```

1 MFRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYSSEAV RTAVAVLDVL
51 GTAGDVGFDA PVRRRASAKS GHSYTGTVSK VYDGDTHLVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLMLQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

m992.seq

```

1 ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51 GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGTGCCTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GGCAGCGCAG GGGACGCGGG TTCCGACGCG CCCGCCGCCG GCCGAGCATC
201 GGCAGAAATCC GGCCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCCT TCACGTTATC GACGGCGACG GCGCGAAACA CAAATCCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
351 GCGCGACAAC CTGCGCGCGG CGGCGGAAGG CAGGAAAGTC AGCGTGCGCG
401 TGTTTCGATC CGACCGCTAC CAGCGCGAAG TGCGCGAGGT TTCTGTCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATT
501 TAAAGATTAT GCTAAAGAAC AGCAGGATAA GGCGGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGAAAGCT
601 AAAAAATCCG AAGCGCCGTG GCGGTACCGC CGAGCAGGCA GGAGCGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

m992.pep

```

1 MFRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYSSEAV RTAVAVLDVL
51 GAAGDAGSDA PARRRASAKS GHRYTGTVSK VYDGDTHLVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLMLQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQ A ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

1411

```

      10      20      30      40      50      60
m992.pep  MFRRHRHLKKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||
g992      MFRRHRHLKKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA
          10      20      30      40      50      60

      70      80      90      100     110     120
m992.pep  PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN
          |||||
g992      PVRRRASAKSGHSYTGTVSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN
          70      80      90      100     110     120

      130     140     150     160     170     180
m992.pep  LRAAAEGRKVS RVFDTDRYQREVAQVSVGKTD LNLMQVQDGA AAWHYKSYAKEQQDKADF
          |||||
g992      LRAAAEGRKVS RVFETDRYQREVAQVSAGKTD LNLMQVQDGA AAWHYKSYAKEQQDKADF
          130     140     150     160     170     180

      190     200     210     220     230
m992.pep  ADYADAQIQAE RERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DAVGEWLGIWX
          |||||
g992      ADYADAQIQAE RERKGLWKAKNPQAPWAYRRAGRS GGGNKDWM DSVGEWLGIWX
          190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

```

a992.seq
1  ATGTTTCAGAC GGCATCGGCA TTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCT TGTCGCTTTT GGGTGCCTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GCGCGGCAG GGGACGCGGG TTCCGACGCG CCCGCCGCC GCGGAGCATC
201 GCGCAAATCC GGCACCCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCTT TCACGTTATC GACGGCGACG GCGCGAAACA CAAAATCCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
351 GCGCGACAAC CTGCGCGCGG CGGCGGAAGG CAGGAAAGTC AGCGTCCGCG
401 TGTTTCGACAC CGACCCGTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCCGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGGCGG CGTGGCATT
501 TAAAAGTTAT GCTAAAGAAC AGCAGGATAA GCGCGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 KTDLNLQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQ AERERKGLWA
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA

```

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

```

a992.pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGYGSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGT VSK VYDGD TLHVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFDTDRY QREVAQVSVG
151 KTDLNLQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQ AERERKGLWA
201 KNPQAPWAYR RAGRS GGGNK DWM DAVGEWL GIW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

```

      10      20      30      40      50      60
a992.pep  MFRRHRHLKKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          |||||
m992      MFRRHRHLKKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA
          10      20      30      40      50      60

      70      80      90      100     110     120
a992.pep  PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN
          |||||
m992      PARRRASAKSGHRYTGT VSKVYDGD TLHVIDGDGAKHKIR MAYIDAPEMKQAYGTRSRDN
          70      80      90      100     110     120

      130     140     150     160     170     180

```

1412

```

a992.pep      LRAAAEGRKVSVRVFDTDYQREVAQVSVGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF
|||||
m992          LRAAAEGRKVSVRVFDTDYQREVAQVSVGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF
              130      140      150      160      170      180

              190      200      210      220      230
a992.pep      ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX
|||||
m992          ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWMDAVGEWLGIWX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTCTT CGATATCCCG ATGGTGGAAA
101 TTACCGGGCA GTATCTGCAC TATATTGCCC AAATGGAAGC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGTC TTGCCTACGA GCAAATGAAA
301 CTGGCGGCGC AGGGTTTGGG CGCGCTGCCG CGTGCGGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCGAC CGAGACGAAG CTGCCCAGAG
401 TTTACATCGC CGATTTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCTTT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGOYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTEAVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLSVRAQMT AILRRLNEHG ICRFHAFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATCCCG ATGGTGAAGA
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGTC TGGCTTACGA ACAGATGAAG
301 CTGGCGGCGC AGGGTTTGGG CGCGCTGCCG CGAGCCGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCAGAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCCAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCGTCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGOYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTEAVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDIT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRRLNHHG ICRFHDLPNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLGSFQGPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			
g993	LKVVLGSFQGPLDLLLYLIRKQNI	DVLDIPMVEITGQYLHYIAQMEAYQ	FDLAAEYLLMA			
	70	80	90	100	110	120
m993.pep	AMLEIEIKSRLLLPRTETVEDEEADP	RAELVRRLLAYEQMKLAAQGLDALP	RAGRDFAWAY			
g993	AMLEIEIKSRLLLPRTETVEDEEADP	RAELVRRLLAYEQMKLAAQGLDALP	RAGRDFAWAY			
	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQAWLG	ILSRKHKRSHEVIKETISVRAQMTA	ILRRNLNGHG			
g993	LPLEIAAETKLPEVYIADLMQAWLG	ILSRKHKRSHEVIQETLSVRAQMTA	ILRRNLNEHG			
	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAAYVVVNFIALLE	LAKEGLVRIVQEDGFGEIRISLNHEG	AHSDGISG			
g993	ICRFHALFNPQGAAAYVVVNFIALLE	LAKEGLVGIVQEDGFGEIRISLNHEG	AHSDGIFG			
	249					
m993.pep	TRGGRDVF					
g993	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

```

1   CTGAAAGTCG TATTGAGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTCT CGATATCCG ATGGTGAAGA
101 TTACCGAACA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTGTGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAAC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCCTGC TGGCTTACGA GCAGATGAAG
301 CTGGCGGCAC AAGGGTTGGA TGCCTTCCT CGTGGCGGCC GGGATTTCGC
351 ATGGGCATAC CTGCCACTGG AAATTGCCGT CGAAGCCAAG CTGCCCCAAG
401 TCTATATTAC CGACTTGACG CAGGCGTGGC TGAGTATTTT GTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTTATCAA GAAACCATCT CCGTGCGCGC
501 GCAAATGACG GCAATCCTGC GCCGTTTGAA CAAACACGGG ATATGCAGGT
551 TTCACGACCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GGTCTGTAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGTTGGTTCG GAATCGTACA
651 GGAAGTCGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGGGGCG GCGCGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3006; ORF 993.a>:

a993.pep

```

1   LKVVLSFQGPLDLLLYLIRKQNI DVLDIPMVKITEQYLHYIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LPRTETVED EADPRAELV RRLLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLSILSRA
151 KHRSHEVIK ETISVRAQMT AILRRLNKHG ICRFHDLPNP EQGAAYVVVN
201 FIALLELAKE GLVGIVQEVG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSSFQGPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			
m993	LKVVLGSFQGPLDLLLYLIRKQNI	DVLDIPMVKITEQYLHYIAQIETYQ	FDLAAEYLLMA			

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GGCGCGTTGC  TTCTTACCGC
51  CTGCGGCAGA  AAATCCGCCC  GAACCCACGC  CAAAATTCCC  GAAGGAAGCA
101 CCGTGCTTGC  CTTGGGCGAT  TCGCTCACCT  TCGGCTACGG  AGCAAACCCC
151 GGCGAATCCT  ACCCCGCGCA  ACTGCAAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACGTCCGC  GCAAGCCCTA  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAAA  CCAAGCTTG  TGATTGTCGG  CATAGGCGGC
301 AACGACTTTC  TCGCGCAAAGT  TCCCGAGGAG  CAGACCCGCG  CCAATATCGC
351 GAAAATCATC  GAAACCGTGC  AAAAGGAAAA  CATTCCCGCC  GTCCTCGTCG
401 GCGTGCCGCA  CATCACACTG  GGCGCGTTGT  TCGGGCATT  GAGCGACCAT
451 CCGCTGTATG  AGGATTTGTC  CGAGGAATAC  GGCATTCCGT  TGTTCGGCGG
501 CGCGTGGGCG  GAAATTTTGG  GCAATAATAA  TCTGAAATCC  GACCAATCC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTCG  CCGAAAATTT  GAATCAATTT
601 TTGAGAAAAC  ATGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPAQLQK  LTGWNIVNGG  VSGD TSAQAL  SRLPALLARK  PKLVIVIGIG
101 NDFLRKVPPE  QTRANIAKII  ETVQKENIPA  VLVGVPHITL  GALFGHLSDH
151 PLYEDLSEY  GIPLFGGAWA  EILGNLNLKS  DQIHANGKGY  RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA  GAACCTTCCT  CCTCGGCGCA  GGCGCGTTGC  TGCTTACCGC
51  CTGCGGCAGA  AAATCCGCCC  GAACCCACGC  CAAAATTCCC  GAAGGAAGCA
101 CCGTACTTGC  CTTGGGCGAT  TCGCTTACCT  TCGGCTACGG  CGCAAACCCCT
151 GGCGAATCCT  ACCCCGCGCA  ACTGCAAAAA  CTGACGGGTT  GGAATATTGT
201 CAACGGCGGC  GTATCGGGCG  ATACATCTGC  CCAAGCCCTG  TCGCGCCTGC
251 CCGCGCTGTT  GGCACGCAAA  CCAAGCTTG  TGATTGTCGG  CATAGGCGGC
301 AACGACTTTC  TCGCGCAAAGT  TCCCAAGGAG  CAGACCCGCG  CCAATATCGC
351 GAAAATCATC  GAAACCGTGC  AGAAGGAAAA  CATCCCGGCC  GTCCTCGTCG
401 GCGTGCCGCA  CATCACACTG  GGTGCGTTGT  TCGGGCATT  GAGCGATCAT
451 CCGCTGTATG  AGGATTTGTC  CGAGGAATAC  GGCATTCCGT  TGTTCGGCGG
501 CGCGTGGGCG  GAAATTTTGG  GCGATAATAA  TCTGAAATCC  GACCAATCC
551 ACGCCAACGG  CAAAGGCTAT  CGGAAATTTG  CCGAAGATTT  GAATCAATTT
601 TTGAGAAAAC  AGGGGTTTAG  ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLLGA  GALLLTACGR  KSARTHAKIP  EGSTVLALGD  SLTFGYGANP
51  GESYPAQLQK  LTGWNIVNGG  VSGD TSAQAL  SRLPALLARK  PKLVIVIGIG

```

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101 NDFLRKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
 151 PLYEDLSEY GIPLFGGAWA EILGDNNLKS DQIHANGKGY RKFAEDLNQF
 201 LRKQGFR

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

	10	20	30	40	50	60
m996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQLOK					
g996	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQLOK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m996.pep	LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
g996	LTGWNIVNGGVSGDTSQAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII					
	70	80	90	100	110	120
	130	140	150	160	170	180
m996.pep	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS					
g996	ETVQKENIPAVLVGVPHITLALFGHLSHDHPLYEDLSEYGIPLFGGAWAEILGNNLKS					
	130	140	150	160	170	180
	190	200				
m996.pep	DQIHANGKGYRKFAEDLNQFLRKQGFR					
g996	DQIHANGKGYRKFAENLNQFLRKHGFRX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGCGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CGGTACTTGC	CTTGCGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCACGCAAA	CCCAAGCTTG	TGATTGTCGG	CATAGGCGGC
301	AACGACTTTC	TGCGCAAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAAATCATC	GAACCGTGC	AGAAGGAAA	CATCCCGGCC	GTCCTCGTCG
401	GCGTGCGGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATTT	GAGCGATCAT
451	CCGCTGTATG	AGGATTGTG	CGAGGAATAC	GGCATTCCGC	TGTTCCGGCG
501	CGCGTGGGCG	GAAATTTTGG	GCGATAATAA	TCTGAAATCC	GACCAATATC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAAGATT	GAATCAATTT
601	TTGAGAAAAC	AGGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPAQLQK	LTGWNIVNGG	VSGDTSQAAL	SRLPALLARK	PKLVIVGIGG
101	NDFLRKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHITL	GALFGHLSDH
151	PLYEDLSEY	GIPLFGGAWA	EILGDNNLKS	DQIHANGKGY	RKFAEDLNQF
201	LRKQGFR*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

	10	20	30	40	50	60
a996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQLOK					

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```

|||||
m996      MNRRTFLLGAGALLLTACGRKSARTHAKEIPEGSTVLALGDSLTFYGANPGESYPAQLQK
              10      20      30      40      50      60

              70      80      90      100     110     120
a996.pep   LTGWNIVNGGVSGDTSQAQALSRLPALARKPKLVIVIGGNDFLRKVPKEQTRANIAKII
|||||
m996      LTGWNIVNGGVSGDTSQAQALSRLPALARKPKLVIVIGGNDFLRKVPKEQTRANIAKII
              70      80      90      100     110     120

              130     140     150     160     170     180
a996.pep   ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
|||||
m996      ETVQKENIPAVLVGVPHITLGALFGHLSDHPLYEDLSEYGIPLFGGAWAEILGDNNLKS
              130     140     150     160     170     180

              190     200
a996.pep   DQIHANGKGYRKFAEDLNQFLRKQGFRX
|||||
m996      DQIHANGKGYRKFAEDLNQFLRKQGFR
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TEGGCGCAGG
51 CTGGGCGGCG TTGTCCGCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCTGTGTTGA AGCCGGCCGG CAGGCGGGCG GAAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGCGGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCCAGACC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCGCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGG CAGCCCTTGG TCTGGGCGCG GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG CGACGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCCCTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAGC GCGCGTATGC CGTCTGAACA CCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CTTTCGCTAC CACGCCATCA CCACCGCTA TCTGCGCTAC
901 GCCGAACCCG TCCGcCTGcc CGCCCCGCTG AccGGCAttg CCGAcggcAC
951 ggcaCaatgG CTGCTTTgcc cgGGGcAGGC tccggactgc CcccaaAacg
1001 aagTCTCCGC cGTCAttagc GTTTCGAcG GCGtcggcgG Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRMLMTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGAGG CTGTCCGCCG CCGTCACCTT GGCGCGGCAC GCCGACGTTA
101 CCTGTGTTGA AGCCGGCCGG CAGGCGGGCG GCAGGGCGCG CACACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ACATTTTGCT
201 CGCGGCATAC CGGGGCGTGT TGCGCCTGAT GAAAACCATC GGTTCCGATC
251 CCCGTGCCGC CTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CCGCCCGCG CCGCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGTG CACCGACTGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCGCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTGAT
501 GCAGTTTGGG CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAA

```

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```

551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCCCTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCGTATGC CGTCTGAACA CCCTCCCGGA CGGGAAAGTG
751 CTCGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCTGCG CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGCGC CGCCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGGT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCCGCG GACTTGTGCT GGTGACCG GCACCGCATC
1201 TTCCCCCGCG GCGACTACCT CCACCCGGAC TACCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

```

m997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GNTDGFGLD NGQHILGAY RGVRLRMKTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSDGVL
201 KKSGSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQWV LLCRGRGLP ENEVSAVISV SDRVGAFANR
351 AWADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPD DLSWLHRHRI
401 FPAGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

```

g997.pep      10      20      30      40      50      60
MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGLD
|||||
m997          10      20      30      40      50      60
MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLFEAGRQAGGRARTLAGNTDGFGLD

g997.pep      70      80      90      100     110     120
NGQHILGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL
|||||
m997          70      80      90      100     110     120
NGQHILGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGGLQFRALPLPAPLHILGGVLL

g997.pep     130     140     150     160     170     180
ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
|||||
m997         130     140     150     160     170     180
ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT

g997.pep     190     200     210     220     230     240
PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC
|||||
m997         190     200     210     220     230     240
PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC

g997.pep     250     260     270     280     290     300
RLNTLPDGKVLVNGEAFDAAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
|||||
m997         250     260     270     280     290     300
RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY

g997.pep     310     320     330     340     350
AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFANR
|||||
m997         310     320     330     340     350
AEPVRLPAPLTGLADGTQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHAD

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1   ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTC A TCGGCGCAGG
51  CTGGGCGCGG TTGTCCGCGG CCGTTACCTT GGCGCGGCAC GCCGACGTTA
101 CCCTGTTTGA AGCCGGCGCG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGAAATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGTGT TGC GCCTGAT GAAAACCATC GGTTCAGACC
251 CCCATGCCGC CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGTGCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTGCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCAGTTTGGC CAGCCCTTGG TTTGGGCGCG GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCGGAA CCCGCCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCCTCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAGTG
751 CTCGTCACCG GCGAACCTTT CGATGCCGCC GTCCCCGCCA CCGCGCCCTA
801 CCACGCGGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAT CACGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCCGAACCCG TCCGCTTGCC TGCCCCGCTG ACCGGACTTG CCGACGGCAC
951 GGTGCAATGG CTGCTTTGCC GGGGCGAGGT CGGACTGCCT GAAAACGAAG
1001 TGTCCGCGGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCGTGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GGGCGAACCC GAAGCCGTGC GCGTCATCAC CGAAAAACGC GCCACAACCG
1151 CAGCCGATGC CCCGCCGCGG GATTTGTCGT GGTTCACCG GCACCGCATC
1201 TTCCCCGCGG GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1251 CGCCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1   MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVRLMKT I GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPSAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVNQFW QPLVWGALNT PLETASLRVL CNVLSGVLT
201 KKS GSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEPFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTQVQW LLCRGRGLP ENEVSAVISV SDRVGAFA NR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRHRI
401          FPGADYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

a997/m997 98.2% identity in 437 aa overlap

	10	20	30	40	50	60
a997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
a997.pep	NGQHILLGAYRGVRLMKTIGSDPHAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILLGAYRGVRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
a997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
a997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
	190	200	210	220	230	240
a997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPALELQRLGADIRLETRIC					

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```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

a997.pep   250      260      270      280      290      300
           RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRyhAITTVYLRY
           |||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRyhAITTVYLRY
           250      260      270      280      290      300

a997.pep   310      320      330      340      350      360
           AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
           |||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

a997.pep   370      380      390      400      410      420
           KRILPHLGEPEAVRVITEKRATTAADAPPPDLswLHRHRIFPAGDYLHPDYPATLEAAVQ
           |||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLswLHRHRIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

a997.pep   430
           SGFASAEACLQSLSDAVX
           |||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA  AAAAAATTGAT  TTCCGCAATT  TGTGTTTCAA  TTGTTTTATC
51  AGCCTGCAAC  CAACAATCAA  AAACGGCACA  AGCCGAAGAA  CCTGTCCAAA
101  GTATCCAGGC  TGCTGATTGT  ACCGCCCCAA  TGGACATCAC  AGTTGAACAA
151  TATCTCATCA  ATTTGGAGCA  AGCATTAAAA  ACTCAGAACG  TCTCAACAAA
201  AATCCATAAT  AAAAAATTG  TCAAGACCGA  TTGTGGTTAT  GACCTTACTT
251  TGGTAATGGA  TTTTGGGGCG  ATTGCGCTCA  AACTGGACGA  GCAGCAAAAA
301  ATTAGAGCTA  TCTCAGTAGG  CTACATTTTA  AAAACCGACG  GAGAGAAAGG
351  ACAAATCTA  GTCAATAATG  CCATAAATGG  ATTACACAGT  ATTCAGGCAG
401  TTCTGTCTTT  AACTACCACA  GACAAATTGG  GCGAATCGGA  AGCAGGAAAA
451  CAACTTTTAA  CAGCTTTAAC  CGAAGTCGTC  AAAGAATCCA  ATCAGACAGG
501  AGCAACAGCG  CAAAAGACG  TTCCGGCAGA  TGGTATTTTA  TATAGCGTTG
551  TTTTGA AAA  AGAAACAAAC  ACCATTGCAA  TAATCGGCAG  AAAACAACCC
601  TAA

```

This corresponds to the amino acid sequence <SEQ ID 3020; ORF 999>:

```

m999.pep
1  MNMKKLISAI  CVSIVLSACN  QSKTAQAE  PVQSIQAADC  TAPMDITVEQ
51  YLINLEQAFK  TQNVSTKIHN  KNIVKTD  DCGY  DLTLMDFGA  IALKLDEQQK
101  IRAISVG IIL  KTDGEKGQNL  VNNAINGLHS  IQAVLSLTTT  DKLGESEAGK
151  QLFTALTEVV  KESNQTGATA  QKDV PADGIL  YSVVFEKETN  TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

FIG. 1A

919 (46 kDa)

PURIFICATION

M1 919

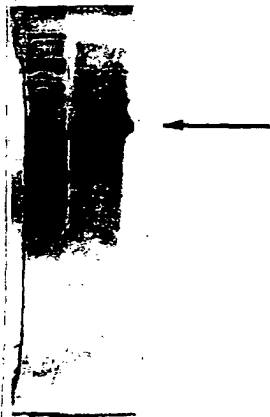


FIG. 1B

919 (46 kDa)

WESTERN BLOT

OMV TP PP

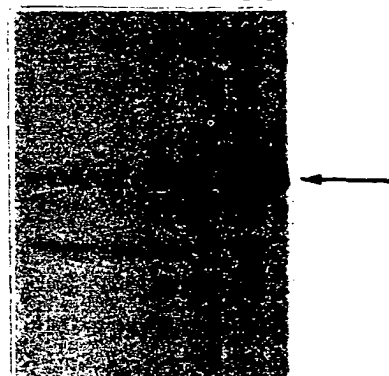


FIG. 1C

919 (46 kDa)

FACS

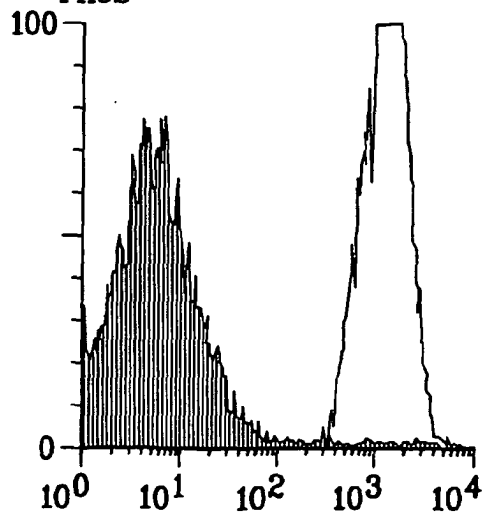


FIG. 1D

919 (46 kDa)

BACTERICIDAL ASSAY

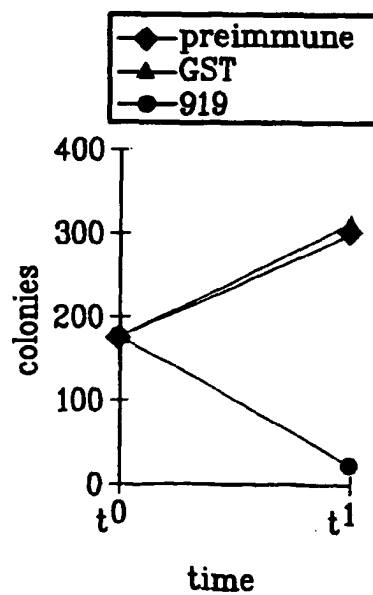


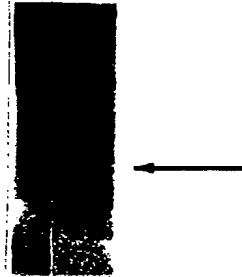
FIG. 1E

919 (46 kDa)

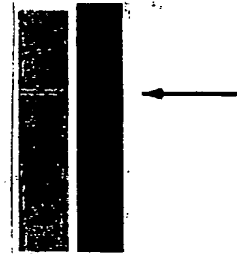
ELISA assay: positive

FIG. 2A

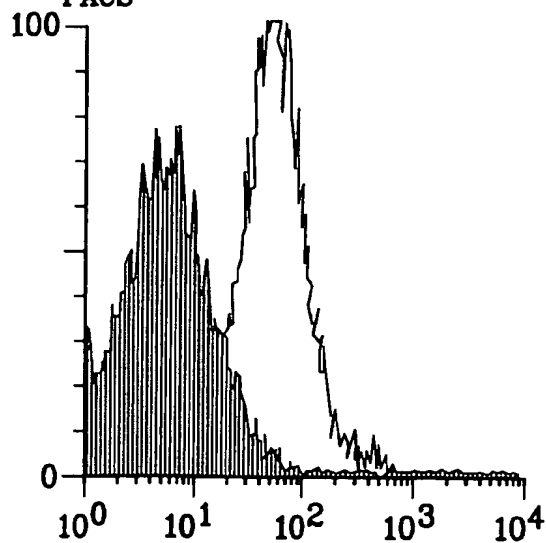
279 (10.5 kDa)
PURIFICATION
M1 279

*FIG. 2B*

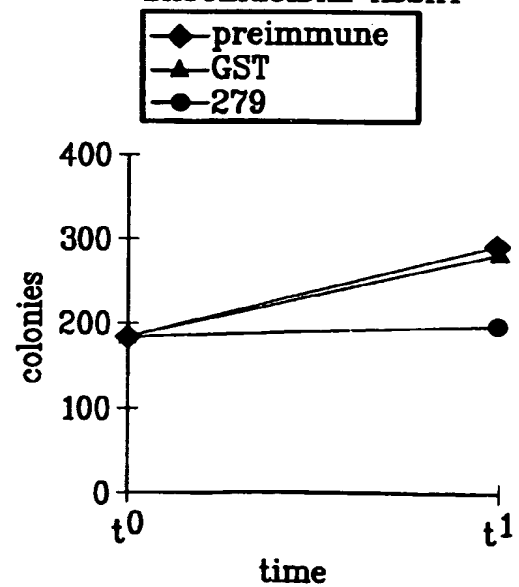
279 (10.5 kDa)
WESTERN BLOT
TP OMV

*FIG. 2C*

279 (10.5 kDa)
FACS

*FIG. 2D*

279 (10.5 kDa)
BACTERICIDAL ASSAY

*FIG. 2E*

279 (10.5 kDa)
ELISA assay: positive

FIG. 3A

576 (27.8 kDa)

PURIFICATION

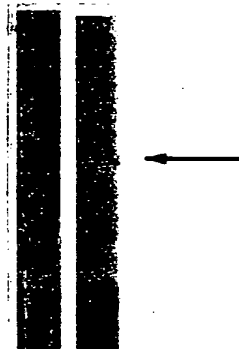
M1 576

*FIG. 3B*

576 (27.8 kDa)

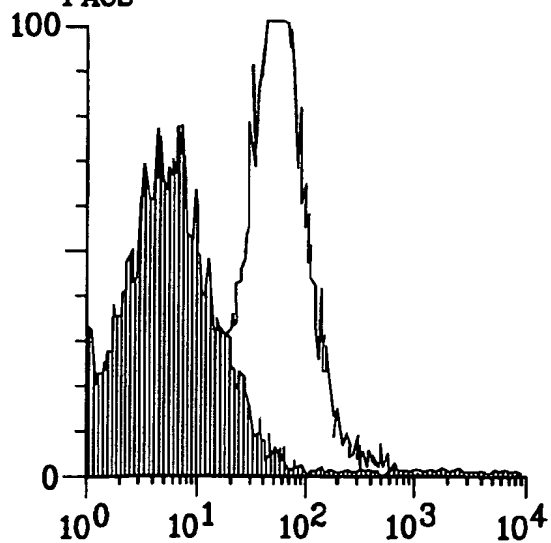
WESTERN BLOT

TP OMV

*FIG. 3C*

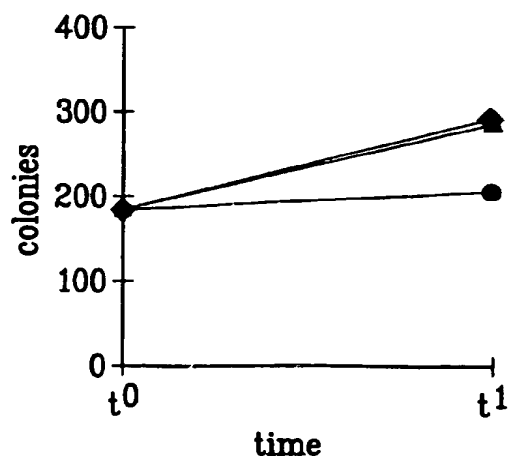
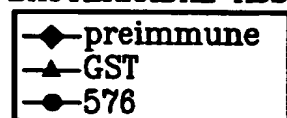
576 (27.8 kDa)

FACS

*FIG. 3D*

576 (27.8 kDa)

BACTERICIDAL ASSAY

*FIG. 3E*

576 (27.8 kDa)

ELISA assay: positive

FIG. 4A

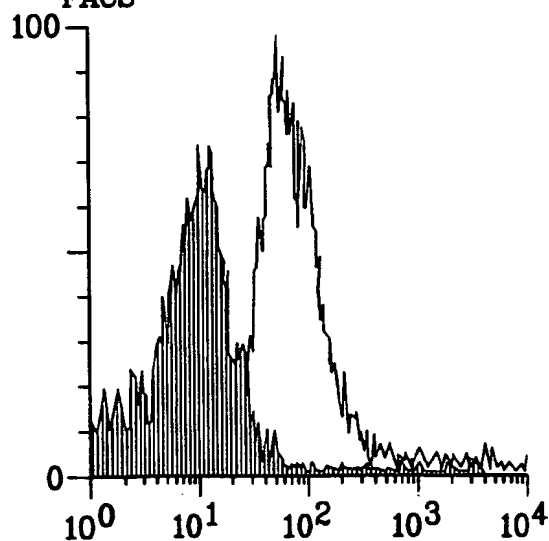
519 (33 kDa)
PURIFICATION
M1 519

*FIG. 4B*

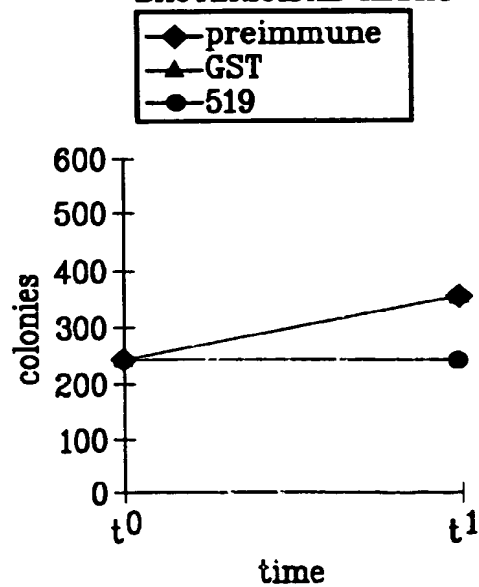
519 (33 kDa)
WESTERN BLOT
TP OMV

*FIG. 4C*

519 (33 kDa)
FACS

*FIG. 4D*

519 (33 kDa)
BACTERICIDAL ASSAY

*FIG. 4E*

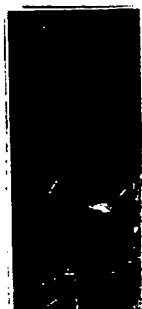
519 (33 kDa)
ELISA assay: positive

FIG. 5A

121 (40 kDa)

PURIFICATION

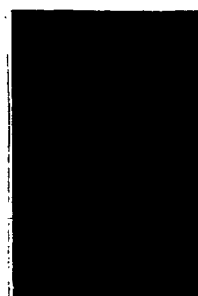
M1 121

*FIG. 5B*

121 (40 kDa)

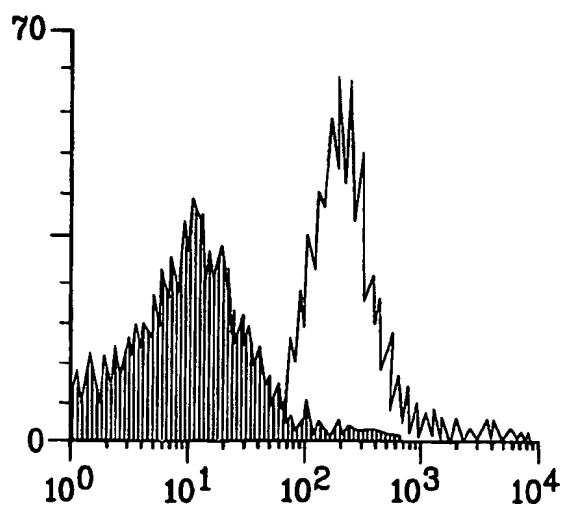
WESTERN BLOT

TP OMV

*FIG. 5C*

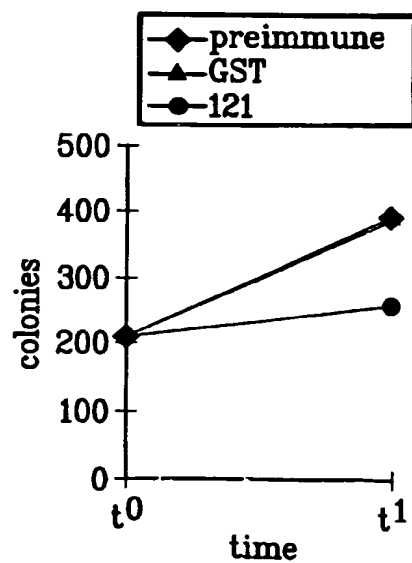
121 (40 kDa)

FACS

*FIG. 5D*

121 (40 kDa)

BACTERICIDAL ASSAY

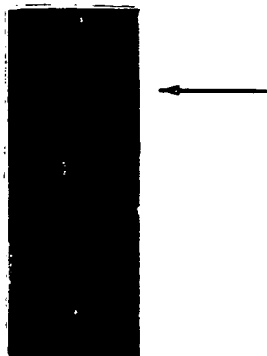
*FIG. 5E*

121 (40 kDa)

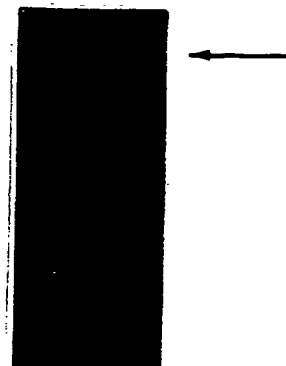
ELISA assay: positive

FIG. 6A

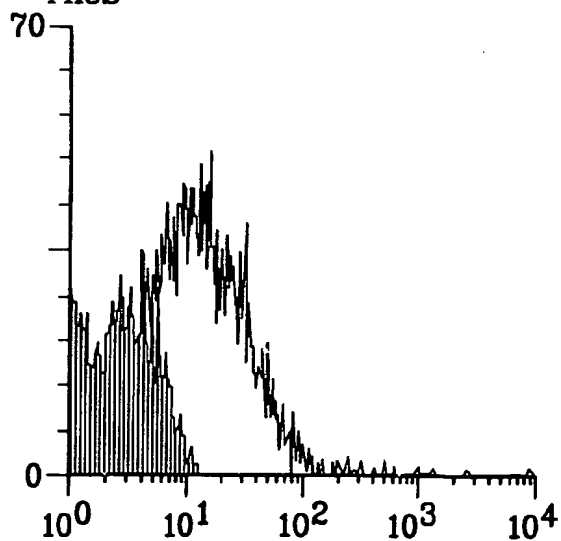
128 (101 kDa)
PURIFICATION
M1 128

*FIG. 6B*

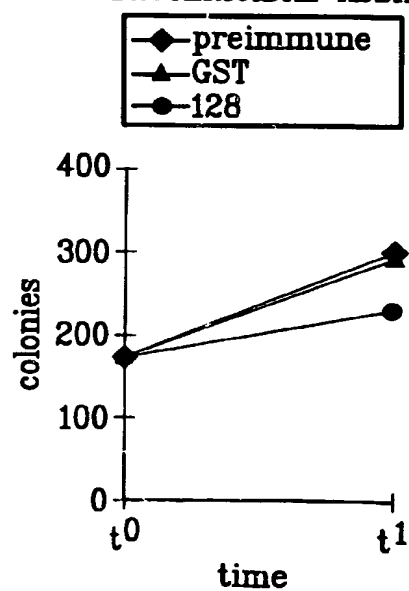
128 (101 kDa)
WESTERN BLOT
TP OMV

*FIG. 6C*

128 (101 kDa)
FACS

*FIG. 6D*

128 (101 kDa)
BACTERICIDAL ASSAY

*FIG. 6E*

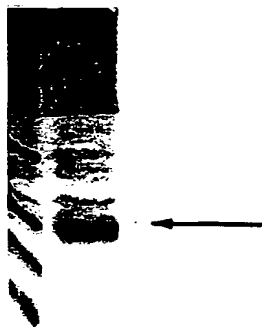
128 (101 kDa)
ELISA assay: positive

FIG. 7A

206 (17 kDa)

PURIFICATION

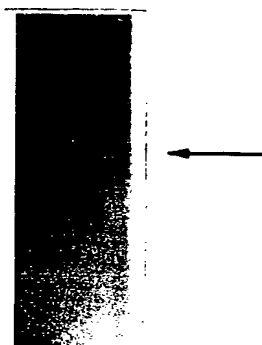
M1 206

*FIG. 7B*

206 (17 kDa)

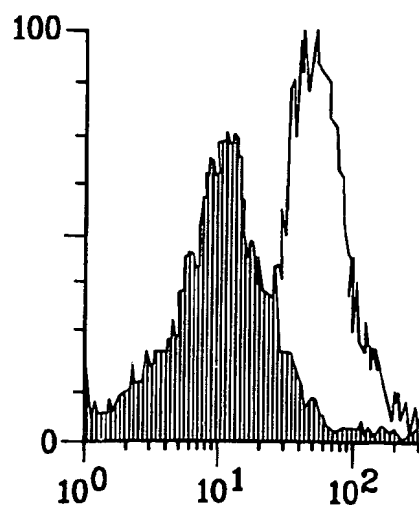
WESTERN BLOT

TP OMV

*FIG. 7C*

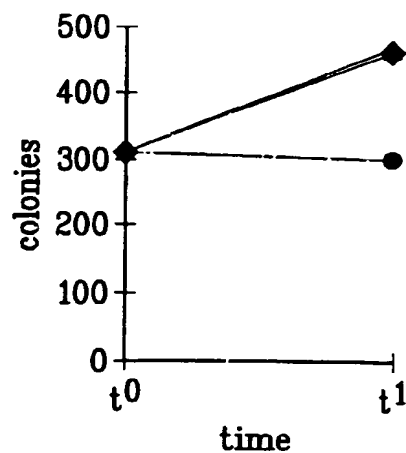
206 (17 kDa)

FACS

*FIG. 7D*

206 (17 kDa)

BACTERICIDAL ASSAY

*FIG. 7E*

206 (17 kDa)

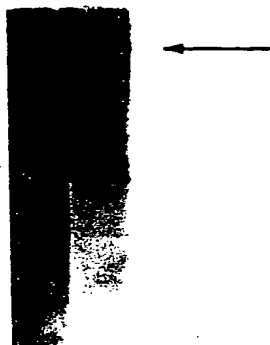
ELISA assay: positive

FIG. 8A

287 (78 kDa)

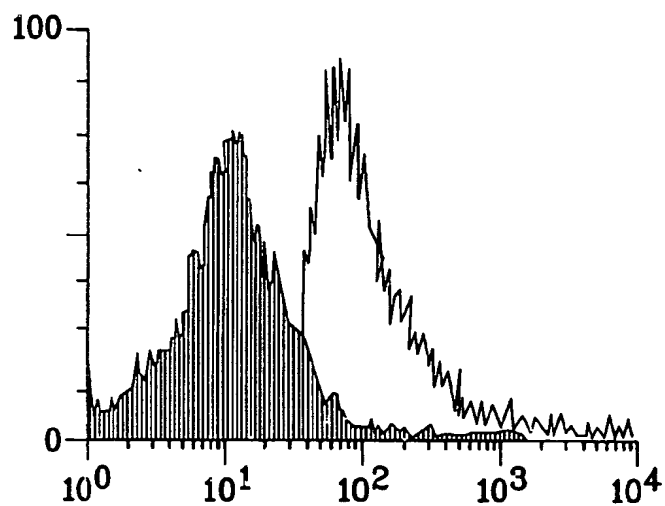
PURIFICATION

M1 287

*FIG. 8B*

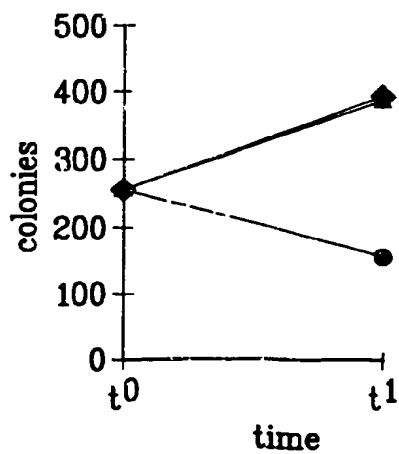
287 (78 kDa)

FACS

*FIG. 8C*

287 (78 kDa)

BACTERICIDAL ASSAY

*FIG. 8D*

287 (78 kDa)

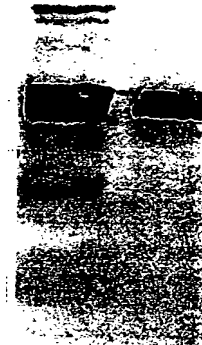
ELISA assay: positive

FIG. 9A

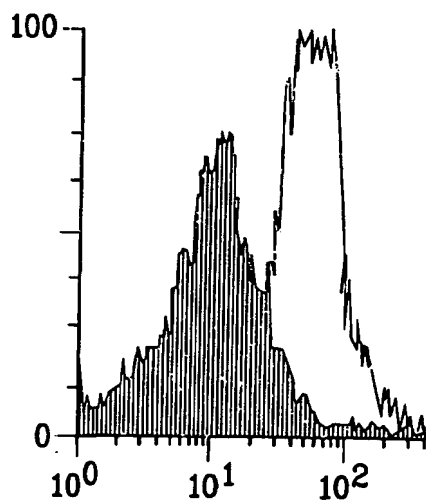
406 (33 kDa)
PURIFICATION
M1 406

*FIG. 9B*

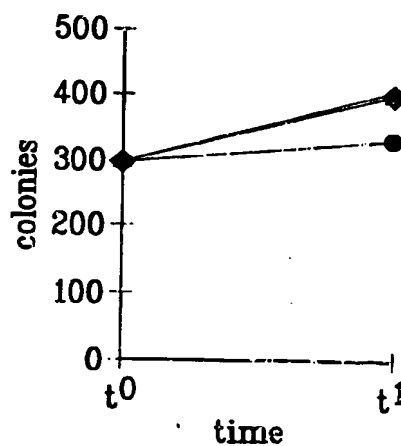
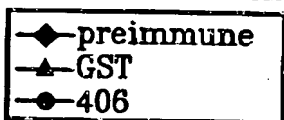
406 (33 kDa)
WESTERN BLOT
TP OMV

*FIG. 9C*

406 (33 kDa)
FACS

*FIG. 9D*

406 (33 kDa)
BACTERICIDAL ASSAY

*FIG. 9E*

406 (33 kDa)
ELISA assay: positive

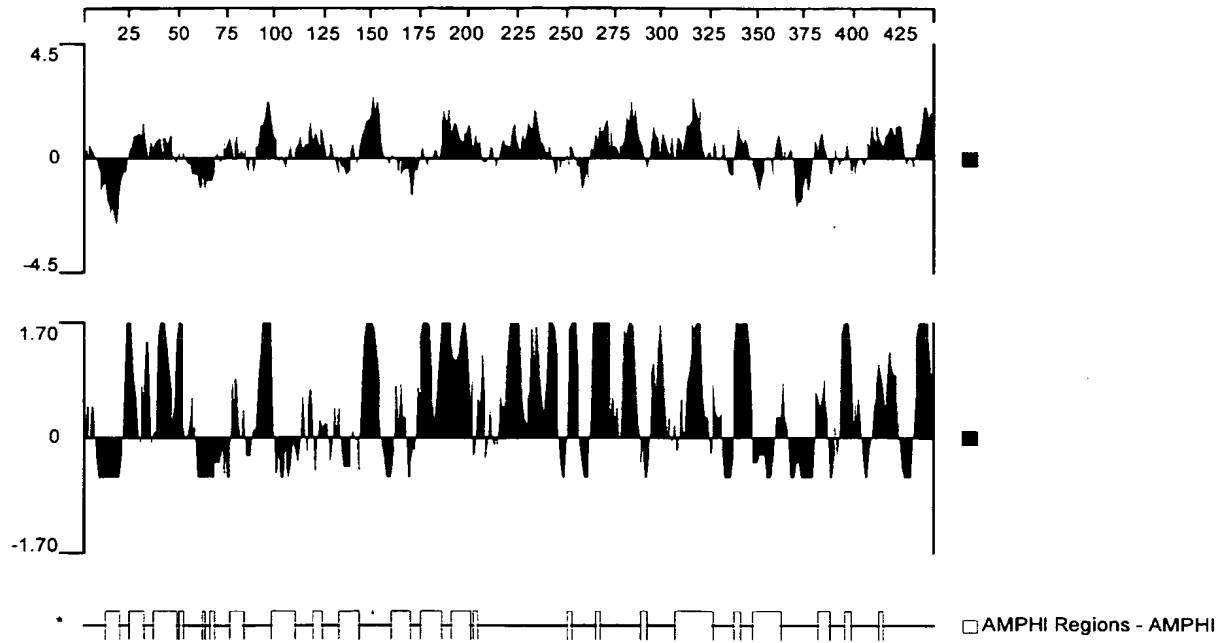
919Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10